

```
OY 398 GCAGCCGGGCTCCG-----GGAGAGAAAGCGAGCGCGGAGCGG 439
      |||||
Db 62 LeuProGlyLeuAlaGlyAspHisGlyIuLeuGlyIuLysGlyAspAlaGlyIlePro 81
      |||||
OY 440 GGACTGCGG-----GGACTCGAGAGGAGCCCGGCGCGAGAGAGCGGAGACC 490
      |||||
Db 82 GlyIleProGlyLysValGlyProLysGlyProValGlyProLysGlyAlaProGlyPro 101
      |||||
OY 491 GCGGGGCGCCCGGCGCT-----GCCGGGAGTCTCGGTCTCCGCGATCCGCC 541
      |||||
Db 102 ProGlyProArgGlyProLysGlyLysSerGlyLysPyrLysAlaThrGlnLysValAla 121
      |||||
OY 542 TTCAGCGCGAGCGCTCCGAGAGCGGCGGCTCCCGCTCGAGCGACACCTCGGCTTC 601
      |||||
Db 122 PheSerAlaLeuAlaGlyThrValAsnSerAlaLeuArgProAsnGlnAla---IleArgPhe 140
      |||||
OY 602 GACCGCGTGTGTGACGAGCAGGACGACATTACGAGCGCGTACCGGCGCAAGTTCACCTGC 661
      |||||
Db 141 GluLysValIleThrAsnValAsnAspAsnTyrGluProArgSerGlyLysPheThrCys 160
      |||||
OY 662 CAGGTGCTGGGGTCTACTTCCGCTCCATGCGCACCGTCTACCGGCGCACGCTGCAG 721
      |||||
Db 161 LysValProGlyLeuTyrPheThrTyrHisAlaSer---SerArgGlyAsnLeuCys 179
      |||||
OY 722 TTGATCTGTGAGAGATGCG-----GAATCATTCCTCTTC----- 760
      |||||
Db 180 ValAsnIleValArgGlyArgAspArgAspArgMetGlnLysValIleThrPheCysAsp 199
      |||||
OY 761 -----TTCACGTTTTCGGGGGCTGCGCCCAAGCCAGCCTCGCTCTCGGGG 805
      |||||
Db 200 TyrAlaGlnAsnThrPheGlnVal-----ThrThrGly 210
      |||||
OY 806 GGGGCCATGTGTGAGCTGTGAGACCTGAGACCAAGTGTGGTGCAC---GTGGGTGTGGT 862
      |||||
Db 211 GlnValValIleLysLeuGlnGlnGlnValIleHisLeuGlnAlaThrAspLysAsn 230
      |||||
OY 863 GACTACATTGTCATCTATGCGACATCAAGACAGACAGACCTTCTCCGATTCTGTGTG 922
      |||||
Db 231 SerLeuLeuGlyValGlnGlyAla-----AsnSerIlePheThrGlyPheLeuLeu 247
      |||||
OY 923 TACTCCGAC 931
      |||||
Db 248 PheProAsp 250
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Search completed: June 21, 2003, 16:07:42
Job time : 63.5 secs

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Db 409 PheProGlyProIySgLyGlnGlyIleVal---GlyProGlnGlyProProGlyPro 427
Qy 217 TGCCAGCGCATGATGAGGCGCATCCCGCTGCTGCTGCTGCGGCGGCGGCGGCGG 276
Db 428 LysGlyGlyProGlyLeuGlnGlyPheProGlyIySgProGlyPheLeuGlyGlnValGly 447
Qy 277 CCCACTGAGCAGACAAAGATCCCGACCT----- 306
Db 448 ProProGlyMetArgGlyPheProGlyProIleGlyProIySgLyGlnGlySgLyS 467
Qy 307 -----CTGCGCGGCGGCGGCGGCGGCTT-----CGAGCGAC 336
Db 468 GlyValProGlyLeuProGlyVal---ProGlyLeuGlyProIySgLyGlnProGlyI 487
Qy 337 GCGGCGGCGCATGAGCGAGCGAG-----GGCTGCGCGGCGGCGGCGGCGGCGG 387
Db 487 eProGlyAspGlnGlyLeuGlnGlyProProGlyIleProGlyIleGlyIyProSerg 507
Qy 388 CCGGAGCGGCGGCGGCGGCGGCGGAGAAAGCGGAGCGGCGGCGGCGGAGCTGCC 447
Db 507 yProIleGlyProProGlyIleProGlyProIySgLyGlnProGlyLeuProGlyPro 527
Qy 448 G----- 448
Db 527 oGlyPheProGlyIleGlyIySgProGlyValAlaGlyLeuHisGlyProProGlyIyS 547
Qy 449 -----GGACTTCGAGGAGGAGCGGCGGCGGCGGAGAGCGGAGCGGCGGCGG 498
Db 547 oGlyAlaLeuGlyIleProGlnGlyGlnProGlyLeuProGlyProProGlyPro 567
Qy 499 CACCGGGGCTT----- 508
Db 567 oProGlyProAlaValMetProProthProProProGlnGlyIyGlyIyLeuProAs 587
Qy 509 -----GCCGGGAGAGCTCGGCGGCGGCGGCGGCGGCTTCGAGCGGCGGCGG 561
Db 587 pMetGlyLeuGlyIleAspGlyValIySgProGlnHisAlaThrGlyAlaIySgLy 607
Qy 562 GACCGGGGCTT-----CC 576
Db 607 sAsnGlyIyProAlaIyGlnMetProAlaPheThrAlaGlyLeuThrAlaProPhePr 627
Qy 577 GCGGCTGAGCAGCAGCTTCGCTTCAGCGGCGGCTGCTGAGCAGCAGGAGCATTCGA 636
Db 627 oProValGlyIyProValIySgPheAsnIySgLeuLeuTyAsnGlyIyGlnAsnTyAs 647
Qy 637 CCGCGTCACCGGAGTACCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
Db 647 nProGlnThrGlyIlePheThrIySgIyValProGlyValIyTyIyPheAlaTyHisVa 667
Qy 697 CACCGTCCTACCGGCGGCGGCGGCGGAGTTCGATGCTGAGTGAAGATGCGCATTCG 754
Db 667 HisCysIySgIyGlyAsnValIyPheValAlaLeuPheIySgAsnValIyProValMetTy 687
Qy 755 -TCTTCTTCACATTTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
Db 687 rTrpTyAspGlnIyTyIySgIyPheLeuAspGlnAla-----SergIySeraIyVa 705
Qy 814 GGTGAGGCTGAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 873
Db 705 IleuLeuLeuArgProGlyAspArgValIlePheLeuGlnMetProSergIyGlnAlaIaG 725
Qy 874 CATCTATGCGAGCATCAAGACAGACAGCATTCCTCGGATTCCTGCTGCTGCTAC 925
Db 725 yLeuTyAlaGlnIyGlnTyValHisSerSerPheSerGlyTyIyLeuLeuTy 742

```

RESULT 12

S23779
collagen alpha 1(VIII) chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S23779
R:Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Nishimura, Y.

Eur. J. Biochem. 207, 895-902, 1992
A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polype
A:Reference number: S23779; MUID:92362626; PMID:1499564
A:Accession: S23779
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <MOR>
A:Cross-references: EMBL:X66976; NID:950493; PIDN:CAA47387.1; PID:q1359953
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
F:616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>

Alignment Scores:

Pred. No.:	5,02e-18	Length:	743
Score:	408.50	Matches:	119
Percent Similarity:	42.51%	Conservative:	40
Best Local Similarity:	31.82%	Mismatches:	123
Query Match:	16.08%	Indels:	92
		Gaps:	12

US-09-944-944-41 (1-1377) x S23779 (1-743)

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Qy 70 GGCAGGCGCAGGCGGCGGCGGCGGAGAAAGCGGCGGCGCTGAGCAGCA----- 123
Db 372 GlyProArgGlyGlnGlySgIyProIleGlyAlaProGlyMetGlyIyProProGlyGln 391
Qy 124 ACTGAGGCTCCGAGTACGAGC-----GCCCGAAGAGGCGCATCGGAGAGCGGGA 177
Db 392 ProGlyLeuProGlyIleProGlyProMetGlyProProGlyAlaIleGlyPheProGly 411
Qy 178 -----GGGGGAGCTGCGAGAGACCCCGGCGCTCCGGGCTCCCGTCCAGCGC 225
Db 412 ProIySgLyGlnGlyIyValAla---GlyProGlnGlyProProGlyProIySgLyGln 430
Qy 226 TATGAGGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
Db 431 ProGlyLeuGlnGlyPheProGlyIySgProGlyPheLeuGlyIyValGlyProProGly 450
Qy 286 CGACAAACAGATCCCGACCT-----CTGCC 312
Db 451 MetArgIyLeuProProGlyProIleGlyProIySgLyGlnGlyHisIySgLyLeuPro 470
Qy 313 GGGGCGCGGCGGCTTCAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372
Db 471 GlyLeu---ProGlyValProGlyLeuGlnGlyProIySgLyGlnProGlyIleProGlyAs 490
Qy 373 CGATGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 432
Db 490 pGlnGlyLeuGlnGlyProProGlyIleProGlyIleValGlyProSergIyProIleG 510
Qy 433 GAGGCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
Db 510 yProProGlyIleProGlyProIySgLyGlnProGlyLeuProGlyProProGlyPhePr 530
Qy 466 ----- 466
Db 530 oGlyValGlyIySgProGlyValAlaGlyLeuHisGlyProProGlyIySgProGlyAla 550
Qy 467 -GGGCGCGAGGAGAG-----GGGAGACCGGCGGCGGCGGCGGCGGCGGCGG 516
Db 550 uGlyProGlnGlyGlnProGlyLeuProGlyProProGlyProProGlyProProGlyPr 570
Qy 517 GTGCTGCTGCTCCGCGA----- 535
Db 570 oProAlaValMetProthProSerProGlnGlyIyTyIyLeuProAspMetGlyLeuG 590
Qy 536 -----TCGCGCTTCACGCCAGCGC----- 556
Db 590 yIleAspGlyValIySgThrProHisAlaTyAlaGlyIySgLyGlnHisIySgLyPr 610
Qy 557 -----TCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 588
Db 610 oAlaTyIyGlnMetProAlaPheThrAlaGlnGlyValIyProPheProProValGlyAl 630

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[illegible]

Alignment Scores:			
Pred. No.:	1,39e-18	Length:	635
Score:	417.50	Matches:	134
Percent Similarity:	41.99%	Conservative:	26
Best Local Similarity:	35.17%	Mismatches:	120
Query Match:	16.44%	Indels:	102
DB:	2	Gaps:	15
US-09-944-944-41 (1-1377) x A57131 (1-635)			
QY	28	GSAAAGCGGAGCCGCGACGGAGACCAACGACGCTGGGTGAC-----	69
Db	272	GLYAsprgrglYgluPrroglYgluAspsrJLYAsPrroglYgluGlnGlyProGlnGlyLeu	291
QY	70	-----GCCAGGCGAGGGGGGCC--TGGCGGGGAGA-----	99
Db	292	GLYglYPrroPrroglYLeuPrroglYserLaagLYLeuPrroglYArgrglYPrroglY	311
QY	100	-----AGCGCGGGGGCTGGAGACCAACA-----	120
Db	312	LeuArgrglYgluLaagLYPrroglYglYPrroglYglYAlPrroglYLeaTgrLYAspGln	331
QY	127	GGAAGGTCGCGAGTATCGACGAGCGCCCGAAGAGGACCATGGGAGACCGGAGGGGGACT	186
Db	332	GLYPrroserglYLeuLaagLYAsPro--GLYAlPrroglYgluArgrglYLeuPrroglY	350
QY	187	GCGAGAGGACCCCGGGCTCCGGCTCCGACCCATATGAGGC-----ACTCCT	240
Db	351	AlaHISglYPro-----PrroglYPrroHrgrglYProglYglYgluPrroglYpheHrgrglY	368
QY	241	CGMCTCTCTCTCTCTGGGCGCTGGGGCGCGGCTGCGCCCGCCACATGGAGCAGCAAGATCCC	300
Db	369	ArgrProglYglYPrroglYAlaLaagLYAlaLeuGlnLYsGly-Asp-----	384
QY	301	CAGCTCTGCCCCGGGCGACCCGCGCTTCAGAGCAGCGCGGCGACCATGGACCCAGG	360
Db	385	-----LeuGlyLeuPrroglYgluPrroglYLeuArgrglYPrrosergl	398
QY	361	CTTGGCGGGCGCGATGGCGCGGAGCGCGCGGCGCGCGCGCGCGCTCCGGAGAGAA	420
Db	398	YILePrroglYLeuGlnGlyPrroLaagLYPrroLleglYPrroGlnGlyLeuPrroglYLeuLY	418
QY	421	AGCGAGGCGGGAGGCGCGGACCTGCGGAGCTCGAGGGAC-----CCGCGCGCGG	474
Db	418	SGLYglu-----PrroglYLeuPrroglYPrroPrroglYgluLaagLYgluPr	435
QY	475	AGAGAGCGCGGACCCGCGGGCGCCACCGCGGCTCCGGGAGTGTGCGTGC-----	537
Db	435	OGLYThrLaagLY-PrroArgrglYPrroPrroglYAlPrroglYserPrroglYLeHrgrglY	455
QY	528	-----CTCGCGAGTCCGCGCTTCAGCGGCCAGCGCT-----	557
Db	455	roPrroglYLeuPrroglYPrroPrroglYAlPrroglYAlaPheAspGlnHrgrglYLeaIag	475
QY	558	-----CCGAGACGCGGGGTGCT-----	574
Db	475	LYLeuHISLeuPrroAsnGlyglYAlaGlnGlyAlaValLeuGlnLYsGlnLYsPrroG	495
QY	574	-----	574
Db	495	LnPheglYLeuGlnLYLeuSerAlaHISAlaThrProAlaPheHrgrAlaValLeuHrgrs	515
QY	575	-----CGCGGTGTGACGACACCTTGCTGCTTGACGCGGTGCTGTGACGACGAG	626
Db	515	erPrroLeuPrroAlaSerglYmetPrroLYAsPheAsPArgrThrLeuLYAsnLYHIS	535
QY	627	GACATTACGACGCGCGGACGATTCACCTGCGAGGAGCTGCGGGGTCTACTACTCTCG	686
Db	535	erGlyLYAsnPrroAlaHrgrglYILePheHrgrCysPrroAlaGlnGlyAlaLYrTYrgrhea	555
QY	687	CGGTCAATGCGACACGTCTACCGGCGCAGCTTGACGTTTGATCTGTGTGAAGATGCG--G	743


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QY 458 -----GGGACCCCGCGCGAGAGAGCG-----GGACCCGC 492
Db 483 yProProGlyProProGlyProLysAsnSerGlyLeuProGlyLeuProGlyPro 503
QY 493 GGGGCCACCGGGCTCCGGGAGTCTGGTCC----- 529
Db 503 oglyProProGlyProProGlyInsThrLeProGlyGlyTyrValLysGlyLys 523
QY 529 ----- 529
Db 523 rArgGlyLeuSerGlyMetSerPheMetLysAlaGlyAlaAsnGlnAlaLeuThrGly 543
QY 530 -CGCGATCCGCGCTTCAGCCGCAAGCGCTCGAGAGCGGGCTGCCGCGTGTGACG 588
Db 543 tProValSerAlaPheThrValLeuSerLysAlaTyr-----ProGlyAlaThrVa 561
QY 589 ACCCTTGCCCTTGACCGCGCTGCTGTGAAGACAGACGACATTACAGCGCGTACCG 648
Db 561 lProIleLysPheAspLysIleLeuTyrAsnArgGlnGlnIleTyrAspProAla 581
QY 649 CAAGTTCACCTGGCGAGTGGCGTCTACTACTGCGCGTCCATGCGACCGCTACCG 708
Db 581 yllePheThrCysArgGlyLeuProGlyLeuTyrTyrPheSerTyrHisValHisAlaLysG 601
QY 709 GCGCAGCGCTCAAGTTGATCTGTGAAGAAATGCGGAATCCATTGCC---TCTTCTTCA 765
Db 601 yThrAsnValAlaThrValAlaLeuTyrLysAsnGlySerProValMetTyrThrTyrAsp 621
QY 766 GTTTTGGGGGGGGCGCAAGCGCTCGCTCTCGGGGGCGCGCATGCGAGCGTGA 825
Db 621 uTyrGlnLysGlyTyrLeuAspGlnAla-----SerGlySerAlaValIleAspLeu 639
QY 826 GCGTAGAGCAAGTGTGGTGCAGTGTGGTGTGGATTCATTCATTCATTCAG 885
Db 639 tGluAsnAspGlnValThrLeuGlnLeuProAsnSerGlySerAsnIleLeuTyrSer 659
QY 886 CATCAGACAGACAGACATCTTCGGATTCTG 919
Db 659 rGluTyrValHisSerSerPheSerGlyPheLeu 670

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RESULT 4

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S13301
collagen alpha 1(X) chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C:Accession: S13301
R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
Biochem. J. 273, 141-148, 1991
A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. EV
A:Reference number: S13301; MUID:9113131; PMID:1703407
A:Accession: S13301
A:Molecule type: mRNA
A:Residues: 1-674 <TPRO>
A:Cross-references: EMBL:X53556; NID:9263; PIDN:CAA37624.1; PID:9264
C:Genetics:
A:Gene: COL10A1
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #stratus predicted <SIG>
F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:347-673/Domain: complement C1q carboxyl-terminal homology <CIQ>

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Alignment Scores:

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Pred. No.: 7.37e-21 Length: 674
Score: 454.00 Matches: 122
Percent Similarity: 44.93% Conservative: 42
Best Local Similarity: 33.42% Mismatches: 116
Query Match: 17.87% Indels: 85
DB: 2 Gaps: 13

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US-09-944-944-41 (1-1377) x S13301 (1-674)

QY 46 GGAGCGAAGCAGACTGGGT-----GACGCGAGGCGAGGCGCGCTGCGCG 93

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Db 320 GlyValLysGlyGlnGlnGlyProAlaGlyHisProGlyGlnAlaGly-----LeuPro 337
QY 94 GGAAGAAGCGCGGGGCTGGAGACACACCACTGAGAGGTCGAGTAGAGAGCGCCCG 153
Db 338 GlyProSerGlyAsnMetGly-----ProGlnIleProLysGlyIleProGlyAsnPro 355
QY 154 AAGAGGCCATCGGGGAGCGGGGAGGAGCTCCGAGAGACCC-----CGG 201
Db 356 -----GlyLeuProGlyProLysGlyLysIleMetGlyProValGlyProAlaGly 371
QY 202 CGTCCGAGCTCCCGGCTCCAGCGCTATAGAGCC-----ACTCCGCTCCGCTGCTCT 255
Db 372 AsnProGlyAlaLysGlyGlnArgGlySerSerGlyLeuAsnAspGlyLysProGlyTyrPro 391
QY 256 GGGCTGCGGCGCGCTCGCCCGCCACTGACAGACACAGATCCCAAGCT----- 306
Db 392 GlyLeuProGlyLeuAsnGlyProLysGlyAsnProGlyLeuProGlyProLysGlyAsp 411
QY 307 -----CTGCCCGGGGACCGCGCGCTTCAGAGCAGCGCGGCGCACCATGCGACCGAGG 360
Db 412 ProGlyIleAlaGlySer-ProGlyLeuProGlyProValGlyProAlaGlyAlaLysG 431
QY 361 CTTCGCGGCGCGCATGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGAGAA 420
Db 431 yValProGlyHisAsnGlyGlnAlaGlyProArgGlyValProGlyIleProGlyThrAr 451
QY 421 AAGCGAGGCGGGGCGCGCGGAGCTGCGG----- 448
Db 451 gGlyProIleGlyProProGlyIleProGlyPheProGlySerLysGlyAspValGlyTh 471
QY 449 -----GGAGCC 453
Db 471 rProGlyProProGlyProAlaGlyIleAlaValLysGlyLeuAsnIleProThrGlyPr 491
QY 454 TCGAGGGAGCCCGCGCGCGCGAGAGAGCG-----GGAGCCGCGG 495
Db 491 oProGlyProProGlyProArgGlyAsnAlaGlyGlnProGlyLeuProGlyProProG 511
QY 496 GCCCAGCGGCGCGCGGAGAGTCTGCGGCT----- 529
Db 511 yProProGlyProProGlyGlnValAlaLeuProLysAspPheValLysAlaGlyGlnAr 531
QY 530 -----CGCGATCCGCGCTTCAGCGCAA 552
Db 531 gProPheValSerAlaAsnGlnGlyAlaThrGlyMetProValSerAlaPheThrVal 551
QY 553 GCGCTCCGAGAGCGCGGCTCCGCGCTGAGAGCAACCTTCGCTTCGACCGCGTGT 612
Db 551 eLeuSerLysAlaTyr-----ProAlaIleGlyThrProIleProPheAspLysIle 569
QY 613 GGTCAAGCAGCAGGAGACATACAGAGCGCGCGACCGGACGGAATTCACCTCCAGAGTGG 672
Db 569 uTyrAsnLysGlnGlnIleHisThrAspProArgThrGlyIlePheThrLysLysIleProG 589
QY 673 GGTCTACTACTGCGCGCTCCATGCGCACCGCTACCGCGGCGCAAGCTTCGATCTGT 732
Db 589 ylleTyrTyrPheSerTyrHisIleHisValLysGlyThrHisAlaThrValGlyLeuTyr 609
QY 733 GAAGATGCGGAATTCATTGCC---TCTTCTTCAGATTTTTCGGGGGTGGCCCAAGCC 789
Db 609 rLysAsnGlyThrProValMetTyrThrTyrAspGlyTyrLysGlyLysIleAspG 629
QY 790 AGCGTCCCTTCGCGGGGGCGCATGCGAGAGCTGAGACCTCGAGACCAATGTTGGGTGA 849
Db 629 nAla-----SerGlySerAlaValIleAspLeuThrGluAsnAspGlnValThrLeuG 647
QY 850 GGTGGGTGTGGTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 909
Db 647 nLeuProAsnAlaGlySerAsnIleLeuTyrSerProGlyTyrValHisSerSerPhe 667
QY 910 CGGATTTCTGCTG 922

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Db 361 SerProglySer-----AspGlyLysProGlyTyrProGlyLysProGly 395
QY 250 GCTCTGGGCGCGCGCGCGCTCGCCCTGAGACAGACAGATCCAGCGCTTG 309
Db 396 LeuAspGlyProGlyGlyAsnProGlyLeuProGlyProGlyAspProGlyVal-- 414
QY 310 CCCGGGAGACCCCGGCTTCACAGGACCGGGGACCATGATGACGAGGCTTGCGG 369
Db 415 -GlyGlyProGlyLeuProGlyProGlyProValGlyProAlaGlyAlaLysGlyMetProGly 434
QY 370 CCGCATGGCCCGACGCGCGGAGCGCGCGCGCGGCTCCGGGAGAGAAAGGCGAGG 429
Db 434 YH1asnGlyGlyAlaGlyProArgGlyAlaProGlyLysProGlyTyrArgGlyProGly 454
QY 430 CGGAGAGCGCGGAGCTGCGG----- 448
Db 454 eGlyProProGlyLysProGlyPheProGlySerLysGlyAspProGlySerProGlyLys 474
QY 449 -----GGACCTCGAGGGA 462
Db 474 oProGlyProAlaGlyIleAlaThrLysGlyLeuAsnGlyProThrGlyProProGlyLys 494
QY 463 CCGCGGCGCGCGAGAGAGCGG-----GGACCGCGGCGCGCGCGCGG 504
Db 494 oProGlyProArgGlyH1asnSerGlyLysProGlyLeuProGlyProGlyProGlyProGly 514
QY 505 GCGTCCGCGGAGAGTCTCGGTCCT----- 529
Db 514 yProProGlyGlnAlaValMetProGlyLysPheLysAlaGlyGlnAlaArgProSerLys 534
QY 530 -----CCGCGATCCGCGCT 543
Db 534 uSerGlyThrProLeuValSerAlaAsnGlnGlyValThrGlyMetProValSerAlaPhe 554
QY 544 CAGCCCGCAAGCGCTCCGAGAGCGCGGCTGCTCCGCGTACGACACCTTGCTGCA 603
Db 554 eThrValIleLeuSerLysAlaTyr-----ProAlaIleGlyThrProLysProPheAs 572
QY 604 CCGCGTCTGGTGAACGAGAGGACATTACGACCGCGCGCGGACCGGCAAGTTCACCTGCA 663
Db 572 pLysIleLeuTyrAsnAlaGlnGlnHisTyrAspProArgThrGlyLysPheThrCysGly 592
QY 664 GGTGCTGGGCTGTACTACTGCGCGCGTCCAGTCCACCGGCGCGGCTGCACT 723
Db 592 nIleProGlyLysIleTyrPheSerLysValHisValLysGlyThrHisValTyrPhe 612
QY 724 TGATGTGGTGAAGATGGCGAATCCATGCG-----TCTTCTTCGAGTTTTCGGGGG 780
Db 612 lGlyLeuTyrLysAsnGlyThrProValMetLysThrTyrAspGlyTyrThrLysGlyTyr 632
QY 781 GCCCAAGCCAGCGCTGCTCGGGGGGCGGCGGAGGCTGAGAGCTGAGAGCAAGT 840
Db 632 rLeuAspGlnAla-----SerGlySerAlaIleIleLysPheLysGlnAlaAsnAspGln 650
QY 841 GTGGGTGCAAGTGGGTGGGTGACTACATGGCATGATGACCATGACATCAAGACAG 900
Db 650 lTyrPheGlnLeuProAlaGlnLysSerAsnGlyLeuTyrSerSerGlyTyrValHisSe 670
QY 901 CACCTTCCGCGATTTCGCG 922
Db 670 rSerPheSerGlyPheLeuVal 677

RESULT 3
S23297
collagen alpha 1(X) chain precursor - chicken
N:Alternate names: type X collagen
C:Species: Gallus gallus (chicken)
C:Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text change 13-Aug-1999
R:Accession: S23297; A31896; S65594; S77711; I50218
R:Ninomiya, Y.; Castagna, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvallie, P.; McCamguch, N.; Olsen, B.R.
A:Title: The molecular biology of collagens with short triple-helical domains.

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A:Reference number: S22243
A:Accession: S23297
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-674 <NIN>
R:Luvallie, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J: Biol. Chem. 263, 18378-18385, 1988
A:Title: The type X collagen gene. Intron sequences split the 5'-untranslated region
A:Reference number: A31896; MUID:89054019; PMID:2461368
A:Accession: A31896
A:Molecule type: mRNA
A:Residues: 1-75 <LUV>
R:Ninomiya, Y.; Gordon, M.; Van der Rest, M.; Schmid, T.; Linsemaier, T.; Olsen, B.R.
J: Biol. Chem. 261, 5041-5050, 1986
A:Title: The developmentally regulated type X collagen gene contains a long open read
A:Reference number: I50218; MUID:86168227; PMID:3082876
A:Accession: S65594
A:Molecule type: DNA
A:Residues: 'T','G','D','11-12','EDGMKLYLFTW','30-31','TCKSGRAFTYMILONVMDLVSSH','48-89','
629','POAVLSLWSMTCGSGSCQIONMVSIPLMFYLILSVSYLKSNNIPLMVS' <NINI>
A:Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
A:Accession: S77711
A:Molecule type: protein
A:Residues: 104-112,'X','114-117,453-466 <NIN2>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyprol
F:1-18/Domain: signal sequence #status predicted <SIG>
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Percent Similarity: 45.45% Conservative: 40
Best Local Similarity: 34.09% Mismatches: 111
Query Match: 17.91% Indels: 81
DB: 2 Gaps: 13

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Db 365 ---PheProGlyAlaLysGlyGlyLysGlyLeuPro-----GlyLeuAsp 378
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Db 379 GlyLysPro-----GlyTyrProGlyGlnGlnGlyLeuProGlyProLysGly 394
QY 202 -----CGTCCGCGCTCCCGGTCCAGCGCTATGAGCCCATCTCTGCTCTGCT 252
Db 395 HisProGlyLeuProGlyGlnLysGlyAspThrGlyHisAlaGlyPro---ProGlyLeu 413
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Db 414 ProGlyProValGly---ProGlnGlyValLys 423
QY 313 GGGGACCCCGGCGCTTCAGGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372
Db 424 GlyVal-ProGlyLysAsnGlyGlnProGlyProArgGlyProSerGlyLysProGlyTyr 443
QY 373 CGATGCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGAGAGGCGGCGG 432
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QY 433 GAGCGCGGAGCTCCCGGAGCTCGA----- 457
Db 463 yAlaProGlyLeuProGlyProAlaGlyIleAlaThrLysGlyLeuArgGlyPrometGly 483

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2003, 16:01:52 ; Search time 48 Seconds

(without alignments)
\$41.261 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325
Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSTFGSLVYSIDWHSPPVFA 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	1325	100.0	243	9	US-09-944-907-42
6	1325	100.0	243	9	US-09-944-929-42
7	1325	100.0	243	9	US-10-028-072-362
8	1325	100.0	243	9	US-10-121-049-362
9	1325	100.0	243	9	US-10-123-904-362
10	1325	100.0	243	9	US-10-140-470-362
11	1325	100.0	243	9	US-09-796-753-68
12	1325	100.0	243	9	US-10-175-746-362
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29	1325	100.0	243	9	US-10-140-921-362	Sequence 362, App
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32	1325	100.0	243	9	US-10-123-292-362	Sequence 362, App
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37	1325	100.0	243	9	US-10-160-498-362	Sequence 362, App
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ALIGNMENTS

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; Sequence 42, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,082
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 42
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-413-42

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 FFGGMPKPRASISGGAMVLEPEDQVWVGVGYDYIGIYASIKTDTSESGFLVSDMHSPP 240
Qy 241 VFA 243
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Db 241 VFA 243

RESULT 2
US-09-944-403-42
Sequence 42, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
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PRIOR APPLICATION NUMBER: 60/069,684
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 23, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
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PRIOR FILING DATE: July 28, 1999
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PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
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PRIOR APPLICATION NUMBER: 09/254,311
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PRIOR FILING DATE: September 15, 1999
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 42
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-403-42

Query Match 100.0% Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRPLVLLGLAASPPDDNKKIPSLCPGHGLPGTPGHHSOGLPGDGRDGRGANG 60
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DB 181 FFGMPKPASLSGGAMVRLPEPDQVWVGVGDYIGIYASIKTDTSTFSGFLVYSDMHSSP 240
QY 241 VFA 243
DB 241 VFA 243
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US-09-944-896-42
Sequence 42, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guiney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kjaavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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PRIOR FILING DATE: January 5, 1998
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PRIOR FILING DATE: February 9, 1998
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PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 23, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998


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: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 42
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-944-42

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Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pctd. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHGILPTPGHHGSGGLPGRDGRDGPAG 60
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHGILPTPGHHGSGGLPGRDGRDGPAG 60
QY 61 APGEKGGGRPLGPPGDEGPPGEGAGPAGTGPAGGCSVPPRSASFSAKSSSESVPPSPD 120
DB 61 APGEKGGGRPLGPPGDEGPPGEGAGPAGTGPAGGCSVPPRSASFSAKSSSESVPPSPD 120
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DB 181 FFGGMPKASLSGGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTDSFGFLVYSDWHSPP 240
QY 241 VFA 243
DB 241 VFA 243

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RESULT 4
US-09-944-944-42
: Sequence 42, Application US/0944944
: Patent No. US20020173463A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David

```

```

: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,944
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020173463A1ember 30, 1999

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: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 42
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-944-42

```

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Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPCTGHHGSGCLPGRDGRDGDAG 60
    |||||||
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPCTGHHGSGCLPGRDGRDGDAG 60
    |||||||
OY 61 APGEKGGRRGLPGRDPPGPRGEGAGPPTGPAEGCSVPRSAFSAKRSRVPSPSD 120
    |||||||
DB 61 APGEKGGRRGLPGRDPPGPRGEGAGPPTGPAEGCSVPRSAFSAKRSRVPSPSD 120
    |||||||
OY 121 APPEDRVLVNQGHDYAVTGKFTCQVPGVYVFAVHATVYRASLOFDLVKNGESTIASFEQ 180
    |||||||
DB 121 APPEDRVLVNQGHDYAVTGKFTCQVPGVYVFAVHATVYRASLOFDLVKNGESTIASFEQ 180
    |||||||
OY 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYTGITASITDSTFSGFLVYSWMHSSP 240
    |||||||
DB 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYTGITASITDSTFSGFLVYSWMHSSP 240
    |||||||
OY 241 VFA 243
    |||
DB 241 VFA 243

```

RESULT 5
US-09-944-907-42
Sequence 42, Application US/09944907
Publication No. US20020198147A1
GENERAL INFORMATION:

```

: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret

```

```

: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,907
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 42
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-907-42

```

```

Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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OY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPCTGHHGSGCLPGRDGRDGDAG 60
    |||||||
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPCTGHHGSGCLPGRDGRDGDAG 60
    |||||||
OY 61 APGEKGGRRGLPGRDPPGPRGEGAGPPTGPAEGCSVPRSAFSAKRSRVPSPSD 120
    |||||||
DB 61 APGEKGGRRGLPGRDPPGPRGEGAGPPTGPAEGCSVPRSAFSAKRSRVPSPSD 120
    |||||||
OY 121 APPEDRVLVNQGHDYAVTGKFTCQVPGVYVFAVHATVYRASLOFDLVKNGESTIASFEQ 180
    |||||||
DB 121 APPEDRVLVNQGHDYAVTGKFTCQVPGVYVFAVHATVYRASLOFDLVKNGESTIASFEQ 180
    |||||||
OY 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYTGITASITDSTFSGFLVYSWMHSSP 240
    |||||||
DB 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYTGITASITDSTFSGFLVYSWMHSSP 240
    |||||||
OY 241 VFA 243
    |||
DB 241 VFA 243

```

RESULT 6
US-09-944-929-42
Sequence 42, Application US/09944929
Publication No. US20020197612A1
GENERAL INFORMATION:

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: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,929
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 42
: LENGTH: 243
: TYPE: PRT

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ORGANISM: Homo Sapien
US-09-944-929-42
Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNKIPSLCPGHPGLPGTPGHHGSGGLRGDRDGDGAPG 60
DB 1 MRPLVLLLLGLAAGSPPLDNKIPSLCPGHPGLPGTPGHHGSGGLRGDRDGDGAPG 60
QY 61 APGKGGGGRGGLPGPPGDDGPPRGAGPAGTGTGAGGCSVPPRAFAKRSRVPSPSD 120
DB 61 APGKGGGGRGGLPGPPGDDGPPRGAGPAGTGTGAGGCSVPPRAFAKRSRVPSPSD 120
QY 121 APLEPDLVNEGGHYAVTGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180
DB 121 APLEPDLVNEGGHYAVTGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180
QY 181 FFGGMPKASLSSGCAWVLEPEDQVWVQVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240
DB 181 FFGGMPKASLSSGCAWVLEPEDQVWVQVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240
QY 241 VFA 243
DB 241 VFA 243

RESULT 7
US-10-028-072-362
Sequence 362, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028, 072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-29
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPPIDDKIPSLCPGHPGLPGRPHNGSGLPGNDGXDGAAG 60
DB 1 MRPLVLLLLGLAASPPIDDKIPSLCPGHPGLPGRPHNGSGLPGNDGXDGAAG 60
QY 61 APGEKGEGRPLPGPRDGPGRGAPGPTGPAGECSVPRSAFSAKRSRVPSPD 120
DB 61 APGEKGEGRPLPGPRDGPGRGAPGPTGPAGECSVPRSAFSAKRSRVPSPD 120
QY 121 APLPFDRLVYNEQHYDAVTGKFTQVPGVYFAVHATVYRASLPDLVKNESIASFEQ 180
DB 121 APLPFDRLVYNEQHYDAVTGKFTQVPGVYFAVHATVYRASLPDLVKNESIASFEQ 180
QY 181 FFGWPKPASLSGAMVRLPEPDQWVGVDYIGIYASIKTDSFSGFLVYSWHSPP 240
DB 181 FFGWPKPASLSGAMVRLPEPDQWVGVDYIGIYASIKTDSFSGFLVYSWHSPP 240
QY 241 VFA 243
DB 241 VFA 243

RESULT 8

US-10-121-049-362
Sequence 362, Application US/10121049
Publication No. US2003002239a1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-362

Query Match 100.0%; Score 1325; DB 9; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
Db 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
Db 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
Db 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
QY 241 VFA 243
Db 241 VFA 243

RESULT 9

US-10-123-904-362
Sequence 362, Application US/10123904
Publication No. US20030022328A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
PRIORITY FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-362

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
Db 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
Db 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180

Db 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
Db 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
QY 241 VFA 243
Db 241 VFA 243

RESULT 10

US-10-140-470-362
Sequence 362, Application US/10140470
Publication No. US20030022331A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
PRIORITY FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-362

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
Db 61 APGEKGGGRGRLPGPRGDPGPRGEAGPAGTGPAGCSVPPRSASFSAKRSSESVPPSPD 120
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
Db 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
Db 181 FFGGMPKRPASISGGAMVRLPEPDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240
QY 241 VFA 243
Db 241 VFA 243

RESULT 11

US-09-796-753-68

```

; Sequence 68, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 68
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-68

```

```

Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSQGLPGRDGRDGRGARG 60
|||||

```

```

Db      1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSQGLPGRDGRDGRGARG 60
QY      61 APGEKGGGRPGIPGRGDPGRGEGAPGTGPGEGCSVPPRSASFARSRSRVPSPD 120
        |||||
Db      61 APGEKGGGRPGIPGRGDPGRGEGAPGTGPGEGCSVPPRSASFARSRSRVPSPD 120
QY      121 APLPFDRLVYNQGHDAVTGKFTQCPVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
        |||||
Db      121 APLPFDRLVYNQGHDAVTGKFTQCPVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
QY      181 FFGWPKPASLSGAMVRLPEPDQWVGVGDYIGIYASIKTDSFTSGFLVYSQWHSPP 240
        |||||
Db      181 FFGWPKPASLSGAMVRLPEPDQWVGVGDYIGIYASIKTDSFTSGFLVYSQWHSPP 240
QY      241 VFA 243
        |||
Db      241 VFA 243

```

RESULT 12

```

US-10-175-746-362
; Sequence 362, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 2002-06-19
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-362

```

```

Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSQGLPGRDGRDGRGARG 60
|||||
Db      1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSQGLPGRDGRDGRGARG 60
QY      61 APGEKGGGRPGIPGRGDPGRGEGAPGTGPGEGCSVPPRSASFARSRSRVPSPD 120
        |||||
Db      61 APGEKGGGRPGIPGRGDPGRGEGAPGTGPGEGCSVPPRSASFARSRSRVPSPD 120
QY      121 APLPFDRLVYNQGHDAVTGKFTQCPVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
        |||||
Db      121 APLPFDRLVYNQGHDAVTGKFTQCPVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
QY      181 FFGWPKPASLSGAMVRLPEPDQWVGVGDYIGIYASIKTDSFTSGFLVYSQWHSPP 240
        |||||
Db      181 FFGWPKPASLSGAMVRLPEPDQWVGVGDYIGIYASIKTDSFTSGFLVYSQWHSPP 240

```

QY 241 VFA 243
Db 241 VFA 243

RESULT 13

US-10-176-918-362
; Sequence 362, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C382
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-918-362

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAG 60
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAG 60
QY 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120
Db 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120
QY 121 APLEPDRVLVNEQGHYDAVTGKFTCOVPGVYFFAVHATVYASIQFDLVKNGESTIASPFO 180
Db 121 APLEPDRVLVNEQGHYDAVTGKFTCOVPGVYFFAVHATVYASIQFDLVKNGESTIASPFO 180
QY 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240
Db 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240
QY 241 VFA 243
Db 241 VFA 243

RESULT 14

US-10-176-921-362
; Sequence 362, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C288
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-921-362

Query Match 100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAG 60
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAG 60
QY 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120
Db 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120
QY 121 APLEPDRVLVNEQGHYDAVTGKFTCOVPGVYFFAVHATVYASIQFDLVKNGESTIASPFO 180
Db 121 APLEPDRVLVNEQGHYDAVTGKFTCOVPGVYFFAVHATVYASIQFDLVKNGESTIASPFO 180
QY 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240
Db 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240
QY 241 VFA 243
Db 241 VFA 243

RESULT 15

US-10-137-865-362
; Sequence 362, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K

```

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-362

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Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPLIVLLGLAAGSPPLDNDKIPSLCPGHPGLPGTGHGSGGLPGRDGRDGRDAPG 60
    |||||||
DB 1 MRPLIVLLGLAAGSPPLDNDKIPSLCPGHPGLPGTGHGSGGLPGRDGRDGRDAPG 60
    |||||||
QY 61 APGEKGEGRPGPLPGRGDPPGPRGEAGPAGPTGPAGECVPPRSASFSAKRSESRVPPSD 120
    |||||||
DB 61 APGEKGEGRPGPLPGRGDPPGPRGEAGPAGPTGPAGECVPPRSASFSAKRSESRVPPSD 120
    |||||||
QY 121 APLPFDRLVNEQGHYDAVTGKFTQVPGVYFAVHATVYRASLQFDLVKNGESIASFQ 180
    |||||||
DB 121 APLPFDRLVNEQGHYDAVTGKFTQVPGVYFAVHATVYRASLQFDLVKNGESIASFQ 180
    |||||||
QY 181 FFGGWPKPASLSGGAMVRLEPEDQVQVGVGDYTGITASIKTSTFSGFLVSDMHSSP 240
    |||||||
DB 181 FFGGWPKPASLSGGAMVRLEPEDQVQVGVGDYTGITASIKTSTFSGFLVSDMHSSP 240
    |||||||
QY 241 VFA 243
    |||
DB 241 VFA 243

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Search completed: June 13, 2003, 16:11:09.
 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 16:09:26 ; Search time 2664 Seconds

(without alignments)
2654.048 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLLVLILLGLAAGSPPLD.....DSTFGSLVSDMHSPPVEA 243

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+2pn.model -DEV=x1h
-O/cgn2.1/USPTO/US0944944/runat_13062003_150046_24241/app_query.fasta.1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0944944.ecgn.1.1.2496_@runat_13062003_150046_24241 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
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22: em_ov:*
23: em_pat:*
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25: em_pl:*
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27: em_sts:*
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29: em_vl:*
30: em_hcg_hum:*
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32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
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37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1325	100.0	1337	9	AF329841
2	1325	100.0	1347	6	AR138193
3	1325	100.0	1377	6	AX464228
4	1321	99.7	1370	9	BC029485
5	1258	94.9	4220	10	AF469650
6	1254	94.6	1234	10	BC025174
7	1254	94.6	1271	10	BC023068
8	1239.5	93.5	191362	9	AP003396
9	1239.5	93.5	219574	9	AP002956
10	1207	91.1	1068	9	HSMB00923
11	1183.5	89.3	173657	2	AC112557
12	1167.5	88.1	249283	2	AC124577
13	1072	80.9	729	6	AR138195
14	914.5	69.0	182429	2	AP001557
15	765	57.7	150653	2	AC107174
16	584	44.1	173038	2	AP001003
17	452	34.1	150653	2	AC107174
18	436	32.9	947	10	BC028770
19	436	32.9	1276	6	AR034252
20	436	32.9	1276	6	AX195209
21	436	32.9	1276	6	AX358519
22	436	32.9	1276	6	AX358519
23	434	32.8	767	10	MMU37222
24	432.5	32.6	1313	6	AR034253
25	432.5	32.6	4517	6	AR138194
26	432.5	32.6	4517	6	AX195211
27	432.5	32.6	4517	6	AX335029
28	432.5	32.6	4517	6	AX358521
29	432.5	32.6	4517	6	HMMPEST2
30	432.5	32.6	4545	6	AX134174
31	432	32.6	194674	2	AC124477
32	428.5	32.3	1886	5	AB067770
33	427	32.2	1134	4	AF269230
34	424.5	32.0	1152	6	AX195207
35	424.5	32.0	1152	6	AX358517
36	424.5	32.0	1152	10	MMU49915
37	422.5	31.9	1282	6	AX054815
38	422	31.8	734	9	AF404407
39	421.5	31.8	178850	9	AL359736
40	418.5	31.6	1973	9	HS10A1COL
41	418.5	31.6	3215	9	HS10A1COL
42	418.5	31.6	10058	9	HS10A1COL
43	418.5	31.6	107553	9	HS10A1COL
44	418.5	31.6	205594	2	AL355373
45	417.5	31.5	3226	6	AX333243

RESULT 1

ALIGNMENTS

LOCUS	AF329841		1337 bp	mRNA	linear	PRI 12-MAR-2001
DEFINITION	Homo sapiens complement-clq tumor necrosis factor-related protein (CTRP5) mRNA, complete cds.					
ACCESSION	AF329841					
VERSION	AF329841.1		GI:13274527			
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens.					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
AUTHORS	1 (bases 1 to 1337)					
JOURNAL	Sheppard,P.O. and Humes,J.M.					
REFERENCE	Unpublished					
AUTHORS	2 (bases 1 to 1337)					
TITLE	Sheppard,P.O. and Humes,J.M.					
JOURNAL	Direct Submission					
FEATURES	Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA					
source	Location/Qualifiers					
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	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/chromosome="11"					
	/map="11q23.3"					
gene	1..1337					
	/gene="CTRP5"					
	/note="ZSIC39"					
CDS	198..929					
	/gene="CTRP5"					
	/codon_start=1					
	/product="complement-clq tumor necrosis factor-related protein"					
	/protein_id="AAK17965.1"					
	/db_xref="gi:13274528"					
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BASE COUNT	235 a 417 c 459 g 226 t					
ORIGIN						
Alignment Scores:						
Pred. NO.:	2.83e-48					1337
Score:	1325.00					Matches: 243
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Best Local Similarity:	100.00%					Mismatches: 0
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Oy	1 MetArgProLeuLeuValLeuLeuLeuLeuAlaAlaGlySerProProLeuAsp					20
Db	198 ATGAGGCCACTCCGCGCCTGCCTGCTGTGGGCGCGGCGCGCCACTGGAC					257
Oy	21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis					40
Db	258 GACACACAAGATCCCACCCTCTGCGCGGCGCACCCCGCCCTTCCAGGCACACCCCGGCCAC					317
Oy	41 HisGlySerGlnGlyLeuProGlyAArgAspGlyAArgAspGlyAArgAspGlyAArgGly					60
Db	318 CATGGACACCGCGGCTTGCCGGGCGCGCATGGCCGACAGCGCCCGCGCGGCCCGGG					377
Oy	61 AlaProGlyIuLysGlyGluGlyLysArgProGlyLeuProGlyProArgGlyAspPro					80
Db	378 GCCTCGGAGAGAAGCGAGGCGGCGGCGCGGAGACTGCCGGGAGCTCGAGGGAGCCCC					437
Oy	81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerVal					100
Db	438 GGCGCGGAGAGAGGGGAGCCCGCGGCGGCCACCGGCTGCGCGGGAGTGTCTCGGTG					497

QY	101	PROPARGSERALAPHERSERALAYASRGISERARGVALPROPROSERASP	120
Db	498	CCTCCGGCATCCGCTTACGGCCAGAGCGCTCCGAGACCGGGTCCCTCCGGCTGAC	557
QY	121	ALAProLeuProPheAspArgValLeuValAsnGlnGlnIstYrAspAlaValThr	140
Db	558	GCACCCCTTGCCCTTGACCGGGGTGGTGAACGAGCAGGGCATTACGAGCGGTACC	617
QY	141	GlyIysPheThrCysGlnValProGlyValIleYrTyPheAlaValHisAlaThrValTyr	160
Db	618	GGCAAGTTCCACTGCGCAGGTGCTGGGGTCACTACTTCCTGCGCTCCAGCCAGCTTCAC	677
QY	161	ArgAlaSerLeuGlnPheAspLeuValIlyAsnGlnIylGluSerIleAlaSerPhePheGln	180
Db	678	CGGGCCACCTGCGACTTGATCTGGTGAAGATGGCGAATTCATTGGCTTTCTTCCAG	737
QY	181	PhePheGlyGlyTyrProIlyProIlyAsSerLeuSerGlyGlyAlaMetValArgLeuGln	200
Db	738	TTTTTCGGGGGGGTGGCCCAAGCAGCCCTCGCTCTCGGGGGGGCCATGGTAGGGCTGAG	797
QY	201	ProGluAspGlnValTyrValGlnValGlnValGlyValGlyAspTyrIleGlyIleAsp	220
Db	798	CCTGAGGACCAAGTGGGTGCAGAGTGGGTGTGGGTGACTACATTGGCATGTATGCCAGC	857
QY	221	IleIlyThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPHisSerSerPro	240
Db	858	ATCAAGACAGACAGCACTTCTCCGAGATTTCGTGGTACTCTCCAGTCCGACAGCTCCCA	917
QY	241	ValPheAla 243	
Db	918	GTCTTTGCT 926	
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LOCUS	DEFINITION	Sequence 1 from patent US 6197930.	
AR138193	ACCESSION	AR138193	
VERSION	AR138193.1	GI:14479702	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1347)		
TITLE	Sheppard, P.O. and Humes, J.M.		
JOURNAL	Adipocyte-specific protein homologs		
FEATURES	Patent: US 6197930-A 1 06-MAR-2001;		
	Location/Qualifiers		
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BASE COUNT	235 a	421 c	465 g 226 t
ORIGIN			
Alignment Scores:			
Pred. No.:	2.85e-48	Length:	1347
Score:	1325.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Db	198	ATGAGGGCCACCTCCGTGCTCTGCTGCTGCGGCTGGGCGGCGGCTGCCCCACTGGAC	257
QY	21	AspAsnIlyIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis	40
Db	258	GACAAACAAGATCCCAAGCTTGCTGCCCGGGGACACCCCGGCTTCCAGGACGCGGGCCAC	317
QY	41	HisIylSerGlnIlyLeuProGlyIlyArgAspIlyIlyArgAspIlyIlyArgAspIlyAlaProGly	60

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Db	318 CATGCAACGACGGGCTTCCGGGCGCCGCGATGCGCCGACGGCCGACGGGCGCCCGG	377	2.9e-48	100.00%
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Db	378 GCTCCGGGAGAAAGCGGAGCGGAGCGCCGGAGCTGCCGGGACCTCGAGGGGAGACCC	437	100.00%	0
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Db	438 GGGCGCGGAGAGAGCGGGGACCGCGGGGCCACCGGCGCTCGCGGGGAGTGTCTGGTG	497		
Qy	101 ProProa1rG1e1r1a1Phe1e1r1a1y1a1rG1e1r1u1S1e1r1a1rG1e1r1a1V1a1P1rO1Pro1S1e1r1a1P	120		
Db	498 CCTCCGGCATCGCCTTCAGCGCCAGCGCTCCAGAGCCGGGTCCTCCGCGCTGCAC	557		
Qy	121 A1a1rO1e1u1P1rO1Phe1a1rG1a1l1e1u1V1a1a1S1nG1u1nG1y1h1S1T1y1a1S1P1a1V1a1Th1r	140		
Db	558 GCACCCCTTGCCCTTCGACCGCGCTGCTGGTGAACAGACAGGAGACATTTCAGACGGCTCAC	617		
Qy	141 G1y1y1S1Phe1h1rC1y1S1G1n1V1a1P1rO1G1y1V1a1T1r1T1y1r1Phe1a1V1a1H1S1a1Th1V1a1T1r	160		
Db	618 GGCAGATTCACCTCCAGAGTCCCTCGGGGCTACTACTTCGCCGTCACATGCACACGCTCAC	677		
Qy	161 A1rG1a1a1S1e1r1e1u1nG1n1Phe1a1S1P1e1u1V1a1l1y1a1S1nG1u1S1e1r1I1e1a1S1e1r1Phe1phe1n	180		
Db	678 CGGGCGACCGCTCGCAGTTTGATCTGGTGAAGATGGCGCATTCATTCCTTTCTTCAG	737		
Qy	181 Phe1phe1G1y1G1T1r1P1rO1y1S1P1rO1a1S1e1r1e1u1S1e1r1G1y1G1a1M1e1V1a1A1rG1e1u1	200		
Db	738 TTTTTCGGGGGCTGCGCCAGCCAGCTCGCTTCGGGGGGGCGCATGTAGGCTGGAG	797		
Qy	201 ProG1u1a1S1P1G1V1a1T1r1P1a1G1n1V1a1G1y1V1a1G1y1a1S1P1T1r1I1e1G1y1I1e1T1y1a1S1e1r	220		
Db	798 CCTAGAGACCAAGTGGGTGCAGGTGGGTGGGTGGGTGCATTCATTCGATTCATTCAGC	857		
Qy	221 I1e1y1S1h1r1a1S1e1r1h1Phe1S1e1r1G1y1Phe1e1u1V1a1Y1S1e1a1P1T1P1H1S1e1S1e1r1P1rO	240		
Db	858 ATCAAGACAGACACACCTTCCTCCGATTTCGTGGTGTACTTCGACTGACACAGCTCCCA	917		
Qy	241 ValPhe1a1 243			
Db	918 GTCCTTGGCT 926			
RESULT 3	AX464228	1377 bp	DNA	linear
LOCUS	AX464228	Sequence 361 from Patent WO0140466.		
DEFINITION	AX464228			
ACCESSION	AX464228.1	GI:21899130		
VERSION				
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Wetanabe,C.K., Wood,W.L. and Zhang,Z.			
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding same			
JOURNAL	Patent: WO 0140466-A 361 07-JUN-2001;			
FEATURES	Genentech Inc. (US)			
SOURCE	Location/Qualifiers			
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ORIGIN				
Alignment Scores:				
Pred. No.:	2.9e-48	Length:	1377	
Score:	1325.00	Matches:	243	
Percent Similarity:	100.00%	Conservative:	0	

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BASE COUNT	873 a 1282 c 1147 g 918 t
ORIGIN	
Alignment Scores:	
Pred. No.:	4.5e-45 Length: 4220
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Percent Similarity:	96.30% Conservative: 6
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Query Match:	94.94% Indels: 0
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OY	21 AspAsnLysLieProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis 40
Db	3157 GACAACAGATCCCAGCTGTGTCGGGGGAGCCCCGGCTTCCAGGACACCAGGTAC 3216
OY	41 HisGlySerGlnGlyLeuProGlyValArgAspGlyValArgAspGlyValArgProGly 60
Db	3217 CATGGCAGCCAAAGCGCTGCGGCGCGTAGCGCGGTATGGCCGCAAGGTGCACCCGGA 3276
OY	61 AlaProGlyGluLysGlyGlnGlyValArgProGlyLeuProGlyProArgGlyAspPro 80
Db	3277 GCTCCGGAGAGAAGGCGAGGGGGGAGACCGGACTACTCGGCCAACGCGGGAGACCC 3336
OY	81 GlyProArGlyGlnAlaGlyProAlaGlyProThrGlyProAlaGlyGlnCysSerVal 100
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OY	101 ProProArGSerAlaPhaSerAlaLysArgSerGluSerArgValProProProSerAsp 120
Db	3397 CCCCCAGATCAGGCTTCAAGTGCACAGCATCCGAGACCGCGTACTCCGCCAGCCGAC 3456
OY	121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrrAspAlaValThr 140
Db	3457 ACACCCCTACCTTTGCACCGCTGCTCTTAATAGCAGAGGCGCATTCAGACCCCACTACT 3516
OY	141 GlyLysPheThrCysGlnValProGlyValTyrrTyrrPheAlaValHisAlaThrValTyrr 160
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REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
161	Arglase	serleugln	phleapleu	vallysas	nclygusertlealeaser
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3577	CGGGCCAGC	CTTGCA	CTTTGAT	CTTGTCTAAAAACGGGAC	GTCCACATCGGCTCTTCTTCTCAG
3636					
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200					
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3696					
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220					
3697	CCTGAGG	CCAGCGTGTGGT	GTGTCAGGTGGGCGTGGGT	GATTAACATTTGCACTATGAC	CGACG
3756					
221	Illey	thr	asp	ser	trp
240					
3757	ATCAAGC	ACAGAC	ACTTCTCTGTG	ATTCTCGTATTTCTGACTG	GCACAGCTCCCA
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3817	GTCTTC	CGCT	3825		
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BC025174					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
house mouse.					
Mus musculus.					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
1 (bases 1 to 1234)					
Strausberg,R.					
Direct Submission					
Submitted (05-MAR-2002) National Institutes of Health, Mammalian					
Gene Collection (MGC), Cancer Genomics Office, National Cancer					
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					
USA					
NIH-MGC Project URL: http://mgc.ncl.nih.gov					
Contact: MGC help desk					
Email: cgapbs-rt@mail.nih.gov					
Tissue Procurement: Gilbert Smith, Ph.D.					
cDNA Library Preparation: Life Technologies, Inc.					
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
DNA Sequencing by: Baylor College of Medicine Human Genome					
Sequencing Center					
Center code: BCM-HGSC					
Web site: http://www.hgsc.bcm.tmc.edu/cdna/					
Contact: amgdbcm.tmc.edu					
Gunnarone, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,					
Yoon, V.S., Kovais, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,					
Richards, S., Gibbs, R.A.					
Clone distribution: MGC clone distribution information can be found					
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov					
Series: IRAK Plate: 61 Row: f Column: 24					
This clone was selected for full length sequencing because it					
passed the following selection criteria: Hexamer frequency ORF					
analysis.					
Location/Qualifiers					
1. 1234					
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112. 843					
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Oy	109	LysArSerSerGluSerArgValProProRoSerAspAlaProLeuProPheAspArgVal	128
Db	6271	AAGCGCTCCGAGAGCGGGGTCCCTCCGCCGCTCTGACGCAACCTTGCCCTTGACCGCGTG	621212
Oy	129	LeuValAsnGluGlnGlyHisTyrAspAlaValThrGlyLysPheThrCysGlnValPro	148
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Oy	149	GlyValTyrTyrPheAlaValAlaHisAlaThrValTyrArgAlaSerLeuGlnPheAspLeu	168
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Oy	169	ValLysAsnGlyGluSerLeuAlaSerPhePheGlnPhePheGlyTyrProLysPro	188
Db	6091	GTGAAGAAATGCGCAATCCATGCTCTTCTTCCAGTTTTCGGGGGTGGCCCAAGCCA	603222
Oy	189	AlaSerLeuSerGlyGlyAlaMeValArgLeuGlnProGluAspGlnValTyrValGln	208
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Oy	209	ValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysTyrAspSerThrPheSer	228
Db	5971	GTGGGTGTGGGTGACTCATATTGGCATCTATATCCAGCATCAGACAGACAGACACTTCTCC	59121
Oy	229	GlyPheLeuValTyrSerAspTyrPheSerSerProValPheAla	243
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ACCESSION	AP002956		
VERSION	AP002956.1	GI:22255355	
KEYWORDS	HTG.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., 1 Totoroki,Y., Matanabe,H. and Sakaki,Y.		
TITLE	Human Sapiens 219,574 genomic DNA of 11q		
JOURNAL	Published Only in Database (2002)		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoroki,Y., Matanabe,H. and Sakaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, Yori:http://hgpc.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
COMMENT	Overlapping Clones: pD114, PQ3868 Cytogenetic Position: 21q22.1, region:D21S226-AML STS Markers (ePCR): stsG53747, SHGC-16045, D11S2450, SHGC-7143, WI-16056, stsG31054, sts-X57110, WI-8978, GDB:198117, stsG29284, SHGC-130657, D11S1941E, WI-14589, stsG60191, stsS50535, A002048, stsS26946, stsG41092, TIGR-A005D38, Bdaa7902, D11S869E, RH80030 Contamination: none detected non-ACGT bases: none Additional author information Arai,Y., Kubo,T.,Ohki,M. National Cancer Center Research Institute Cancer Genomic Division		

	5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN zip: 104-0045 phone: +81-3-3542-2511 ex4752, fax: +81-3-3542-0688 e-mail: yatalenc.go.jp.
FEATURES	Location/Qualifiers
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ORIGIN	
Alignment Scores:	
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Percent Similarity:	68.17%
Best Local Similarity:	68.17%
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DB:	Gaps: 1
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Dd	209668 ATGAGGCCATCTCCTCGTGTGGTCCTCCGCGGCCTGGGGCCGCGCTCCCCCCACTGGAC 209609
OY	21 AspaAsnlystlerProserLeucysPproglYHIsPProglYleuProglYThProglYHis 40
Dd	209608 GACAACAAGTATCCCACGACCTCTGCCCCGGGGCACCCCGGCTTTCAAGACACC CGGGCCAC 209549
OY	41 HisglySerclnglyLeuProglYArGaSpglYArGaSpglYArGaSpglYAlaProgly 60
Dd	209548 CATGGCAGCCAGCGGCTTGCCGGGGCGCGATGGCCGCGACGGCGCGGAGCGCGCCCGGG 209489
OY	61 AlaProglyshluyslsglyLuglytlyArGaProglyLeu----- 73
Dd	209488 GCTCCGGGAGAAGAAAGCGAGGGCGGAGCGGGTA--GAAGCACCCCGCGGCTATC 209430
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Dd	209189 CTTAGAGTGGCGCGCCCGCTGGGGGCTGAGCCGCCCTACTCTACACCTGGCGCCCGCT 209130
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Dd	209129 TACCCCGCAGAGACTGCGGGGACTCGAAGGGAGCCCCGGGGCGCGAGGAGGGGAGACC 209070
OY	89 AlaglyProThglyProAlaIaglyLucysSerValProProArngSerAlaIapheserAla 108
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OY	109 LysArgSercluserArgValProProProserAspAlaProleuProphesAspArgVal 128
Dd	209009 AAGCGCTCCGAGAGCGGGGTGCTCCGCCGCTGACGACACCTTGCCCTTCGACCGGCTG 208950
OY	129 LeuValAsncluglnclyHIsTyfAspAlaValThrglyLyspherhCySGlnValPro 148

Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbala, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bowick, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavaros, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, R.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Donthate, K.J., Draper, H., Dugan-Rocha, S., Durbin, R.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, R., Harris, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Huliy, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratoch, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkwo, S., Oguh, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ran, X., Rivas, M., Rojas, A., Rojuben, I., Rolfe, M., Ruiz, S., Savary, G., Scherier, S., Scott, G., Shen, H., Shoshitari, N., Slisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umami, K., Vasquez, L., Vera, Y., Villalón, D., Vinson, R., Wang, Q., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Unpublished
2 (bases 1 to 173657)
Direct Submission
Morley, K.C.
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173657)
Morley, K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced g1:18660143.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKAB
Center clone name: CH230-904
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 105614 bases at least Q40
Consensus quality: 111210 bases at least Q30
Consensus quality: 115587 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1137: contig of 1137 bp in length
1138 1237: gap of unknown length
1238 2720: contig of 1483 bp in length
2721 2820: gap of unknown length
2821 3984: contig of 1164 bp in length
3985 4084: gap of unknown length
4085 5158: contig of 1074 bp in length
5159 5258: gap of unknown length
5259 6307: contig of 1048 bp in length
6308 6406: gap of unknown length
6407 7523: contig of 1117 bp in length
7524 7623: gap of unknown length
7624 8632: contig of 1008 bp in length
8633 8731: gap of unknown length
8732 9806: contig of 1075 bp in length
9807 9906: gap of unknown length
9907 11155: contig of 1249 bp in length
11156 11255: gap of unknown length
11256 12568: contig of 1313 bp in length
12569 12658: gap of unknown length
12659 13704: contig of 1036 bp in length
13705 13804: gap of unknown length
13805 14931: contig of 1127 bp in length
14932 15031: gap of unknown length
15032 16084: contig of 1053 bp in length
16085 16184: gap of unknown length
16185 17858: contig of 1674 bp in length
17859 17958: gap of unknown length
17959 19035: contig of 1077 bp in length
19036 19135: gap of unknown length
19136 20291: contig of 1156 bp in length
20292 20391: gap of unknown length
20392 21643: contig of 1252 bp in length
21644 21743: gap of unknown length
21744 22846: contig of 1103 bp in length
22847 22946: gap of unknown length
22947 24684: contig of 1738 bp in length
24685 24784: gap of unknown length
24785 26405: contig of 1621 bp in length
26406 26505: gap of unknown length
26506 27716: contig of 1211 bp in length
27717 27816: gap of unknown length
27817 28876: contig of 1060 bp in length
28877 28976: gap of unknown length
28977 30019: contig of 1043 bp in length
30020 30119: gap of unknown length
30120 31550: contig of 1431 bp in length
31551 31650: gap of unknown length
31651 33128: contig of 1478 bp in length
33129 33228: gap of unknown length
33229 34763: contig of 1535 bp in length
34764 34863: gap of unknown length
34864 36404: contig of 1541 bp in length
36405 36504: gap of unknown length
36505 37957: contig of 1453 bp in length
37958 38057: gap of unknown length
38059 40293: contig of 2236 bp in length
40294 40393: gap of unknown length
40394 41698: contig of 1305 bp in length
41699 43155: gap of unknown length
43156 43255: contig of 1357 bp in length
43256 45193: gap of unknown length
45194 45293: contig of 1938 bp in length
45294 47217: gap of unknown length
47218 47317: gap of unknown length

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* 47318 49231: contig of 1914 bp in length
* 49332 49331: gap of unknown length
* 49332 51305: contig of 1874 bp in length
* 51306 51305: gap of unknown length
* 51306 53117: contig of 1812 bp in length
* 53118 53217: gap of unknown length
* 53218 55542: contig of 2325 bp in length
* 55543 55642: gap of unknown length
* 55643 57451: contig of 1809 bp in length
* 57452 57551: gap of unknown length
* 57552 60851: contig of 3300 bp in length
* 60852 60951: gap of unknown length
* 60952 62718: contig of 1767 bp in length
* 62719 62818: gap of unknown length
* 62819 64976: contig of 2158 bp in length
* 64977 65076: gap of unknown length
* 65077 67855: contig of 2779 bp in length
* 67856 67955: gap of unknown length
* 67956 71313: contig of 3358 bp in length
* 71314 71413: gap of unknown length
* 71414 73659: contig of 2246 bp in length
* 73660 73760 75549: gap of unknown length
* 73760 75549: contig of 1790 bp in length
* 75550 79106: gap of unknown length
* 75650 79206: contig of 3457 bp in length
* 79107 83551: gap of unknown length
* 79207 83552 83651: gap of unknown length
* 83552 86053: contig of 2402 bp in length
* 86054 86153: gap of unknown length
* 86154 88659: contig of 2506 bp in length
* 88660 88759: gap of unknown length
* 88760 90078: contig of 1319 bp in length
* 90079 90178: gap of unknown length
* 90179 92201: contig of 2023 bp in length
* 92202 92301: gap of unknown length
* 92302 94877: contig of 2576 bp in length
* 94878 94977: gap of unknown length
* 94978 96946: contig of 1969 bp in length
* 96947 97046: gap of unknown length
* 97047 99897: contig of 2851 bp in length

```

Alignment Scores:

Pred. No.:	1,05e-40	Length:	173657
Score:	1183.50	Matches:	225
Percent Similarity:	69.07%	Conservative:	5
Best Local Similarity:	67.57%	Mismatches:	6
Query Match:	89.32%	Indels:	97
DB:	2	Gaps:	1

US-09-944-944-42 (1-243) x AC112557 (1-173657)

```

OY 8 LeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAspAspAsnLysIleProSerLeu 27
DB 43284 CTGCTTCGGGCTGCGATCGAGGCTCTCTCTCGAGCAACAAATCCCGCCGCTG 43343
OY 28 CysProGlyHisProGlyLeuProGlyThrProGlyHisHisGlySerGlyLeuPro 47
DB 43344 TGTCCCGGAGACCGCGCTCCACAGCACACAGGCGCACAGGAGCGGAGGCTGCT 43403
OY 48 GlyArgAspGlyArgAspGlyArgAspGlyAlaProGlyAlaProGlyGluGlyGlu 67
DB 43404 GGGCGGTGAGCGCGGTGATGGCGGAGCGGTGACCGGAGCGTCCGGAGAGAAAGCG 43463
OY 68 GlyGlyArgPro----- 71
DB 43464 GGGCGGAGACCGGAGTAAGACTATTTCGTTGAGTCATGATGGTGCATCTGTGAACA 43523
OY 71 ----- 71
DB 43524 CAGCCCTGCTCTGATGATCTTTGGGGGTCAGAGGTCGCCGAGGGGGCGCTACTCTC 43583
OY 71 ----- 71

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DB 43584 COTCATTCAGTCAGCAGAGCGGGGAGGTGGGCTGCGGGTGGAGGGGTGATCAG 43643
OY 71 ----- 71
DB 43644 CCCCAGGAAATCAGAAACCTGATCCCTACTACAGCACTTCAGATCTGCCCGCAGG 43703
OY 71 ----- 71
DB 43704 AGGTACAGCCTGGAGGCTGGAGGCTTTCGACTTCCTCCCTTCCTCATCCCT 43763
OY 72 ---GlyLeuProGlyProArgGlyAspProGlyProArgGlyGluAlaGlyProAlaGly 90
DB 43764 GCAGACATACCTGGGCGCACAGTGGGAGGCGCGCGCGCGGAGAGCAGAGACTGGGG 43823
OY 91 ProThrGlyProAlaGlyGlyGlySerValProProArgSerAlaPheSerAlaLysArg 110
DB 43824 GCTATCGGCGCTCGCGGAGAGTCTCGGGTCCCGCCAGATCAGCTTCAGTCCAAAGCG 43883
OY 111 SerGlySerArgValProProProSerAspAlaProLeuProPheAspArgValLeuVal 130
DB 43884 TCAGAGAGCGGGTACCTCCGCGAGCGACACACCCCTTACCTTGACCGGTGCTGCTC 43943
OY 131 AsnGlyGlnGlyHisTyrAspAlaValThrGlyLysPheThrCysGlnValProGlyVal 150
DB 43944 AATGAGCAGGAGCATTAAGATGACGACCTACCGGCAAGTTCACCTGCCAAGTGGCTGTC 44003
OY 151 TyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeuGlnPheAspLeuValLys 170
DB 44004 TACTACTTTCGCTGCTCCATGCACTGCTACCGGCGGCGCACCTACACTTTCATCTGCAAA 44063
OY 171 AsnGlyGlySerIleAlaSerPhePheGlnPhePheGlyTyrProLysProAlaSer 190
DB 44064 AATGCGCAATCATAGCTTCTTCTTCCAGTTTGGGGGTGGCGCAAGCGACCTCG 44123
OY 191 LeuSerGlyGlyAlaMetValArgLeuGluProGlyAspGlnValTyrValGlnValGly 210
DB 44124 CTCCTAGGGGGGTGCGATGTGAGGCTTAACCTGAGCAGCAGTATGGGTTCAGGTGGGT 44183
OY 211 ValGlyAspTyrIleGlyTyrLeuAlaSerIleLysThrAspSerThrPheSerGlyPhe 230
DB 44184 GTGGGTGATTCATTCATGCGATCATGTCAGCATCAAAAGACAGTACCTTCCTGATTT 44243
OY 231 LeuValTyrSerAspThrPheSerProValPheAla 243
DB 44244 CTCGCTATTCGACTGCGACAGCTCCCGAGCTTCGCT 44282
RESULT 12
AC124577 249283 bp DNA linear HTG 11-AUG-2002
LOCUS AC124577
DEFINITION Mus musculus chromosome UNK clone R23-162p10, WORKING DRAFT
AC124577
VERSION AC124577.2 GI:22203905
SOURCE HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILLTOP.
ORGANISM house mouse.
MUS musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 249283)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
2 (bases 1 to 249283)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 249283)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (11-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

```


QY 173 GlusertleAlaserPhepneGluPhepneGlyTyrProLysProAlaserLeuser 192
 Db 46810 CAGTCATCGCCTCTTTCTTCAGATTTTGGGGGCTGCCCAACCCAGCTCTCA 46869
 QY 193 GllgylAlaMetValArgLeuGluProLysAspGlnValTyrValGlnValGly 212
 Db 46870 GGGGGTGGAGTGTAAAGCTAGAACCTAGAGCACAGGTGGGTGAGTGGGTGGGT 46929
 QY 213 AspTyrIleGlyIleTyrAlaSerIleLysThrAspSerThrPheSerGlyPheLeuVal 232
 Db 46930 GATTACATTCATATGATGACAGCATCAAGACAGCACTTCTCTGATTTCTCTGC 46989
 QY 233 TyrSerAspTyrPheLysSerSerProValPheAla 243
 Db 46990 TATTCTGACTGGCACAGCTCCCACTCTTCTGCT 47022
 RESULT 13
 ARI38195 ARI38195 729 bp DNA linear PAT 16-JUN-2001
 LOCUS Definition Sequence 10 from patent US 6197930.
 ACCESSION ARI38195
 VERSION ARI38195.1 GI:14479704
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Sheppard,P.O. and Humes,J.M.
 TITLE Adipocyte-specific protein homologs
 JOURNAL Patent: US 6197930-A 10-06-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..729
 BASE COUNT 77 a 101 c 160 g 81 t 310 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.96e-38 Length: 729
 Score: 1072.00 Matches: 191
 Percent Similarity: 78.60% Conservative: 0
 Best Local Similarity: 78.60% Mismatches: 52
 Query Match: 80.91% Indels: 0
 Gaps: 0
 DB: 6
 US-09-944-944-42 (1-243) x ARI38195 (1-729)
 QY 1 MetArgProLeuLeuValLeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAsp 20
 Db 1 ATGMCNCCNTNTNTNTNTNTNTNTNTNTGNGNCGNCGNCGNCGNCGNCGNCGNCGN 60
 QY 21 AspAsnLysIleProSerLeuGlyProGlyHisProGlyLeuProGlyThrProGlyHis 40
 Db 61 GATTAAT 120
 QY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyArgAspGly 60
 Db 121 CAYGNGNMGNCARGNYTNCNGNMGNCARGNYTNCNGNMGNCARGNYTNCNGNMGNCARGNYTNC 180
 QY 61 AlaProGlyGluLysGlyGlyGlyGlyArgProGlyLeuProGlyProArgGlyAspPro 80
 Db 181 GCNCCNCGNGARAAARGNGARGNGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 240
 QY 81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerVal 100
 Db 241 GGNCCNMGNGNGARGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 300
 QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProSerSerAsp 120
 Db 301 CCNCCNMGNMGNCCTTYWNGNCNARBMGNMNGNMGNCCTTYWNGNCNCGNCGNCGNCGNCGN 360
 QY 121 AlaProLeuProPhePheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThr 140
 Db 361 GCNCCNNTNCCNTTYGATGNGTNTNTGTAAYGARCARCGNCAATATGAYGCGNCGNCGNCGN 420

QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
 Db 421 GGNAAATTTACNTGTCACATGNCNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 480
 QY 161 ArgAlaSerIleGlnPheAspLeuValLysAsnGlyLysSerIleAlaSerPheGln 180
 Db 481 MGNCGNMSNTNTCATTTTGATTTGTTTNTNARAAAGGNGARGNARMSATATGCMMSNTTYYTCAR 540
 QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200
 Db 541 TTYTTGGNGNTGGCCNAARCCNMSNTNTNMGNGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 600
 QY 201 ProGluAspGlnValTyrValGlnValGlyAlaGlyAspTyrIleGlyIleTyrAlaSer 220
 Db 601 CCNGARGAYACATGTGGTNCARGTNGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 660
 QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheLysSerPro 240
 Db 661 ATHAARACGAYWMACTTYSNCGNNTTYTNTNTATYWSNGAYTGGCAVMSMNSNCGN 720
 QY 241 ValPheAla 243
 Db 721 GTTNTYGCN 729
 RESULT 14
 APO01557 182429 bp DNA linear HTG 03-NOV-2000
 LOCUS Homo sapiens chromosome 11 clone RP11-680A7 map 11q23, WORKING
 DEFINITION DRAFT SEQUENCE, 21 unordered pieces.
 ACCESSION APO01557
 VERSION APO01557.3 GI:11094164
 KEYWORDS HTG, HTGS, PHASE1, HTGS, DRAFT.
 SOURCE Homo sapiens DNA, clone:RP11-680A7.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 182429)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
 Homo sapiens 182,429 genomic DNA of 11q23
 Published Only in Database (2000)
 2 (bases 1 to 182429)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
 Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 On Nov 3, 2000 this sequence version replaced gi:8117391.
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center(GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center project name: HumDraft11
 Center clone name: RP11-680A7
 ----- Summary Statistics
 Sequencing vector: PCR products: 100% of reads
 Chemistry: dye-terminator ET-amersham: 100% of reads
 Assembly program: Phrap, version 0.990329
 Consensus quality: 175397 bases at least Q40
 Consensus quality: 178555 bases at least Q30
 Consensus quality: 179768 bases at least Q20
 Insert size: 180429; sum-of-contigs
 Quality coverage: 9.01x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
 21 contigs. The true order of the pieces is not known and the
 order in this sequence record is arbitrary. Gaps between the

*	1	30107:	contlg of	30107 bp	in	length
*	30108	30207:	gap of	100 bp		
*	30208	54357:	contlg of	24150 bp	in	length
*	54458	54457:	gap of	100 bp		
*	54458	69839:	contlg of	15382 bp	in	length
*	69840	69939:	gap of	100 bp		
*	69940	84048:	contlg of	14109 bp	in	length
*	84049	84148:	gap of	100 bp		
*	84149	95177:	contlg of	11029 bp	in	length
*	95178	95277:	gap of	100 bp		
*	95278	107653:	contlg of	12486 bp	in	length
*	107764	107863:	gap of	100 bp		
*	107864	119057:	contlg of	11194 bp	in	length
*	119058	119157:	gap of	100 bp		
*	119158	128134:	contlg of	8977 bp	in	length
*	128135	128234:	gap of	100 bp		
*	128235	136903:	contlg of	8669 bp	in	length
*	136904	137003:	gap of	100 bp		
*	137004	145887:	contlg of	8884 bp	in	length
*	145888	145987:	gap of	100 bp		
*	145988	153199:	contlg of	7212 bp	in	length
*	153200	153299:	gap of	100 bp		
*	153300	159555:	contlg of	6266 bp	in	length
*	159566	159665:	gap of	100 bp		
*	159666	163580:	contlg of	3915 bp	in	length
*	163581	163680:	gap of	100 bp		
*	163681	165152:	contlg of	1472 bp	in	length
*	165153	165252:	gap of	100 bp		
*	165253	166901:	contlg of	1649 bp	in	length
*	166902	167001:	gap of	100 bp		
*	167002	170460:	contlg of	3459 bp	in	length
*	170461	170560:	gap of	100 bp		
*	170561	172761:	contlg of	2201 bp	in	length
*	172762	172861:	gap of	100 bp		
*	172862	175605:	contlg of	2744 bp	in	length
*	175606	175705:	gap of	100 bp		
*	175706	178308:	contlg of	2603 bp	in	length
*	178309	178408:	gap of	100 bp		
*	178409	180918:	contlg of	2510 bp	in	length
*	180919	181018:	gap of	100 bp		

70 -----ArgPro-----GlyLeuProGlyProArgGlyAspProGly 81

Db 107983 CTCACACCCGCGCCGCTTACCCGCGAGACTGCGGAGACCTCGAGGGAGCCCGG 108042
 Oy 82 ProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerValPro 101
 Db 108043 CCGCAGAGAGAGCGCGGAGCCCGCGGCGCCACCGGCGCTCGCGGGAGAGCTGGTGCTT 108102
 Oy 102 ProArgSerAlaPheSerAlaLysArgSerGluSerArgValProProProSerAspAla 121
 Db 108103 CCGGACATCCGCTTACGCGCCAGAGCGCTCCGAGAGCCGGGTGCTCCCGCGCTACAGCA 108162
 Oy 122 ProLeuProPheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThrGly 141
 Db 108163 CCGTGGCCCTTCGAGCGCGGTGCTGCGTGAACGGCA-GGACCATTTACGAGCGCTCACCGCG 108221
 Oy 142 LysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyrArg 161
 Db 108222 AAGTTCACCTGCGAGGTGCTGCGGTCTACTACTTCCGCGCTCAGTCCAGCCGCTACGCG 108281
 Oy 162 AlaSerLeuGlnPheAspLeuValLysAsnGlyGluSerIleAlaSerPhePheGlnPhe 181
 Db 108282 GCCACCTGCAAGTTGATCTGGTGAAGAATGCGCAATGCCTCTTCTTCCAGTTT 108341
 Oy 182 PheGlyGlyTyrProGlyProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluPro 201
 Db 108342 TTTGGGGGGTGGCCCAACCCAGCTCTGCTGCGGGGGGCGCATGTGAGGCTGAGGCT 108401
 Oy 202 GluAspGlnValTyrPheValGlnValGlyAlaGlyAspTyrIleGlyIleTyrAlaSerIle 221
 Db 108402 GAGGACCAAGTGTGGGTGAGGTGGGTGGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 108461
 Oy 222 LysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheIleSerSerProVal 241
 Db 108462 AAGACAGACAGACACCTTCCGAGTTTCTGGTGTACTGCTGCTGCTGCTGCTGCTGCTGCT 108521
 Oy 242 PheAla 243
 Db 108522 TTTGCT 108527

RESULT 15
 AC107174/c
 LOCUS Rattus norvegicus clone CH230-215D1, *** SEQUENCING IN PROGRESS
 DEFINITION *** 78 unordered pieces.
 AC107174
 AC107174.3 GI:21737488
 HTG: HTGS.PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 150653)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
 Bouck,J., Benton,J., Blumage,K., Blankenburg,K., Bonini,D.,
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
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 Scherer,S., Scott,G., Shen,H., Shoohart,N., Sisson,I.,
 Sodergren,E., Sonaite,T., Sparks,A., Stanley,H., Stone,H.,
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 Taneey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
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 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,
 Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 150653)
 Worley,K.C.
 Direct Submission
 Submitted (16-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 150653)
 Worley,K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 12, 2002 this sequence version replaced gi:18702083.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFFT
 Center clone name: CH230-215D1
 ----- Summary Statistics
 Sequencing vector: Plasmid.
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap, version 0.990329
 Consensus quality: 86959 bases at least Q40
 Consensus quality: 95630 bases at least Q30
 Consensus quality: 102140 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drat_data.html).
 * NOTE: This is a "working draft" sequence. It currently
 * consists of 78 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 1222 1221: contig of 1221 bp in length
 * 1322 1321: gap of unknown length
 * 1322 1322: gap of unknown length
 * 2838 2837: gap of 1516 bp in length
 * 2838 2838: gap of unknown length
 * 2938 2937: gap of 1103 bp in length
 * 4041 4040: contig of 1103 bp in length
 * 4141 4140: gap of unknown length
 * 5496 5495: contig of 1356 bp in length
 * 5497 5496: gap of unknown length
 * 5597 5596: gap of unknown length
 * 7003 7002: contig of 1406 bp in length
 * 7103 7102: gap of unknown length
 * 8483 8482: contig of 1380 bp in length
 * 8583 8582: gap of unknown length
 * 9994 9994: contig of 1412 bp in length

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 16:07:46 ; Search time 266 Seconds

(without alignments)
2057.277 Million cell updates/sec

Title: US-09-944-944-42

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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
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24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	100.0	1347	20	AAK24684	Human adipocyte-sp
2	1325	100.0	1377	20	AAK87258	CDNA clone encodin
3	1325	100.0	1377	20	AAK80052	Human PRO344 nucle
4	1325	100.0	1377	21	AAK58626	Human PRO344 prote
5	1325	100.0	1377	21	AAAD01241	Human PRO344 prote
6	1325	100.0	1377	21	AAAA46907	CDNA encoding nove
7	1325	100.0	1377	21	AAAA49560	Human PRO344 CDNA
8	1325	100.0	1377	22	AAK21424	Human CDNA sequenc
9	1295	97.7	728	22	AAK44971	Human TANGO 253 OR
10	1295	97.7	728	22	AAK44995	Human secreted pro
11	1295	97.7	728	22	AAK44997	Human secreted pro
12	1295	97.7	1338	22	AAK44970	Human TANGO 253 co
13	1295	97.7	1338	22	AAK44998	Human secreted pro
14	1293	97.6	728	22	AAK44994	Human secreted pro
15	1293	97.6	1338	22	AAK45001	Human secreted pro
16	1291	97.4	728	22	AAK44996	Human secreted pro
17	1291	97.4	1338	22	AAK44999	Human secreted pro
18	1291	97.4	1338	22	AAK45000	Human secreted pro
19	1271	95.9	1001	21	AAK61745	CDNA encoding rat
20	1271	95.9	1001	22	AAK99678	SKIN cell CDNA, SE
21	1271	95.9	1001	24	ABL34830	Rat CDNA isolated
22	1271	95.9	1015	21	AAK61635	CDNA encoding rat
23	1271	95.9	1015	22	AAK99568	SKIN cell CDNA, SE
24	1271	95.9	1015	24	ABL34720	Rat CDNA isolated
25	1258	94.9	729	22	AAK44973	Murine TANGO 253 O
26	1258	94.9	1263	22	AAK44972	Murine secreted pr
27	1256	94.8	729	22	AAK45001	Murine secreted pr
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29	1254	94.6	729	22	AAK45038	Murine secreted pr
30	1254	94.6	729	22	AAK45039	Murine secreted pr
31	1254	94.6	729	22	AAK45040	Murine secreted pr
32	1254	94.6	1263	22	AAK45006	Murine secreted pr
33	1254	94.6	1263	22	AAK45007	Murine secreted pr
34	1254	94.6	1263	22	AAK45008	Murine secreted pr
35	1183	89.3	1082	23	AAK76911	DNA encoding novel
36	1072	80.9	729	20	AAK24685	Degenerate DNA enc
37	1048	79.1	3248	24	AAK39624	Human secreted pro
38	659	49.7	764	24	AAK62228	CDNA sequence #15
39	535.5	40.4	601	22	AAK44991	Rat TANGO 253 codi
40	478	36.1	536	23	AAK56910	DNA encoding novel
41	449.5	33.9	678	24	ABL57719	Human sbg103026C1
42	442.5	33.4	1002	24	ABL57718	Human sbg103026C1
43	436	32.9	1276	18	AAK51048	Murine adipocyte c
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ALIGNMENTS

RESULT 1

AAK24684

AAK24684 standard: CDNA: 1347 BP.

AAK24684; 21-JUN-1999 (first entry)

Human adipocyte-specific protein zsig39 CDNA.

Adipocyte-specific protein; zsig39; human; fatty acid metabolism;

energy balance; nutrition; antimicrobial; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 198..929

FT CDS 198..929

FT CDS 198..929

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QY	121	ALAProLeuPProPheASPARGVALLeuValAsnGLuGLuIHisTyrTRASPALAVALThr	140
Db	587	GCACCCCTTGCCCTTCGACCGCGCTGCTGGTGAACGACAGGAGCATTCACACGCGCTCAC	646
QY	141	GLYTPSPHERHRCYSGINVALPRoGLYVALTYRTYRPhEALAVAlHISAlAThrVALTYR	160
Db	647	GGCAAGTTCACCTCGCAGGTGCGTGGGGTCTACTACTTCGCGCTCATGCCACCGCTTAC	706
QY	161	ARGVALSERLEuGINPheASPLeuVALYLSANGLYGLUSERLLEALASERPhEPheGIN	180
Db	707	CGGGCGACCCGTCAGATTGTGATCTGGTGAAGAATGGCGAATTCATTGCCCTTCTTCCAG	766
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QY	221	ILELYSTRASPSErThrPhESerGLYPheLeuVALTYRSerASPTrpHISerSerPro	240
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QY	241	VALPheALa 243	
Db	947	GTCTTTTGGCT 955	

DE	Human secreted protein related coding sequence SEQ ID NO: 80.
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KW	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KM	INTERCEPT 258; coronary disorder; olfactory disorder;
KW	neurological disorder; pulmonary disorder; immunological disorder;
KW	developmental disorder; kidney disorder; ss.
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OS	Homo sapiens.
XX	
FN	WO20078608-A1.
XX	
PD	28-DEC-2000.
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PF	19-JUN-2000; 2000WO-US16883.
XX	
PR	18-JUN-1999; 99US-0336536.
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PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Leibyl KR, McKay C, Bossone S;
DR	WPI; 2001-050109/06.
XX	
PT	New nucleic acids for treating diseases and disorders, e.g.
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT	sclerosis and asthma -
XX	
PS	Disclosure; Page 260; 332pp; English.
XX	
CC	The present invention provides the protein and coding sequences of the
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC	coronary, pulmonary, olfactory, immunological, neurological,
CC	developmental and kidney disorders.
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Dd	240 GGCGCCGAGAGAGCGCGGACCCCGGGGGCCACCGGGCCCTGCGGGAGTGTCTCGGTG 299
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Dd	300 CCTCCGGGATCCGCTTCAGCGCAAAGCGCTCGAAGACCGGGTGGCTCCGCGGCTGTGAC 355
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Qy	221	IleGlyThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheSerSerPro	240
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DE		Human secreted protein related coding sequence SEQ ID NO: 109.	
XX			
XX		Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;	
KW		INTERCEPT 258; coronary disorder; olfactory disorder;	
KW		neurological disorder; pulmonary disorder; immunological disorder;	
RV		developmental disorder; kidney disorder; ss.	
XX			
XX		Homo sapiens.	
CS			
XX		WO200078808-A1.	
XX			
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PF		19-JUN-2000; 2000MO-US16683.	
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PR		18-JUN-1999; 99US-0336536.	
XX			
PA		(MILL-) MILLENNIUM PHARM INC.	
XX			
XX		Leiby KR, McKay C, Bossone S;	
XX			
DR		WPI; 2001-050109/06.	
XX			
PT		New nucleic acids for treating diseases and disorders, e.g.	
PT		atherosclerosis, infection, autoimmune diseases, obesity, ear	
PT		disorders, brain disorders, tumors, diabetes, arthritis, multiple	
PT		sclerosis and asthma -	
XX			
XX			
XX		Disclosure; Page 274-275; 332pp; English.	
XX			
CC		The present invention provides the protein and coding sequences of the	
CC		human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,	
CC		TANGO 281 and INTERCEPT 258. These are useful in the treatment of	
CC		coronary, pulmonary, olfactory, immunological, neurological,	
CC		developmental and kidney disorders.	
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RESULT 7
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: Sequence 8, Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leib'y, K.
: APPLICANT: McKay, C.
: APPLICANT: BOSSONE, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336,536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 1263
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-336-536-8

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Alignment Scores:	
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Percent Similarity:	96.308
Best Local Similarity:	93.838
Query Match:	94.94%
DB:	4
Gaps:	0
Length:	1265
Matches:	228
Conservative:	6
Mismatches:	9
Indels:	0
Gaps:	0

US-09-944-944-42 (1-243) x US-09-336-536-8 (1-1263)

[illegible][illegible]

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? RESULT 8
? US-09-140-804-10
? Sequence 10, Application US/09140804
? Patent No. 6197930
? GENERAL INFORMATION:
? APPLICANT: Shepard, Paul O.
? APPLICANT: Humes, Jacqueline M.
? TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
? FILE REFERENCE: 97-49
? CURRENT APPLICATION NUMBER: US/09/140,804
? CURRENT FILING DATE: 1998-08-26
? EARLIER APPLICATION NUMBER: 60/056,983
? EARLIER FILING DATE: 1997-08-26
? NUMBER OF SEQ ID NOS: 47
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 10
? LENGTH: 729
? TYPE: DNA

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; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39
; OTHER INFORMATION: polypeptide of SEQ ID NO:2.

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US-09-140-804-10

Alignment scores:	
Pred. No.:	9.38e-70
Score:	1072.00
Percent Similarity:	78.60%
Best Local Similarity:	78.60%
Query Match:	80.91%
DB:	4
Length:	729
Matches:	191
Conservative:	0
Mismatches:	52
Indels:	0
Gaps:	0

US-09-944-944-42 (1-243) x US-09-140-804-10 (1-729)


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QY 57 gYlaLaProglYalaProglYluYsGlyGluGlylaYargProglYleuProglYPro 76
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Db 250 -----GGCACCCCTGGTGAGAGAGGTGAGAAAGAGATCCAGGCTTATGTCCT 300
QY 77 ArgGlyasp-----ProglYProaYgLYlaLaGly 87
    ||| ||||| ||||| ||||| |||||
Db 301 AAGGAGACATCGGTGAACCGAGATACCCGGGGCTGAAGGTCCCGAGCTTCCGGGA 360
QY 88 ProLaGlyProthrglyProLaGlyGluYsSerValProProaYgSerAlaPheSer 107
    ||| ||||| ||||| ||||| |||||
Db 361 ATCCAAAGCAGGAAGAGAACCTGGAGAGGTGCTATGATACCGCTGAGCTTACGT 420
QY 108 AlaLysArgSerGlySerArgValProProProSerAlaProleuProPheAspArg 127
    ||| ||||| ||||| ||||| |||||
Db 421 GTG---GGATTGGAGACTTACGTACTATCCCC---AACATGCCCATTCGCTTACCAAG 474
QY 128 ValLeuValasnGluGlyHisLysTyraSPalaValThrGlyLysPhehCysGlnVal 147
    ||| ||||| ||||| ||||| |||||
Db 475 ATCTTACATCATCGACAAACCACTATGATGGCTCCACTGTAATTCACACTGCAACATT 534
QY 148 ProGlyValTyrrPheAlaValAlaThrValTyraGlyLysSerLeuGlnPheasp 167
    ||| ||||| ||||| ||||| |||||
Db 535 CCTGGGCTGATCTTCTGCTTACCACATCATCTATGAGAAGATGTAAAGTCAAGC 594
QY 168 LeuValLysasnGlyLysSer---IleAlaSerPhehGlnPhehGlyLysTrpPro 186
    ||| ||||| ||||| ||||| |||||
Db 595 CTCTTCAAGAGAGCAAGAGCTATGCTCTTCACTATGATGACAGCAAGAAATATATGTG 654
QY 187 LysProLaSerLeuSerGlyLysAlaMetValArgLeuGluProGluAspGlnValTrp 206
    ||| ||||| ||||| ||||| |||||
Db 655 GACCAGGCC-----TCCGGCTCTGCTCTCATCTGAGGGGCGACCAAGTCTGG 708
QY 207 ValGlnVal---GlyValGlyAspTyrrIleGlyIleTyraLysSerIleLysThrAspSer 225
    ||| ||||| ||||| ||||| |||||
Db 709 CTCAGGTGATGGGAGAGAGACGTAATGAGACTGATGCTGATATGACAATGACTCC 768
QY 226 ThrPheSerGlyPheLeuValTyrrSerAspTrpHisSerProVal 241
    ||| ||||| ||||| ||||| |||||
Db 769 ACCTTCAAGAGCTTCTTCTTACCATGACACCAATGATCACCACATA 816

RESULT 12
US-09-140-804-9
: Sequence 9, Application US/09140804
: Patent No. 6197930
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Humes, Jacqueline M.
: TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
: FILE REFERENCE: 97-49
: CURRENT APPLICATION NUMBER: US/09/140, 804
: CURRENT FILING DATE: 1998-08-26
: EARLIER APPLICATION NUMBER: 60/056, 983
: EARLIER FILING DATE: 1997-08-26
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-140-804-9

Alignment Scores:
Pred. No.: 1,62e-22 Length: 4517
Score: 432.50 Matches: 111
Percent Similarity: 50.72% Conservative: 29
Best local Similarity: 40.22% Mismatches: 75
Query Match: 32.64% Indels: 61
DB: 4 Gaps: 11

US-09-944-944-42 (1-243) x US-09-140-804-9 (1-4517)
QY 1 MetArgProLeuLeu-----ValLeuLeuLeuLeuGlyLeuAlaLaGlySerPro 17

```

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Db 21 CTCAGAGATGCTGTGCTGGAGAGCTGTCTTACTGCTATATAGCTTG----- 65
QY 18 ProLeuAspAspAnLysIleProSerLeuYsProglYHis----- 31
Db 66 -----CCCGGCAATGACACAGAAACCAAGACT 92
QY 32 -----ProGly-----LeuProGly 36
    |||||
Db 93 CAAGGGCCCGGAGTCTGCTTCCCTGCGCAAGGGGGCTGCACAGGTGGATGGCGGGC 152
QY 37 ThrProGlyHisHisGlySerGlnGlyLeuProGlyLysArgGlyAlaArgAsp 56
    ||||| ||||| ||||| ||||| |||||
Db 153 ATCCAGGCGCATCCGGCCATATGAGGGCCCGCCAGCCGCTGATGGCAAGAT----- 203
QY 57 gYlaLaProglYalaProglYluYsGlyGluGlylaYargProglYleuProglYPro 76
    ||| ||||| ||||| ||||| |||||
Db 204 -----GGCACCCCTGGTGAGAGAGGTGAGAAAGAGATCCAGGCTTATGTCCT 254
QY 77 ArgGlyasp-----ProglYProaYgLYlaLaGly 87
    ||| ||||| ||||| ||||| |||||
Db 255 AAGGAGACATCGGTGAACCGAGATACCCGGGGCTGAAGGTCCCGAGGCTTCCGGGA 314
QY 88 ProLaGlyProthrglyProLaGlyGluYsSerValProProaYgSerAlaPheSer 107
    ||| ||||| ||||| ||||| |||||
Db 315 ATCCAAAGCAGGAAGAGAACCTGGAGAGGTGCTATGATACCCCTGACATTCAGT 374
QY 108 AlaLysArgSerGlySerArgValProProProSerAlaProleuProPheAspArg 127
    ||| ||||| ||||| ||||| |||||
Db 375 GTG---GGATTGGAGACTTACGTACTATCCCC---AACATGCCCATTCGCTTACCAAG 428
QY 128 ValLeuValasnGluGlyHisLysTyraSPalaValThrGlyLysPhehCysGlnVal 147
    ||| ||||| ||||| ||||| |||||
Db 429 ATCTTACATCATCGACAAACCACTATGATGGCTCCACTGTAATTCACACTGCAACATT 488
QY 148 ProGlyValTyrrPheAlaValAlaThrValTyraGlyLysSerLeuGlnPheasp 167
    ||| ||||| ||||| ||||| |||||
Db 489 CCTGGGCTGATCTTCTGCTTACCACATCATCTATGAGAAGATGTAAAGTCAAGC 548
QY 168 LeuValLysasnGlyLysSer---IleAlaSerPhehGlnPhehGlyLysTrpPro 186
    ||| ||||| ||||| ||||| |||||
Db 549 CTCTTCAAGAGAGCAAGAGCTATGCTCTTCACTATGATGACAGCAAGAAATATATGTG 608
QY 187 LysProLaSerLeuSerGlyLysAlaMetValArgLeuGluProGluAspGlnValTrp 206
    ||| ||||| ||||| ||||| |||||
Db 609 GACCAGGCC-----TCCGGCTCTGCTCTCATCTGAGGGGCGACCAAGTCTGG 662
QY 207 ValGlnVal---GlyValGlyAspTyrrIleGlyIleTyraLysSerIleLysThrAspSer 225
    ||| ||||| ||||| ||||| |||||
Db 663 CTCAGGTGATGGGAGAGAGACGTAATGAGACTGATGCTGATATGACAATGACTCC 722
QY 226 ThrPheSerGlyPheLeuValTyrrSerAspTrpHisSerProVal 241
    ||| ||||| ||||| ||||| |||||
Db 723 ACCTTCAAGAGCTTCTTCTTACCATGACACCAATGATCACCACATA 770

RESULT 13
US-09-188-930-217
: Sequence 217, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000,1011c1
: CURRENT APPLICATION NUMBER: US/09/188, 930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 217

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EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 1333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (485)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (486)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (493)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (496)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (587)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (633)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1330)
OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-51

Alignment Scores:
Pred. No.: 1,43e-18 Length: 1333
Score: 369.50 Matches: 97
Percent Similarity: 50.40% Conservative: 28
Best Local Similarity: 39.11% Mismatches: 83
Query Match: 27.89% Indels: 40
DB: Gaps: 7

US-09-944-944-42 (1-243) x US-09-227-357-51 (1-1333)

QY 24 IlleProSerLeu-----CysProGlyHisProGlyLeuProGlyThrProGlyHis 41
DB 212 ATTCTGCTGCTGCTGCACTCCAGGCCCCCTGAGCAAAATGTTCCCTGGGCCCAT 271
QY 42 GlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyArgAspGly 59
DB 272 GGTGCGATCGGCGCTTCAGAGAGATGTAGAGACGGAGAGAGAGAGAGAGAGTGA 331
QY 60 -----GlyAlaProGlyGlyGly 66
DB 332 AAGGAGCTGACAGTTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 391
QY 67 GlnGlyArgProGlyLeuProGlyProArgGlyAspProGlyProArgGlyAla 86
DB 392 GACCAAGGAGAGACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 451
QY 87 GlyProAlaGlyProThrGlyProAlaGlyGlu----- 97
DB 452 GGTCCATTGTCTCTCTGAGACCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 511
QY 98 -----Cys-----SerValProProArgSerAlaPheSerAlaValArgSer 111
DB 512 CTTGAGATTGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 571
QY 112 GluSerArgValProProProSerAspAlaProLeuProPheAspValLeuVal-As 131

DB 572 ACCAGTAC-----CCAGANMAAAGACTACCTATTATTATTAAAGAGTCTCTCCA 625
QY 131 nGlnGlnGlyHisThrAspAlaValThr-GlyLysPheThrCysGlnValPro-GlyVal 150
DB 626 CGAGGAGNAGCAGTACACCTCGCCACAGGAGAGTTCATCTGCTTCTCCAGGAGATC 685
QY 151 TyrTrpPheAlaValHisAlaThrValTyrArgAlaSerLeuGlnPheAspLeuVallys 170
DB 686 TATTACTTTCTTATGATATACATATGCTATTAAGCATCTGCAATCGCATGCTACAC 745
QY 171 AsnGlyGluSerIleAlaSerPhePheGlnPheGlyGlyTyrProLysProAlaSer 190
DB 746 AATGGCAATACCGGATTAAGACCTTCGAGCCCAACAGAGAAACATGATGGCT--- 802
QY 191 LeuSerGlyGlyAlaMetValArgLeuGluProGlyLysGlnValTyrPValGlnValGly 210
DB 803 ---TCGGGGTCCACAGTCATCTATCTGACGACAGAGATGAGTCTGGTGGAGATTTC 859
QY 211 ValGlyAspTyrIleGlyIleTyrAlaSerIlelys---ThrAspSerThrPheSerGly 229
DB 860 TTCACAGACCAAGATGCGCTCTCTCAGACCCAGGTGGGAGACAGACTTATCTCCGG 919
QY 230 PheLeuValTyrSerAsp 235
DB 920 TTCTCTTATACGTTGAC 937

RESULT 15

US-08-383-744-1
Sequence 1, Application US/08383744
Patent No. 5702948

GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
TITLE OF INVENTION: Saccular collagen and Compositions
TITLE OF INVENTION: and
METHOD OF INVENTION: Methods for Making and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5702948rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,744
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 331..1602

US-08-383-744-1

Alignment Scores:	
Pred. No.:	4,53e-17
Score:	351.00
Percent Similarity:	46.488
Best Local Similarity:	37.508
Query Match:	26.498
DB:	1
Gaps:	6

US-09-944-944-42 (1-243) X US-08-383-744-1 (1-1839)

OY		15	GlySerProPheLeuAspAsnLys-----IleProSerLeuCysProGlyHisPro	32
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OY		33	GlyLeuProGlyThrProGlyHisHisGlySerGlnGlyLeuProGlyArg-----Asp	50
Db		859	GGGTAGTCGTGGACAAGGGCTGTGAAGGTGAACAGGGGCTTAAAGGGAGATGTTTACAA	918
OY		51	GlyArgAspGlyArgAspGlyAlaProGlyAlaProGlyIleGlyGlyGlyGlyArg	70
Db		919	GGCAGAGAAGGTGAGCGGGCCCCCTGGTGTGAGAGGTGAGATGGATTGAATGGAAC	978
OY		71	ProGlyLeuProGlyProArgGlyAspProGlyPro-----	82
Db		979	GATGGTGTAAGGAGAGAGAGAGGGGACCAGGCCTCTTGAGAGGAAGGGGCACTGGT	1038
OY		82	-----	82
Db		1039	GCCAGAGGCCCCCAGGTCCTCCAAGAGGAGGGGCAATGGCAGGGTTGAGGGGGAGAG	1098
OY		83	-----ArgGlyIleAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal	100
Db		1099	GGCGTTAAAGGTGTGCGTGGGCCAAGGGGCCCTAAAGGCCCAACAGGTGAAGTGTGAG	1158
OY		101	ProProArgSerAlaPheSerAlaLysArgSerGluSerArgValProProProSerAsp	120
Db		1159	CAGATTGGCTCTGCTTTCAGTAGTGGCGCTGTCCCGAGCAATCTTCCTCCGCCCCAGC	1218
OY		121	AlaProLeuProPheAspArgValIleuValasnGlnGlyHisIleThyAspAlaValThr	140
Db		1219	CTGCCTTGAAAGTTGATAAGGTGTTTTACAACGGGAGGGGCGACCTGGAGCCAAACTC	1278
OY		141	GlyIysrTherTrcysGlnValProGlyValTyrrPhelaValaHisAlaThrValTyrr	160
Db		1279	AACAAATTCAAATGCACCTACCCGCGGGGTCACTATCACTTCACTCACATCACCGCTGGC	1338
OY		161	ArgAlaSerLeuGlnPheAspLeuValLysasnLys---GluSerIleAlaSerPhePhe	179
Db		1339	AACAGCGCTGTGCTGCTGCCCTATGCTTATGGGTGAGCGAAGCTGAGGACCCGGAT	1398
OY		180	GlnPhePheGlyGlyTrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeu	199
Db		1399	TCTCTGTACGGCCAGACATCGACNACGGC-----TCCAACCTCCGACACTGCTGCATCTG	1452
OY		200	GlnProGluAspGlnValTrpValGlnValGlyValGlyAspTyrrIleGlyIleTyrrala	219
Db		1453	ACTGACCGGTGACCGGTGCTGGCTGGAACA---CTGAGAGACTGGAATGGAGGT-TACTCC	1508
OY		220	SerIleTythrAspSerThrPheSerGlyPheLeuValTyrrSerAsp	235
Db		1509	AGCGATGAGATGACACACTTCTCTGGCTTCTTGTGATCCCTGTAC	1556

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Job time : 68 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 17:37:33 ; Search time 192 Seconds

(without alignments)
1857.213 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-THR MIN=0-ALIGN=15-MODE=LOCAL-OUTFMT=ptc-NORM=ext-HEAPSIZE=500-MINLEN=0
-MAXLEN=2000000000-USER=US09944944-@CGN_1_1_156-@runat_13062003_150050_24368
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-FGAPOP=6-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database: Published.Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	1325	100.0	1377	9	US-09-944-413-41		Sequence 41, Appl
2	1325	100.0	1377	9	US-09-944-403-41		Sequence 41, Appl
3	1325	100.0	1377	9	US-09-944-896-41		Sequence 41, Appl
4	1325	100.0	1377	9	US-09-944-944-41		Sequence 41, Appl

5	1325	100.0	1377	9	US-09-944-907-41		Sequence 41, Appl
6	1325	100.0	1377	9	US-09-944-929-41		Sequence 41, Appl
7	1325	100.0	1377	9	US-10-028-072-361		Sequence 361, App
8	1325	100.0	1377	9	US-10-121-049-361		Sequence 361, App
9	1325	100.0	1377	9	US-10-123-904-361		Sequence 361, App
10	1325	100.0	1377	9	US-10-140-470-361		Sequence 361, App
11	1325	100.0	1377	9	US-10-175-746-361		Sequence 361, App
12	1325	100.0	1377	9	US-10-176-918-361		Sequence 361, App
13	1325	100.0	1377	9	US-10-176-921-361		Sequence 361, App
14	1325	100.0	1377	9	US-10-137-865-361		Sequence 361, App
15	1325	100.0	1377	9	US-10-140-474-361		Sequence 361, App
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17	1325	100.0	1377	9	US-10-142-431-361		Sequence 361, App
18	1325	100.0	1377	9	US-10-140-002-361		Sequence 361, App
19	1325	100.0	1377	9	US-10-142-419-361		Sequence 361, App
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21	1325	100.0	1377	9	US-10-142-423-361		Sequence 361, App
22	1325	100.0	1377	9	US-10-121-050-361		Sequence 361, App
23	1325	100.0	1377	9	US-10-141-755-361		Sequence 361, App
24	1325	100.0	1377	9	US-10-143-032-361		Sequence 361, App
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31	1325	100.0	1377	9	US-10-123-292-361		Sequence 361, App
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35	1325	100.0	1377	9	US-10-140-925-361		Sequence 361, App
36	1325	100.0	1377	9	US-10-160-498-361		Sequence 361, App
37	1325	100.0	1377	9	US-09-944-884-41		Sequence 41, Appl
38	1325	100.0	1377	9	US-10-121-041-361		Sequence 361, App
39	1325	100.0	1377	9	US-10-121-043-361		Sequence 361, App
40	1325	100.0	1377	9	US-10-121-047-361		Sequence 361, App
41	1325	100.0	1377	9	US-10-123-215-361		Sequence 361, App
42	1325	100.0	1377	9	US-10-123-908-361		Sequence 361, App
43	1325	100.0	1377	9	US-10-123-908-361		Sequence 361, App
44	1325	100.0	1377	9	US-10-123-909-361		Sequence 361, App
45	1325	100.0	1377	9	US-10-123-910-361		Sequence 361, App

ALIGNMENTS

RESULT 1
US-09-944-413-41
; Sequence 41, Application US/09944413
; Patent No. US20020156004A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25

1	PRIOR APPLICATION NUMBER: 60/067,411	PRIOR FILING DATE: December 3, 1997	PRIOR APPLICATION NUMBER: 60/069,334	PRIOR FILING DATE: December 11, 1997	PRIOR APPLICATION NUMBER: 60/069,335	PRIOR FILING DATE: December 11, 1997	PRIOR APPLICATION NUMBER: 60/069,278	PRIOR FILING DATE: December 11, 1997	PRIOR APPLICATION NUMBER: 60/069,425	PRIOR FILING DATE: December 12, 1997	PRIOR APPLICATION NUMBER: 60/069,696	PRIOR FILING DATE: December 16, 1997	PRIOR APPLICATION NUMBER: 60/069,694	PRIOR FILING DATE: December 16, 1997	PRIOR APPLICATION NUMBER: 60/069,702	PRIOR FILING DATE: December 16, 1997	PRIOR APPLICATION NUMBER: 60/069,870	PRIOR FILING DATE: December 17, 1997	PRIOR APPLICATION NUMBER: 60/069,873	PRIOR FILING DATE: December 17, 1997	PRIOR APPLICATION NUMBER: 60/068,017	PRIOR FILING DATE: December 18, 1997	PRIOR APPLICATION NUMBER: 60/070,440	PRIOR FILING DATE: January 5, 1998	PRIOR APPLICATION NUMBER: 60/074,086	PRIOR FILING DATE: February 9, 1998	PRIOR APPLICATION NUMBER: 60/074,092	PRIOR FILING DATE: February 9, 1998	PRIOR APPLICATION NUMBER: 60/075,945	PRIOR FILING DATE: February 25, 1998	PRIOR APPLICATION NUMBER: 60/112,850	PRIOR FILING DATE: December 16, 1998	PRIOR APPLICATION NUMBER: 60/113,296	PRIOR FILING DATE: December 22, 1998	PRIOR APPLICATION NUMBER: 60/146,222	PRIOR FILING DATE: July 28, 1999	PRIOR APPLICATION NUMBER: PCT/US98/19330	PRIOR FILING DATE: September 16, 1998	PRIOR APPLICATION NUMBER: PCT/US98/25108	PRIOR FILING DATE: December 1, 1998	PRIOR APPLICATION NUMBER: 09/216,021	PRIOR FILING DATE: December 16, 1998	PRIOR APPLICATION NUMBER: 09/218,517	PRIOR FILING DATE: December 22, 1998	PRIOR APPLICATION NUMBER: 09/254,311	PRIOR FILING DATE: March 3, 1999	PRIOR APPLICATION NUMBER: PCT/US99/12252	PRIOR FILING DATE: June 22, 1999	PRIOR APPLICATION NUMBER: PCT/US99/21090	PRIOR FILING DATE: September 15, 1999	PRIOR APPLICATION NUMBER: PCT/US99/28409	PRIOR FILING DATE: No. US200201569041amber 30, 1999	PRIOR FILING DATE: No. US200201569041amber 30, 1999	PRIOR APPLICATION NUMBER: PCT/US99/28301	PRIOR FILING DATE: December 1, 1999	PRIOR APPLICATION NUMBER: PCT/US99/30095	PRIOR FILING DATE: December 16, 1999	PRIOR APPLICATION NUMBER: PCT/US00/03565	PRIOR FILING DATE: February 11, 2000	PRIOR APPLICATION NUMBER: PCT/US00/04414	PRIOR FILING DATE: February 22, 2000	PRIOR APPLICATION NUMBER: PCT/US00/05841	PRIOR FILING DATE: March 2, 2000	PRIOR APPLICATION NUMBER: PCT/US00/08439	PRIOR FILING DATE: March 30, 2000	PRIOR APPLICATION NUMBER: PCT/US00/14042	PRIOR FILING DATE: May 22, 2000	PRIOR APPLICATION NUMBER: PCT/US00/20710	PRIOR FILING DATE: July 28, 2000	PRIOR APPLICATION NUMBER: PCT/US00/32678	PRIOR FILING DATE: December 1, 2000	PRIOR APPLICATION NUMBER: PCT/US01/06520
---	--------------------------------------	-------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	------------------------------------	--------------------------------------	-------------------------------------	--------------------------------------	-------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	----------------------------------	--	---------------------------------------	--	-------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	--------------------------------------	----------------------------------	--	----------------------------------	--	---------------------------------------	--	---	---	--	-------------------------------------	--	--------------------------------------	--	--------------------------------------	--	--------------------------------------	--	----------------------------------	--	-----------------------------------	--	---------------------------------	--	----------------------------------	--	-------------------------------------	--

	PRIOR FILING DATE: February 28, 2001
	: NUMBER OF SEQ ID NOS: 120
	: SEQ ID NO 41
	: LENGTH: 1377
	: TYPE: DNA
	: ORGANISM: Homo Sapien
	US-09-944-413-41
	Alignment Scores:
	Prod. No.: 1.67e-107 Length: 1377
	Score: 1325.00 Matches: 243
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 100.00% Indels: 0
	DB: 9 Gaps: 0
	US-09-944-944-42 (1-243) x US-09-944-413-41 (1-1377)
QY	1 MetArGrProLeuAeuValleuLeuLeuEnglyLeuAlaIlaagLYSerProProLeuAsp 20
Dd	227 ATGAGGGCACTCCTCGCHCCGTGCTGCTGGGCGCTGGGGCCGGCTGCCACCTGAG 286
QY	21 AspAsnLySlIerProSerLeuCySProGLyHISProGLyLLeuProGLyThProGLYHis 40
Dd	287 GACAACAAGATCCCCAGCCCTGCCTCCGGGGGACCCTCCGGCTTCAGAGCACGCCGGGGCAC 346
QY	41 HisGLySerInGLyLeuProGLyARgASpGLyARgASpGLyARgASpGLyALAProGLy 60
Dd	347 CATGGCGACCAAGGGCTTCCGGGGCCCGCATGGCCCGGAAGCGCGCGAGAGGGCCCGGG 406
QY	61 ALAProGLyLuLSglYGLyGLyARgProGLyLeuProGLyProArgLYAsPPro 80
Dd	407 GCCTCCGGAGAAGAAAGCGAGGGCGGAGCGCGGACTGCGCGGACCTCGAGGGGACCCC 466
QY	81 GLYProArgGLyGLuaLaGLyProAlaGLyProThrGLyProAlaGLyGLuCYASerVal 100
Dd	467 GGCGCGGAGAGAGCGCGGAGCCCGGGGGCCACCGGGCTCGCGGGGAGTGTCTGGTG 526
QY	101 ProProArgSerAlaPheseralAlaYSarGSerGLuSarArGVAlProProProSerASP 120
Dd	527 CCTCCGGGATCCCTCTCAGCGCCAGAGCGCTCCGAGAGCGGGGTCTCTCCGCTTGAC 586
QY	121 AlaProLeuProPhesAPrGVAlleuValSaNGlUGlnGLyHISLYrASpAlaValThr 140
Dd	587 GCACCTTGCCCTTCACCGCGGCTGGTGAAGAGAGAGGACATTACGACGGCTCAC 646
QY	141 GLYASPhenrHCysGLInVALProGLyVALTYrTYrPhEALaVALHISAlaThrValTYr 160
Dd	647 GGCAAGTTCACTGCCAGAGGTGGTGGGCTACTACTTGGCGTCAATGCCACCGTCTAC 706
QY	161 ArgAlaserLeuInPhesAPrValLYsaNGLYGluSerLLIalaserPhesGLn 180
Dd	707 CGGGCCAGCCTGCAGTTGATCTGGTGAAGATGGCGAATTCATTGCCCTCTTCTTCAG 766
QY	181 PhePhEGlyGLYrPrOlySProAlaserLeuSERGLyGLyAlamelValArgLeuGLu 200
Dd	767 TTTTTGGGGGGGGGCCAACGACGCTCGCTCGGGGGGGGGCCCATGTGAGGCTGGAG 826
QY	201 ProGLuSpGLInVALTrPVAlGLInVALyALyALSAPryrLIegLYIErYAlaSer 220
Dd	827 CCTGAGGACCAACTGTGGGTGACGAGGGGTGTGGGTGACTCATATGGGATCATTAAGCCAGC 886
QY	221 ILelysrHASperThrPheserGLyPhELeUVALYrSARspTRPHIsSerSerPro 240
Dd	887 ATCAAGACACAGCACCTTCTCCGGAATTCTGTGTACTCGACTGGACAGCAAGTCCCCA 946
QY	241 ValPheAla 243
Dd	947 GTCTTTGCT 955
	RESULT 2
	US-09-944-403-41
	: Sequence 41, Application US/09944403

Patent No. US20020165143A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Bolstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerlitsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kijavrin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,403

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/068,017

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 23, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR FILING DATE: March 3, 1999

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: June 22, 1999

Prior	APPLICATION NUMBER:	PCT/US99/21090
Prior	FILING DATE:	September 15, 1999
Prior	APPLICATION NUMBER:	PCT/US99/28409
Prior	FILING DATE:	No. US20020165143A1ember 30, 1999
Prior	APPLICATION NUMBER:	PCT/US99/28313
Prior	FILING DATE:	No. US20020165143A1ember 30, 1999
Prior	APPLICATION NUMBER:	PCT/US99/28301
Prior	FILING DATE:	December 1, 1999
Prior	APPLICATION NUMBER:	PCT/US99/30095
Prior	FILING DATE:	December 16, 1999
Prior	APPLICATION NUMBER:	PCT/US00/03565
Prior	FILING DATE:	February 11, 2000
Prior	APPLICATION NUMBER:	PCT/US00/04414
Prior	FILING DATE:	February 22, 2000
Prior	APPLICATION NUMBER:	PCT/US00/05841
Prior	FILING DATE:	March 2, 2000
Prior	APPLICATION NUMBER:	PCT/US00/08439
Prior	FILING DATE:	March 30, 2000
Prior	APPLICATION NUMBER:	PCT/US00/14042
Prior	FILING DATE:	May 22, 2000
Prior	APPLICATION NUMBER:	PCT/US00/20710
Prior	FILING DATE:	July 28, 2000
Prior	APPLICATION NUMBER:	PCT/US00/32678
Prior	FILING DATE:	December 1, 2000
Prior	APPLICATION NUMBER:	PCT/US01/06520
Prior	FILING DATE:	February 28, 2001
NUMBER OF SEQ ID NOS:		120
SEQ ID NO 41		
LENGTH:	1377	
TYPE:	DNA	
ORGANISM:	Homo Saplen	
US-09-944-403-41		

Alignment Scores:		
Pred. No.:	1,67e-107	Length: 1377
Score:	1325.00	Matches: 243
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0

US-09-944-944-42 (1-243) x US-09-944-403-41 (1-1377)		
QY 1 MetatgProleuLeuValleuleuLeuEnglyleuaAlaaglySerProProleuAsp 20		
Db 227 ATGAGCGCACTCCTGCTGCTGCTGCTGCTGGGCGTGGGCGCGGCTGCCCCACGTGAC 288		
QY 21 AspaSuLysIleProSerLeucySproglYHISProglYLeuProglYThProglYHis 40		
Db 287 GACAAACAATCCCCACGCCTTCGCCCGGGGACCACCCGGCCCTTCAGAGCACCCGGGGCAC 346		
QY 41 HlsGLYSerGIleuLeuProglYArGspGIYArspsGIYArspsGIYAlaProgly 60		
Db 347 CATGGCAGCGAGGGCTTGCCGGGGCCGCGATGGCCGCGACGGCCGGAGGGGCCCGGG 406		
QY 61 AlaProglYGlulysGIleuGlYalYarPProglYLeuPProglYProarGIYASpPro 80		
Db 407 GCCTCGGAGAGAAGAGCGAGGGCGGAGCGCGGACACTCGCGGACCTCGAGGGGACCCC 466		
QY 81 GlyProarGIleuAlaGIleuProAlaaglYProthrlYProAlaaglYlucySerVal 100		
Db 467 GGCGCCGAGAGAGAGCGCGGACCCCGGGGCCACCGGGGCTCGCGGGAGTCTCGGTG 526		
QY 101 ProProarISerAlaIheSerAlaYsarGserGIUsaraYvalProproProSerAsp 120		
Db 527 CCGCCGCGATCGCCTTCAGCCCAAAGCGCTCCGAGAGCCGGGGTCCCTCGCCCTCGAC 586		
QY 121 AlaProleuPProPhesparYValleuValAsngluIngInLYHISYrASPAValThr 140		
Db 587 GCACCTTGCCCTTCGACCGCGCTGCTGGTAACAGACAGGACATTTACAGACGCCGTACC 646		
QY 141 gLyVsPpheThrCySGlnValaPrOglYValTYrTYrPheaValaIHsAlaThrValTYr 160		

Accession	Protein	Length
Db	647 GCGAAGTTCACCTCGCAGAGGCGCTGGGGCTCACTACTTGGCGGTCCAGTCCACGCTTAC	706
Qy	161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGluSerIleAlaSerPhePheGln	180
Db	707 CGGGCCAGCCTCGAGTTTATCTGGTGAAGAAATGCGAATCCATTGCCCTCTTTTTCAG	766
Qy	181 PhePheGlyGlyTrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu	200
Db	767 TTTTTCGGGGGGTGGCCCAAGCCAGCTCGTCTCGGGGGGGGCCCATGTAGGCTGAG	820
Qy	201 ProGluAspGlnValTrpValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer	220
Db	827 CCTGAGAGCAACATGTGGGTGACAGGTGGTGTGGTGTACTCATTTGGCATTTATGACAGC	886
Qy	221 IleLysThrAspSerThrPheSerGlyPheLeuValIlyrSerAspTrpHisSerSerPro	240
Db	887 ATCAAGACAGACAGACACTTCCGGATTCTTCGGTGTACTCCGACTGGCAAGCTCCCA	946
Qy	241 ValPheAla 243	
Db	947 GTCTTTGGCT 955	

RESULT 3
US-09-944-896-41
Sequence 41, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 2001-08-31
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086

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1 PRIOR FILING DATE: February 9, 1998
2 PRIOR APPLICATION NUMBER: 60/074,092
3 PRIOR FILING DATE: February 9, 1998
4 PRIOR APPLICATION NUMBER: 60/075,945
5 PRIOR FILING DATE: February 25, 1998
6 PRIOR APPLICATION NUMBER: 60/112,850
7 PRIOR FILING DATE: December 16, 1998
8 PRIOR APPLICATION NUMBER: 60/113,296
9 PRIOR FILING DATE: December 22, 1998
10 PRIOR APPLICATION NUMBER: 60/146,222
11 PRIOR FILING DATE: July 28, 1999
12 PRIOR APPLICATION NUMBER: PCT/US98/19330
13 PRIOR FILING DATE: September 16, 1998
14 PRIOR APPLICATION NUMBER: PCT/US98/25108
15 PRIOR FILING DATE: December 1, 1998
16 PRIOR APPLICATION NUMBER: 09/216,021
17 PRIOR FILING DATE: December 16, 1998
18 PRIOR APPLICATION NUMBER: 09/218,517
19 PRIOR FILING DATE: December 22, 1998
20 PRIOR APPLICATION NUMBER: 09/254,311
21 PRIOR FILING DATE: March 3, 1999
22 PRIOR APPLICATION NUMBER: PCT/US99/12252
23 PRIOR FILING DATE: June 22, 1999
24 PRIOR APPLICATION NUMBER: PCT/US99/21090
25 PRIOR FILING DATE: September 15, 1999
26 PRIOR APPLICATION NUMBER: PCT/US99/28409
27 PRIOR FILING DATE: No. US20020166715A1ember 30, 1999
28 PRIOR APPLICATION NUMBER: 09/254,311
29 PRIOR FILING DATE: No. US20020166715A1ember 30, 1999
30 PRIOR APPLICATION NUMBER: PCT/US99/28301
31 PRIOR FILING DATE: December 1, 1999
32 PRIOR APPLICATION NUMBER: PCT/US99/30095
33 PRIOR FILING DATE: December 16, 1999
34 PRIOR APPLICATION NUMBER: PCT/US00/03555
35 PRIOR FILING DATE: February 11, 2000
36 PRIOR APPLICATION NUMBER: PCT/US00/04414
37 PRIOR FILING DATE: February 22, 2000
38 PRIOR APPLICATION NUMBER: PCT/US00/05841
39 PRIOR FILING DATE: March 2, 2000
40 PRIOR APPLICATION NUMBER: PCT/US00/08439
41 PRIOR FILING DATE: March 30, 2000
42 PRIOR APPLICATION NUMBER: PCT/US00/14042
43 PRIOR FILING DATE: May 22, 2000
44 PRIOR APPLICATION NUMBER: PCT/US00/20710
45 PRIOR FILING DATE: July 28, 2000
46 PRIOR APPLICATION NUMBER: PCT/US00/32678
47 PRIOR FILING DATE: December 1, 2000
48 PRIOR APPLICATION NUMBER: PCT/US01/06520
49 PRIOR FILING DATE: February 28, 2001
50 NUMBER OF SEQ ID NOS: 120

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ORGANISM: Homo Sapien
US-09-944-896-41

Alignment Scores:

Pred. No.:	1 67e-107	Length:	1
Score:	1325.00	Matches:	2
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-944-944-42 (1-243) x US-09-944-896-41 (1-1377)

QY	MetFairProteinLeuValIleuLeuLeuengIlyLeuAlaAgiLyserProPoleasp	20
Dd	227 ATAGGCGACCTCCTCTCTCTGTCTCTGGGCGCTGGGGGGGCTGCCTCCCACTGGAC	286
QY	21 AspAsnLysIleProSerLeucCysProGlyHisProGlyLeuProGlyThrProGlyHis	40
Dd	287 GACAAACAATGCCCGCTTCGGCCGGGGGACCCCCGGGCTTCCAGGACGACCGGGGCAC	346


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: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-944-944-41

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Alignment scores:	
Pred. No.:	1,67e-107
Score:	1377
Percent Similarity:	1325.00
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	9
	Length: 1377
	Matches: 243
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-09-944-944-42 (1-243) X US-09-944-944-41 (1-1377)

[illegible]

RESULT 5
US-09-944-907-41
; Sequence 41, Application US/09944907

	Publication No.	US20020198147A1
	GENERAL INFORMATION:	
	APPLICANT:	Baker, Kevin
	APPLICANT:	Botstein, David
	APPLICANT:	Eaton, Dan
	APPLICANT:	Ferrara, Napoleone
	APPLICANT:	Filvaroff, Ellen
	APPLICANT:	Gertlisen, Mary
	APPLICANT:	Godard, Audrey
	APPLICANT:	Godowski, Paul
	APPLICANT:	Grimaldi, Christopher
	APPLICANT:	Gurney, Austin
	APPLICANT:	Hillan, Kenneth
	APPLICANT:	Kjavarin, Ivar
	APPLICANT:	Napier, Mary
	APPLICANT:	Roy, Margaret
	APPLICANT:	Tumas, Daniel
	APPLICANT:	Mood, William
	TITLE OF INVENTION:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
	FILE REFERENCE:	P2546P1
	CURRENT APPLICATION NUMBER:	US-09/944,907
	CURRENT FILING DATE:	2001-08-31
	PRIOR APPLICATION NUMBER:	09/866,028
	PRIOR FILING DATE:	2001-05-25
	NUMBER OF SEQ ID NOS:	120
	SEQ ID NO	41
	LENGTH:	1377
	TYPE:	DNA
	ORGANISM:	Homo Sapien
	US-09-944-907-41	
	Alignment Scores:	
	Pred. No.:	1.67e-107 Length: 1377
	Score:	1325.00 Matches: 243
	Percent Similarity:	100.00% Conservative: 0
	Best Local Similarity:	100.00% Mismatches: 0
	Query Match:	100.00% Indels: 0
	DB:	Gaps: 0
	US-09-944-944-42 (1-243) x US-09-944-907-41 (1-1377)	
OY	1 MetArproleuenuValleuenueuLeuglyLeuaAlaglySerProProleuasp	20
Db		
	227 ATGAGGGCACTCGTCGTCTGCTGCTGCCTGGGCTGGGGCCGGTCCGCCACTGGAC	286
OY	21 AspAsnlysIleProserLeucuspProglYHisProglYLeuProglYThrProglYHis	40
Db		
	287 GACAACAAGATCCCAGCCTCGCCCCGGGGCACCCCGGCGCTTGCAAGGACC GGGGCAC	346
OY	41 HisGIySercInglyLeuProglYArgaspGIyArgaspGIyArgaspGIyAlaProgly	60
Db		
	347 CATGGCGAGCGGGCTTTGGCGGGCCGATGGCCGCGACGGCCGCGAGCGCGCCGGG	406
OY	61 AlaPrOgLyLuLysGLyGlunGLyGlyArgprProglYLeuProglYProArGLYAspPro	80
Db		
	407 GCCTCGGGGAAGAAGGCCAGGGGGGAGGCGGGAGCTCGGGACCTCGAGGGGACCC	466
OY	81 GLYProArGLYLyuALaglYProalAglyProThngLYProalAglyGLucYSerVAl	100
Db		
	467 GGGCCCGAGAGAGAGCGGGGACCCCGGGGCCCATCCGGGCTCGCGGGAGTCTCGGTG	526
OY	101 ProProArGSerAlaBheserAlayArSGerGluSerArgValProProProSerASP	120
Db		
	527 CTTCCGGGAGCCGCTTGACGGGCAAGGCGCTCGAGAGCCGGGGTGGCTCGCGCTTGAC	586
OY	121 AlaPrOleuPrOpheasparYAlleuValasnGLingIngLYHISYrASpAlaValThr	140
Db		
	587 GCACCCCTTGCCCTTCACCGCGCTGCGTGAACGAGCGAGCAATTACGAGCGCGTAC	646
OY	141 GLYSpheRhcYcsglnValnProglYValTYTrYPheAlavAlHISAlaThrValTYr	166
Db		
	647 GGGAAgTTCACCGCCAGGtGCTGGGGGCTTACTGACTTGCGCGTCCAGGACCCAGGTTCAC	706

QY	161	ArgAlaSerLeuGlnInPheAspLeuValLysAsnGlySerIleAlaSerPhePheGln	180
Db	707	CGGGCCACCCGCGCACTGTGATCTGGTGAAGATGGCGAATCCATGGCCCTTTCTTCCAG	766
QY	181	PhePheGlyGlyTyrTrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln	200
Db	767	TTTTTTCGGGGGGTGGCCCAAGCCACCTCGCTCTCGGGGGGGGCCATGGTGAAGGCTGGAG	826
QY	201	ProGluAspGlnValTrpValGlnValAlaGlyAspTyrIleGlyIleTyrAlaSer	220
Db	827	CCTAAGGACCCAGGTGGGTGGGTGGGTGGTGAATCAATGGCATCATATGCCAAC	886
QY	221	IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro	240
Db	887	ATCAAGACAGACAGACACCTCTCCGGATTTTCTGGTGATCTCGACATGGCAGACAGCTCCCA	946
QY	241	ValPheAla	243
Db	947	GTCCTTTGCT	955

RESULT 6
US-09-944-929-41

Alignment Scores:	
Pred. No.:	167-107
Score:	1325_00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
NB:	9
	Gaps: 0
	Mismatches: 0
	Conservative: 0
	Matches: 243
	Length: 1377

US-09-944-944-42 (1-243) x US-09-944-929-41 (1-1377)

[illegible][illegible]

RESULT 7
US-10-028-072-361

PRIOR APPLICATION NUMBER:	60/05697
PRIOR FILING DATE:	1997-08-26
PRIOR APPLICATION NUMBER:	60/059113
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/059115
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/059117
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/059122
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/059184
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/059263
PRIOR FILING DATE:	1997-09-18
PRIOR APPLICATION NUMBER:	60/059352
PRIOR FILING DATE:	1997-09-19
PRIOR APPLICATION NUMBER:	60/055888
PRIOR FILING DATE:	1997-09-19
PRIOR APPLICATION NUMBER:	60/059836
PRIOR FILING DATE:	1997-09-24
PRIOR APPLICATION NUMBER:	60/062255
PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/062285
PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/062287
PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/062814
PRIOR FILING DATE:	1997-10-24
PRIOR APPLICATION NUMBER:	60/062816
PRIOR FILING DATE:	1997-10-24
PRIOR APPLICATION NUMBER:	60/063045
PRIOR FILING DATE:	1997-10-24
PRIOR APPLICATION NUMBER:	60/063082
PRIOR FILING DATE:	1997-10-27
PRIOR APPLICATION NUMBER:	60/063327
PRIOR FILING DATE:	1997-10-27
PRIOR APPLICATION NUMBER:	60/063350
PRIOR FILING DATE:	1997-10-28
PRIOR APPLICATION NUMBER:	60/063561
PRIOR FILING DATE:	1997-10-28
PRIOR APPLICATION NUMBER:	60/063704
PRIOR FILING DATE:	1997-10-29
PRIOR APPLICATION NUMBER:	60/063733
PRIOR FILING DATE:	1997-10-29
PRIOR APPLICATION NUMBER:	60/063755
PRIOR FILING DATE:	1997-10-29
PRIOR APPLICATION NUMBER:	60/063788
PRIOR FILING DATE:	1997-10-29
PRIOR APPLICATION NUMBER:	60/063755
PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/065846
PRIOR FILING DATE:	1997-11-03
PRIOR APPLICATION NUMBER:	60/064809
PRIOR FILING DATE:	1997-11-07
PRIOR APPLICATION NUMBER:	60/065186
PRIOR FILING DATE:	1997-11-12
PRIOR APPLICATION NUMBER:	60/065846
PRIOR FILING DATE:	1997-11-17
PRIOR APPLICATION NUMBER:	60/066364
PRIOR FILING DATE:	1997-11-21
PRIOR APPLICATION NUMBER:	60/066433
PRIOR FILING DATE:	1997-11-24
PRIOR APPLICATION NUMBER:	60/066511
PRIOR FILING DATE:	1997-11-24
PRIOR APPLICATION NUMBER:	60/066770
PRIOR FILING DATE:	1997-11-24
PRIOR APPLICATION NUMBER:	60/069212
PRIOR FILING DATE:	1997-12-11
PRIOR APPLICATION NUMBER:	60/069278

PRIOR FILING DATE: 1997-12-11	PRIOR APPLICATION NUMBER: 60/065333
PRIOR FILING DATE: 1997-12-11	PRIOR APPLICATION NUMBER: 60/065964
PRIOR FILING DATE: 1997-12-16	PRIOR APPLICATION NUMBER: 60/072322
PRIOR FILING DATE: 1998-01-23	PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04	PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-05	PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09	PRIOR APPLICATION NUMBER: 60/077971
PRIOR FILING DATE: 1998-03-12	PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25	PRIOR APPLICATION NUMBER: 60/079666
PRIOR FILING DATE: 1998-02-27	PRIOR APPLICATION NUMBER: 60/079722
PRIOR FILING DATE: 1998-03-22	PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-04-10	PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-16	PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084622
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12	PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085399
PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22	PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22	PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088741


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Db 347 CATGGACAGCCAGGCGCTTCCGGGGCCGGATGCGCGACAGCGCCCGACGCGCGCGCGG 406
QY 61 AAlaProgluyluylsglygluylglYArProgluyluylProgluylProarglyAspPro 80
Db 407 GCTCCGGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGCTCGCGGACCTCGAGGGGAGCCCC 466
QY 81 GlyProarglygluyluylaglyProAlaglyProthrglyProAlaglygluylCysSerVal 100
Db 467 GGGCGCGAGAGAGGCGGAGCGCGCGCGCGCCACCGCGGCGCTGCGGGGAGTGTCTGGTG 526
QY 101 ProProArgSerAlaPheSerAlaLysArgSerLuserArgValProProProSerAsp 120
Db 527 CCTCCGGGATCGGCTTCAGCGCGCCAGCGCTCCAGAGACCGGGGCGCTCGCGCTCGTAC 586
QY 121 AAlaProleupProPheAspArgValIleuValAsnIugInglYHisTyrAspAlaValThr 140
Db 587 GCACCTTGGCCCTTCGACCGCGGTCTGTGTAGACAGAGACATTTACGACCGCTCAC 646
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
Db 647 GGCAGATTACCTCCAGGTGCTGGGGTCTACTTCCGCGCTCCATGCCACCGCTCTAC 706
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnIugLuserTlleAlaSerPhePheGln 180
Db 707 CGGCGCAGCCTGCGATTGATCTGTGAAGAATGGCAATCCATTGCTCTTTCTTCCAG 766
QY 181 PhePheGlyglYTrpProLysProAlaSerLeuSerGlyglYAlaMetValArgLeuGlu 200
Db 767 TTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCGGGGGGGGCGCATGTGAGGCTGGAG 826
QY 201 ProGluAspGlnValTTPValGlnValIglYValIglYAspTyrIleGlyIleTyrAlaSer 220
Db 827 CCTAGAGACCAAGTGTGGTGACAGTGGGTGGGTGACTCATTTGGATGATATAGCCAGC 886
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTTPHLSerSerPro 240
Db 887 ATCAAGACAGACACACCTTCTCCGATTCTGTGTACTCGACTGGACAGCTCCCA 946
QY 241 ValPheAla 243
Db 947 GTCTTTGCT 955

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RESULT 9
US-10-123-904-361
; Sequence 361, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C54
; CURRENT APPLICATION NUMBER: US/10/123, 904
; PRIORITY FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-361
Alignment Scores:
Pred. No.: 1,67e-107 Length: 1377
Score: 1325.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-944-944-42 (1-243) x US-10-123-904-361 (1-1377)
QY 1 MetaArgProleuLeuValIleuLeuLeuGlnIleuAlaIleuAlaGlySerProProleuAsp 20
Db 227 ATGAGGCGACCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 286
QY 21 AspaAsnLysIleProSerLeuCysProGlyHisAspProGlyLeuProGlyThrProGlyHis 40
Db 287 GACAACAAGATCCCGACGCTCTGCGCGGGGACCCCGGCTTCAGAGGACGCGGGGCAC 346
QY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
Db 347 CATGGACAGCCAGGCGCTTCCGGCGCGGATGGCCGACAGCGCGCGCGCGCGCGCGG 406
QY 61 AAlaProgluyluylsglygluylglYArProgluyluylProgluylProarglyAspPro 80
Db 407 GCTCCGGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGCTCGCGGACCTCGAGGGGAGCCCC 466
QY 81 GlyProarglygluyluylaglyProAlaglyProthrglyProAlaglygluylCysSerVal 100
Db 467 GGGCGCGAGAGAGGCGGAGCGCGCGCGCGCCACCGCGGCTCGCGGGAGTGTCTGGTG 526
QY 101 ProProArgSerAlaPheSerAlaLysArgSerLuserArgValProProProSerAsp 120
Db 527 CCTCCGGGATCGGCTTCAGCGCGCCAGCGCTCCAGAGACCGGGTGTCTCGCGCTGTAC 586
QY 121 AAlaProleupProPheAspArgValIleuValAsnIugInglYHisTyrAspAlaValThr 140
Db 587 GCACCTTGGCCCTTCGACCGCGGTCTGTGTAGACAGAGACATTTACGACCGCTCAC 646
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
Db 647 GGCAGATTACCTCCAGGTGCTGGGGTCTACTTCCGCGCTCCATGCCACCGCTCTAC 706
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnIugLuserTlleAlaSerPhePheGln 180
Db 707 CGGCGCAGCCTGCGATTGATCTGTGAAGAATGGCAATCCATTGCTCTTTCTTCCAG 766
QY 181 PhePheGlyglYTrpProLysProAlaSerLeuSerGlyglYAlaMetValArgLeuGlu 200
Db 767 TTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCGGGGGGGGCGCATGTGAGGCTGGAG 826
QY 201 ProGluAspGlnValTTPValGlnValIglYValIglYAspTyrIleGlyIleTyrAlaSer 220
Db 827 CCTAGAGACCAAGTGTGGTGACAGTGGGTGGGTGACTCATTTGGATGATATAGCCAGC 886
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTTPHLSerSerPro 240
Db 887 ATCAAGACAGACACACCTTCTCCGATTCTGTGTACTCGACTGGACAGCTCCCA 946
QY 241 ValPheAla 243
Db 947 GTCTTTGCT 955

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RESULT 10
US-10-140-470-361
; Sequence 361, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen

QY	61	AlAProG1Vg1uysg1yglu1ygl1yAaPProG1y1yLauProG1yProaArgG1yASPro	80
Db	407	GCTCCGGAGAGAAAGGCGAGGGCCGGAGAGCCGGGACTGCCGAGCTCCAGGGAGACCC	466
QY	81	G1yProaArgG1yglu1yAaG1yProAaG1yProthrg1yProAaG1ygluCyASerVal	100
Db	467	GGGCGCCGAGAGAGAGCGGAGCCCGGGGGCCAGCCGGGCGCTGCCGGGAGTGCCTGGTG	528
QY	101	ProProaArgSer1yAaSer1yA1yASaArgSerG1ySerArgValProProProSerAsp	120
Db	527	CGTCCCGGATCCGCTTCAGCCCAAGCGCTCCAGAGCCGAGGTCCCTCCGCGCTGAC	588
QY	121	AlAProLauProPheASparGVal1yLauValasnG1yng1yH1ySTyASpAlaValThr	140
Db	587	GCACCCCTTGCCCTTCAGCCGCGCTGCGTGAAGACAGAGGAGACATTAGACCCGTCACC	648
QY	141	G1yLysPheThrcysGlnValProG1yValTyTyTyPheAlaValH1sAlaThrValTyT	160
Db	647	GGCAAGTTCACTCCGCGCAGCTGCCCTGGGGTCTACTCTAGCCGTCACAGCCACGCTTAC	706
QY	161	ArgAlaSerLeuGlnPheASpleuVal1yLysAsnG1yng1ySer1yAaSerPhePhGln	180
Db	707	CGGGCCAGCCTGCAGTTGATCTGG1yGAAGATGGCGAATCATTCCTCTTTTTCAG	766
QY	181	PhePheG1yG1yTrProLysProAaSerLeuSerG1yG1yAlaMetValArgLeuGlu	200
Db	767	TTTTTGGGGGGGGGGCCAGGCAAGCAGCTCGCTCGGGGGGGCCAGTGAAGCTGAG	828
QY	201	ProG1yASpGlnValTrPVal1yAlnValG1yValG1yASpTyT1yG1y1yTyTAlaSer	220
Db	827	CTGAGAGACCAAGTGGGGTGCAGGTGGGTGGGTGACTCATTTGGCATCTATGACGAGC	886
QY	221	11eLyTThASerSerThrPheSerG1yPheLeuValTyTsrASpTPH1sSerSerPro	240
Db	887	ATCAACACAGACAGACACTTCTCCGGAATTTCTGTGTACTCGACTGGACAGCTCCCA	946
QY	241	Val1yPheAla 243	
Db	947	GTCCTTGCT 955	
RESULT 12			
US-10-176-918-361			
Sequence 361, Application US/10176918			
Publication No. US20030027275A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Beresini, Maureen			
APPLICANT: DeForge, Laura			
APPLICANT: Desnoyers, Luc			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Gerritsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Sherwood, Steven			
APPLICANT: Smith, Victoria			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Watanabe, Colin K			
APPLICANT: Wood, William			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
FILE REFERENCE: P3330R1C382			
CURRENT APPLICATION NUMBER: US/10/176,918			
CURRENT FILING DATE: 2002-06-20			
Prior Application removed - See File Wrapper or Palm			
NUMBER OF SEQ ID NOS: 550			
SEQ ID NO 361			
LENGTH: 1377			
TYPE: DNA			

; ORGANISM Homo Sapien					
US-10-176-918-361					
Alignment Scores:					
Pred. No.:	1,67e-107	Length:	1377		
Score:	1325.00	Matches:	243		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
Dbl:	9	Gaps:	0		
US-09-944-944-42 (1-243) x US-10-176-918-361 (1-1377)					
QY	1	MetArgProLeuDeuValLeuLeuLeuLeuGlyLeuAlaIleArgSerProProLeuAsp	20		
Dl	227	ATGAGGGCACTCCTCGTCTGTGCCTCGTGCCCTGAGGCGTCGGGCCCGGCTGAC	288		
QY	21	AspAsnLysIleProSerLeucySProGIYHISProGIYLeuProGIYThProGIYHIS	40		
Dl	287	GACAACAAAGTCCCCAGCCCTTCGCCCGGGGACCCTCCGACTCCAGGCACGCCGGGCAC	346		
QY	41	HISGIYSerGIInGIYLeuProGIYArAspGIYArAspGIYArAspGIYAlAIProGIY	60		
Dl	347	CATGGCAGCACGAGGCTTGGCCGGGCCCATATGGCCGCCGACGGCCGAGGCGCCCGG	406		
QY	61	AlAProGIYGIYLuSGIYLuGIYLaYArProGIYLeuProGIYProAIYgLYASpPro	80		
Dl	407	GCTCCGGGAGAGAAGGCAAGGCGGAGAGCGCGGACTCCGGGACCTCGAGGGAGACCC	466		
QY	81	GLYProARGLYLuAlaGIYProAlaGIYProHIGLYProAlaGIYLuCYSeServal	100		
Dl	467	GGGCGCGAGAGAGGCGGAGCCGGGGGCCACCGGACCTGGCGGGAGTGTGGTG	526		
QY	101	ProProAIRSerAlaPheSerAlaIalysArASerGIUSeArGvalProProProSerASP	120		
Dl	527	CCTCCGCGATCCGCTTTCAGCGCCAAGGCGCTCCGAGACCGGGGTGGCTCCGCGTGGAC	586		
QY	121	AlAProLeuArProPhAspArgValLeuValAsnGIInGIYHISTYAspAlaValThr	140		
Dl	587	GCACCCCTTGCCCTTCACCGCGGTGGTGGTAAGACGAGGACANTAGACGCGGTACC	646		
QY	141	GIYLySPheThrCYSGInAlProGIYValTYTYrPheAlaValHISAlaThValTYr	160		
Dl	647	GGGAATTACCTCGCCACAGGTGGCTGAGGTCTACTCTTCCGCGTCCATGCCACCGCTTAC	706		
QY	161	ArgAlaSerLeuGIInPheAspleuValLysAsnGIYIUSeTIleAlaSerPhePhcIn	180		
Dl	707	CGGGCCAGCGCTGTGAGTTGATCTGGTGAAGATGGCGAATGCATTCCTCTTCTTCACG	766		
QY	181	PhePhcGIYGIYTrProLySProAlaSerLeuSerGIYGIYAlaMetValArgLeuGIu	200		
Dl	767	TITTTTTGGGGGTGGGCCCAAGCCAGCCCTGCTCTGGGGGGGGCCATGTAGAGCTGAG	826		
QY	201	ProGIUAspGIInValITrPyAlaGIInValAlaGIYAlaGIYAsPTYIleGIYIleTYraLSer	220		
Dl	827	CCTGAGAGACAAGATGGGTGCGAGGTGGGTGGGTGACTCATATGGCATCTATAGCCAGC	886		
QY	221	IleLySThrAspSerThrPheSerGIYPheLeuValTYrSarAPTPrHISserSerPro	240		
Dl	887	AATCAAACAGACAGCACCTTCGCGGATTTCTGTGTACTCCGACTGCACAGCTCCCA	946		
QY	241	ValPheAla 243			
Dl	947	GTCCTTGTCT 955			
RESULT 13					
US-10-176-921-361					
; Sequence 361, Application US/10176921					
; Publication No. US20030027276A1					
GENERAL INFORMATION:					
APPLICANT: Baker, Kevin P.					
APPLICANT: Beresini, Maureen					
APPLICANT: Deforge, Laura					

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:55:46 ; Search time 22 seconds
(without alignments)
458.125 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLGLAGSPPLD.....DSFGFLVSDHSSPVFA 243

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1325	100.0	243	1	COT5_HUMAN
2	433.5	32.7	247	1	Q9BXJ0 homo sapien
3	424	32.0	244	1	APM1_MOUSE
4	418.5	31.6	680	1	APM1_HUMAN
5	417	31.5	674	1	CA1A_CHICK
6	412	31.1	246	1	C1QC_MOUSE
7	411.5	31.0	674	1	CA1A_BOVIN
8	410.5	30.8	289	1	COT7_HUMAN
9	408	30.4	680	1	CA1A_MOUSE
10	403	30.0	285	1	COT2_HUMAN
11	397	28.2	245	1	C1QC_HUMAN
12	374	28.2	744	1	CA18_RABIT
13	373	28.2	419	1	CODE_LEPMA
14	368	27.8	744	1	CA18_HUMAN
15	366.5	27.7	743	1	CA18_MOUSE
16	363	27.4	635	1	CA28_HUMAN
17	362	27.3	251	1	C1OB_HUMAN
18	360.5	27.2	253	1	C1OB_RAT
19	350	26.4	253	1	C1OB_MOUSE
20	314	23.7	245	1	C1QA_HUMAN
21	314	23.7	245	1	C1QA_MOUSE
22	298.5	22.5	255	1	GLIC_MOUSE
23	285.5	21.5	258	1	C1RF_HUMAN
24	282	21.3	258	1	C1RF_MOUSE
25	280.5	21.2	215	1	HP25_TAMSI
26	277.5	20.9	215	1	HP27_TAMSI
27	264.5	20.0	246	1	COT3_HUMAN
28	261.5	19.7	196	1	HP20_TAMSI
29	230.5	17.4	1049	1	CA13_BOVIN
30	228.5	17.3	281	1	COT1_HUMAN
31	228	17.2	684	1	CA39_HUMAN
32	224	16.9	636	1	CA13_RAT
33	223	16.8	1464	1	CA13_MOUSE

34	222.5	16.8	1758	1	CA24_CAEEL	P17140 caenorhabd
35	221.5	16.7	170	1	CA28_MOUSE	P25318 mus musculu
36	221	16.7	1019	1	CA16_CHICK	P20785 gallus galli
37	221	16.7	1262	1	CA13_CHICK	P12105 gallus galli
38	220	16.6	248	1	PSPA_CANFA	P06908 canis fam11
39	220	16.6	360	1	CCD2_CAEEL	P35798 caenorhabd1
40	219.5	16.6	247	1	PSPA_RABIT	P12842 oryctolagu
41	219.5	16.6	1466	1	CA13_HUMAN	P02461 homo sapien
42	219	16.5	671	1	CA11_RAT	P02454 rattus norv
43	218.5	16.5	1453	1	CA11_MOUSE	P11087 mus musculu
44	217.5	16.4	1516	1	CA1H_HUMAN	P39060 homo sapien
45	217	16.4	747	1	CA12_BOVIN	P02459 bos taurus

ALIGNMENTS

RESULT 1
ID COT5_HUMAN STANDARD; PRT; 243 AA.
AC Q9BXJ0; Q90FX4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement-c1q tumor necrosis factor-related protein 5 precursor.
GN C1QTNF5 OR CTRP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SHEPPARD P.O., Humes J.M.;
RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";
RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 25-243 FROM N.A.
RC TISSUE=uterus;
RA Ottenweider B., Obermaier B., Mewes H.-W., Gassenhuber J.,
RA Wiemann S.;
RA Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF329841; AAK17965.1; -
CC EMBL; AL110261; CAB53702.1; -
CC Genew; HGNC:14344; C1QTNF5.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; C1q; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; FALSE_NEG.
DR Collagen; Signal.
FT SIGNAL 1 15
FT CHAIN 16 243
FT DOMAIN 30 95
FT FT 97 243
SQ SEQUENCE 243 AA: 25298 MW: 70CDAA65CD87EB784 CRC64:
Query Match 100.0%; Score 1325; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 17e-85;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNDKIPSLCPGHHGSGGLPGRDGRDGDGAPG 60
 DB 1 MRPLVLLLLGLAAGSPPLDNDKIPSLCPGHHGSGGLPGRDGRDGDGAPG 60
 QY 61 APGKGGGGRGLGPPRDPGPRGAGAGTGTGAGGECVPPRRSAFSAKRSRPPSPD 120
 DB 61 APGKGGGGRGLGPPRDPGPRGAGAGTGTGAGGECVPPRRSAFSAKRSRPPSPD 120
 QY 121 APLEFDRLVNEOGHYDAVTGKFCOVPGVYFFAVHATVYRASLOFEDLVKNGESTIASPFQ 180
 DB 121 APLEFDRLVNEOGHYDAVTGKFCOVPGVYFFAVHATVYRASLOFEDLVKNGESTIASPFQ 180
 QY 181 FFGGMPKPRASISGAMVRLPEPDQWVQVGVGYIGIYASIKTDSFGFLVYSDWHSPP 240
 DB 181 FFGGMPKPRASISGAMVRLPEPDQWVQVGVGYIGIYASIKTDSFGFLVYSDWHSPP 240
 QY 241 VFA 243
 DB 241 VFA 243

RESULT 2

APML_MOUSE STANDARD: PRT: 247 AA.

AC Q60994; Q62400; Q9DC68;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Adiponectin precursor (30 kDa adipocyte complement-related protein)
 GN (ACRP30) (Adipocyte specific protein Adipoc)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE-Adipocyte;
 RX MEDLINE=96070757; PubMed=7592907;
 RA Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;
 RT "A novel serum protein similar to C1q, produced exclusively in
 RT adipocytes".
 RL J. Biol. Chem. 270:26746-26749(1995).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE=96209999; PubMed=8631877;
 RA Hu E., Liang P., Spiegelman B.M.;
 RT "Adipoc is a novel adipose-specific gene dysregulated in obesity".
 RL J. Biol. Chem. 271:10697-10703(1996).
 RN [3]
 RC SEQUENCE FROM N.A.
 RC PubMed=11162643;
 RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;
 RT "Chromosomal localization, expression pattern, and promoter analysis
 RT of the mouse gene encoding adipocyte-specific secretory protein
 RT Acrp30".
 RL Biochem. Biophys. Res. Commun. 280:1120-1129(2001).
 RN [4]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilmshurst L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection".
 RL Nature 409:685-690(2001).
 RN [5]
 RC FUNCTION.
 RX MEDLINE=21372498; PubMed=11479627;
 RA Yamauchi T., Kamon J., Maki H., Terauchi Y., Kubota N., Hara K.,
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
 RA Akamatsu Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
 RA Froguel P., Kadowaki T.;
 RT "The fat-derived hormone adiponectin reverses insulin resistance
 RT associated with both lipodystrophy and obesity".
 RL Nat. Med. 7:941-946(2001).
 RN [6]
 RC FUNCTION.
 RX MEDLINE=21372499; PubMed=11479628;
 RA Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;
 RT "The adipocyte-secreted protein Acrp30 enhances hepatic insulin
 RT action".
 RL Nat. Med. 7:947-953(2001).
 RN [7]
 CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
 CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
 CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING
 CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
 CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE
 CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
 CC -1- SUBUNIT: HOMODIGOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND
 CC SECRETED INTO SERUM.
 CC -1- INDUCTION: DURING HORMONE-INDUCED ADIPOSE DIFFERENTIATION AND
 CC ACTIVATED BY INSULIN.
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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 CC EMBL; U37222; AAA80543.1; -;
 CC EMBL; U49915; AAB06706.1; -;
 CC EMBL; AF304466; AAK13417.1; -;
 CC EMBL; AK003138; BAB2357.1; -;
 CC MGD; MGI:106675; Acrp30.
 CC InterPro: IPR001073; C1q.
 CC InterPro: IPR000087; Collagen.
 CC Pfam: PF00336; C1q; 1.
 CC Pfam: PF01391; Collagen; 1.
 CC PRINTS; PR00007; COMPLEMENTC1Q.
 CC SMART; SM0110; C1Q; 1.
 CC PROSITE; PS01113; C1Q; 1.
 CC Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
 CC Polymorphism.
 CC SIGNAL 1 17
 CC CHAIN 18 247
 CC DOMAIN 45 110
 CC DOMAIN 111 247
 CC DISULFID 39 39
 CC MOD_RES 47 47
 CC MOD_RES 50 50
 CC MOD_RES 56 56
 CC POTENTIAL.
 CC ADIPONECTIN.
 CC COLLAGEN-LIKE.
 CC C1Q.
 CC INTERCHAIN (BY SIMILARITY).
 CC HYDROXYLATION (BY SIMILARITY).
 CC HYDROXYLATION (BY SIMILARITY).
 CC HYDROXYLATION (BY SIMILARITY).

FT MOD_RES 65 65 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 79 79 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 98 98 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 113 113 M -> V.
 FT CONFLICT 50 50 P -> S (IN REF. 2).
 FT CONFLICT 74 74 A -> S (IN REF. 2).
 FT CONFLICT 117 117 A -> G (IN REF. 2).
 FT CONFLICT 148 148 G -> N (IN REF. 2).
 FT CONFLICT 243 243 Y -> F (IN REF. 2).
 SQ SEQUENCE 247 AA: 26841 MW: 1378687D87398BC4 CRC64;

Query Match 32.7%; Score 433.5; DB 1; Length 247;
 Best local Similarity 40.6%; Pred. No. 1.2e-23;
 Matches 102; Conservative 32; Mismatches 92; Indels 25; Gaps 8;

QY 1 MRPLVLLIL-GIAGSPPLDNKIPSLCPGHPG-----LPETPGHSGQLPGRDGRG 54
 DB 4 LQALLFLILPSHAEDDVTYTEELAPALVPPKGTGACGMAGICPHGHNGTPGRDGRD- 62
 OY 55 RDGAGGPGEGGEGGPGI-RGPRGD-----PGREGAPAGTGTGAGCSVPRRA 105
 DB 63 -----GTPEKEKEKGADAGLPGKGTGDMTGABSPKFPPTGPKKSGEPAIYKSA 117
 OY 106 FSAKSESRVPPSDAPLPFDEVLNQGHDVAVTGKTCQVPGVYFAVHAIVYASLQ 165
 DB 118 FGV-GLFTRVTP-NVPIRFETKIFVQGNHYDGSKFCFNIGLYFYHITVYMKDV 175
 OY 166 FLYVNGESIASFFQFGGMPKPSISGAMVRLPEDOVWVY-GVSDYIGIYASIKTD 224
 DB 176 VSLFKRDKAVLFTTYOYOE-KNVDAQSGSVLLHLEVGQVWLVQVGDGDNGLYADNVND 234
 OY 225 STEFGFLVYSD 235
 DB 235 STEFGFLVYHD 245

RESULT 3
 APM1 HUMAN
 ID APM1 HUMAN STANDARD; PRT; 244 AA.
 AC Q15648;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Adiponectin precursor (30 kDa adipocyte complement-related protein) (Acrp30) (adipose most abundant gene transcript 1) (apn-1) (gelatin-binding protein).
 GN APM1 OR ACPR30 OR GBP28.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE-96224171; PubMed-8619847;
 RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y., Matsubara K.,
 RT "cDNA cloning and expression of a novel adipose specific collagen-like factor, apn1 (adipose most abundant gene transcript 1).";
 RL Biochem. Biophys. Res. Commun. 221:286-289(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=adipose tissue;
 RX MEDLINE-96224171; PubMed-8619847;
 RA Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M., Nakano Y., Shimizu N., Tomita M.,
 RT "Organization of the gene for gelatin-binding protein (GBP28).";
 RL Gene 229:67-73(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99333693; PubMed-10403784;
 RA Schaeffter A., Orso E., Paltzsch K.D., Buechler C., Drobnik W., Fuerst A., Schaeffter J., Schmitz G.;

RT "The human apn-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 1q21.3-q23, a susceptibility locus identified for familial combined hyperlipidemia (FCH).";
 RT Biochem. Biophys. Res. Commun. 260:416-425(1999).
 RL [4]
 RP CHARACTERIZATION.
 RX MEDLINE-20417747; PubMed-10961870;
 RA Yokota T., Oritani K., Takahashi T., Ishikawa J., Matsuyama A., Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y., Matsuzawa Y.;
 RT "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages.";
 RL Blood 96:1723-1732(2000).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE-20440368; PubMed-10982546;
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H., Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pathway.";
 RL Circulation 102:1296-1301(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-21372498; PubMed-11479627;
 RA Yamachui T., Kamon J., Maki H., Terauchi Y., Kubota N., Hara K., Mori Y., Ide T., Murakami K., Tsuboyama-Kasato N., Ezaki O., Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H., Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M., Froguel P., Kadowaki T.;
 RT "The fat-derived hormone adiponectin reverses insulin resistance associated with both lipodystrophy and obesity.";
 RL Nat. Med. 7:941-946(2001).
 RN [7]
 RP VARIANT ADIPONECTIN DEFICIENCY CYS-112.
 RX MEDLINE-20378830; PubMed-10918532;
 RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K., Hara K., Boutin P., Mori Y., Tobe K., Kadowaki H., Hagura R., Akanuma Y., Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Genomic structure and mutations in adipose-specific gene, adiponectin.";
 RL Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).
 RN [8]
 RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.
 RX MEDLINE-21671103; PubMed-11812766;
 RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamachui T., Otake S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y., Yazaki Y., Nagai R., Tanigawa M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;
 RT "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population.";
 RL Diabetes 51:536-540(2002).
 RT -I- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
 CC -I- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
 CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
 CC -I- DISEASE: Defects in APM1 are the cause of adiponectin deficiency, resulting in very low concentration of plasma adiponectin.
 CC -I- decreased adiponectin plasma levels are associated with obesity
 CC -I- insulin resistance, and diabetes type 2.
 CC -I- PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.
 CC -I- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -I- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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DR EMBL: D45371; BAA08227.1; -
 DR EMBL: AB012165; BAA86716.1; -
 DR EMBL: AB012164; BAA86716.1; JOINED.
 DR EMBL: AJ131460; CAB52413.1; -
 DR EMBL: AJ131461; CAB52413.1; JOINED.
 DR MIM: 605441; -
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 KW Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
 KW Polymorphism; Disease mutation; Obesity; Diabetes mellitus.
 FT SIGNAL 1 14
 FT CHAIN 15 244
 FT DOMAIN 42 107
 FT DOMAIN 108 244
 FT DISULFID 36 36
 FT MOD_RES 44 44
 FT MOD_RES 47 47
 FT MOD_RES 53 53
 FT MOD_RES 62 62
 FT MOD_RES 71 71
 FT MOD_RES 76 76
 FT MOD_RES 86 86
 FT MOD_RES 95 95
 FT MOD_RES 104 104
 FT MOD_RES 84 84
 FT VARIANT 112 112
 FT VARIANT 117 117
 FT VARIANT 164 164
 FT VARIANT 221 221
 FT VARIANT 241 241
 FT SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;
 Query Match 32.0%; Score 424; DB 1; Length 244;
 Best Local Similarity 40.5%; Pred. No. 5.3e-23;
 Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

RESULT 4
 ID CAIA_HUMAN STANDARD; PRT; 680 AA.
 AC Q03692;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Collagen alpha 1(X) chain precursor.
 GN COL10A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid:9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92109659; PubMed-1764025;
 RA Thomas J.T., Cresswell C.J., Rash B., Nicolai H., Jones T.,
 RA Solomon E., Grant M.E., Boot-Handford R.P.;
 RT "Type human collagen X gene. Complete primary translated sequence and
 RT chromosomal localization.";
 RL Biochem. J. 280:617-623(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93012005; PubMed-1397333;
 RA Reichenberger E., Beller F., Luvalle P., Olsen B.R., von der Mark K.,
 RA Bertling W.M.;
 RT "Genomic organization and full-length cDNA sequence of human collagen
 RT X.";
 RL FEBS Lett. 311:305-310(1992).
 [3]
 RP SEQUENCE FROM N.A.
 RA Beller F., Lammli M.B., von der Mark K.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Williams S.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 [5]
 RP SEQUENCE OF 52-680 FROM N.A.
 RX MEDLINE-92267014; PubMed-1587271;
 RA Apte S.S., Seidlin M.F., Hayashi M., Olsen B.R.;
 RT "Cloning of the human and mouse type X collagen genes and mapping of
 RT the mouse type X collagen gene to chromosome 10.";
 RL Eur. J. Biochem. 206:217-224(1992).
 [6]
 RP SEQUENCE OF 561-666 FROM N.A.
 RX MEDLINE-91243838; PubMed-2037056;
 RA Apte S., Mattei M.-G., Olsen B.R.;
 RT "Cloning of human alpha 1(X) collagen DNA and localization of the
 RT COL10A1 gene to the q21-q22 region of human chromosome 6.";
 RL FEBS Lett. 282:393-396(1991).
 [7]
 RP SEQUENCE OF 547-655 FROM N.A.
 RX MEDLINE-92077285; PubMed-1743401;
 RA Reichenberger E., Aigner T., von der Mark K., Stoeck H., Bertling W.;
 RT "In situ hybridization studies on the expression of type X collagen
 RT in fetal human cartilage.";
 RL Dev. Biol. 148:562-572(1991).
 [8]
 RP REVIEW ON VARIANTS.
 RX MEDLINE-97255959; PubMed-9101290;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
 RT associated collagen (type IX), and network-forming collagen (type X)
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
 RL Hum. Mutat. 9:300-315(1997).
 [9]
 RP VARIANTS SMCD ASP-598 AND PRO-614.
 RX MEDLINE-94136476; PubMed-8304336;
 RA Wallis G.A., Rash B., Sweetman W.A., Thomas J.T., Super M., Evans G.,
 RA Grant M.E., Boot-Handford R.P.;

DB 521 MPEGFIRAGORPSLSGTPLVNSANGVTGMPVSAFTVILSKAY--PAIGTPIPFKILYNR 578
 QY 133 QGHAYATGKFTCCVPEYFAVAHATYRASLOFDLVKNGESIA-SFFQFGGMPKPSAL 191
 DB 579 QGHDPRTGFTTCIPGITYFSYVHAKGNVWALYKNGSPVMTYDEVOKYGLDQA-- 636
 QY 192 SGGAMVRLPEPDVWVGVGDYIGIYASIKTSTSGFLV 232
 DB 637 SGAHIDLTENDQVWLQLPNASENGLYSSEYVHSSFGFLV 677

RESULT 5
 CALA_CHICK STANDARD: PRT: 674 AA.
 ID CALA_CHICK
 AC P08125;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Collagen alpha 1(X) chain precursor.
 GN COL10A1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.
 RX MEDLINE=6616827; PubMed=3082876;
 RA Nishimura Y., Gordon M., van der Rest M., Schmid T., Linsemayer T.,
 RA Olsen B.R.;
 RT "The developmentally regulated type X collagen gene contains a long
 RT open reading frame without introns."
 RL J. Biol. Chem. 261:5041-5050(1986).
 RN [2]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89054019; PubMed=2461368;
 RA Luvalle P., Nishimura Y., Rosenblum N.D., Olsen B.R.;
 RT "The type X collagen gene. Intron sequences split the 5'-untranslated
 RT region and separate the coding regions for the non-collagenous amino-
 RT terminal and triple-helical domains."
 RL J. Biol. Chem. 263:18378-18385(1988).
 RN [3]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=89380199; PubMed=2476437;
 RA Yamaguchi N., Benya P.D., van der Rest M., Nishimura Y.;
 RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
 RT demonstrate that type VIII collagen is a short chain collagen and
 RT contains triple-helical and carboxyl-terminal non-triple-helical
 RT domains similar to those of type X collagen."
 RL J. Biol. Chem. 264:16022-16029(1989).
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
 CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- PM: PROLINS AT THE THIRD POSITION OF THE TRIPETIDE REPEATING
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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 CC
 CC EMBL: M13496; AAA48736.1; ALT_SEQ.
 CC EMBL: J04194; AAA48634.1; -
 CC PIR: A31896; A31896.
 CC InterPro: IPR001073; C1Q.
 CC InterPro: IPR000087; Collagen.
 CC Pfam: PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 8.
 DR PRINTS; PRO0007; COMPLEMENTC1Q.
 DR SMART; SM00110; C1Q; 1.
 DR PROSITE; PS01113; C1Q; 1.
 KW Extracellular matrix; connective tissue; Repeat; Hydroxylation;
 KW Cartilage; Collagen; Signal.
 FT SIGNAL
 FT CHAIN 1 18
 FT CHAIN 19 674 COLLAGEN ALPHA 1(X) CHAIN.
 FT DOMAIN 19 52 NONHELICAL REGION (NC2).
 FT DOMAIN 53 512 TRIPLE-HELICAL REGION.
 FT DOMAIN 513 674 NONHELICAL REGION (NC1).
 FT DOMAIN 539 674 C1Q.
 FT MOD_RES 453 453 HYDROXYLATION.
 FT MOD_RES 456 456 HYDROXYLATION.
 SO SEQUENCE 674 AA; 66434 MW; EAB4B1EF174B145 CRC64;

Query Match 31.5%; Score 417; DB 1; Length 674;
 Best Local Similarity 36.0%; Pred. No. 4.4e-22;
 Matches 96; Conservative 34; Mismatches 84; Indels 53; Gaps 6;

QY 14 AGSPPLDNDKIPSLCPGHPGLPTGPHHSGGLPGRDRDGRDAPGAPGEGGGRPL 73
 DB 408 AGHFGLEGPGVPGGVKVPGLNGEPGRGPGITGVGPGIPGPGMPGAPKAGAPGL 467
 QY 74 GPRP-----GDEPRGEA-----GPAGPTGPGGCSVP----- 101
 DB 468 GPGAGIYTKGLRGPGLGPGPKNGSGEPGLPGPPGPPGPGOSTIPEGYKGSRELS 527
 QY 102 -----PRSAFSARSRSPVPDPAPLPDPRLVYNQGHDAVTGKFTC 145
 DB 528 GMSFPMKAGANALTMGPVSAFTVILSKAY--PGATVPKPKDKILYNQGHDPRTGFTC 585
 QY 146 QVPEYFAVAHATYRASLOFDLVKNGESIA-SFFQFGGMPKPSALSGAMVRLPEPD 204
 DB 586 RIGPLTYFSYVHAKGNVWALYKNGSPVMTYDEVOKYGLDQA--SGSAVIDLMENDQ 643
 QY 205 VVWVGVGDYIGIYASIKTSTSGFL 231
 DB 644 VMLQPLPNSSENGLYSSEYVHSSFGFL 670

RESULT 6
 C1QC_MOUSE STANDARD: PRT: 246 AA.
 ID C1QC_MOUSE
 AC Q02105;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C1q subcomponent, C chain precursor.
 GN C1QG OR C1QC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Liver;
 RX MEDLINE=96186528; PubMed=8606057;
 RA Petry F., Reid K.B.M., Loos M.;
 RT "Isolation, sequence analysis and characterization of cDNA clones
 RT coding for the C chain of mouse C1q. Sequence similarity of
 RT complement subcomponent C1q, collagen type VIII and type X and
 RT prececebelin."
 RL Eur. J. Biochem. 209:129-134(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Liver;
 RX MEDLINE=96186528; PubMed=8606057;
 RA Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;
 RT "The mouse C1q genes are clustered on chromosome 4 and show
 RT conservation of gene organization."
 RL Immunogenetics 43:370-376(1996).
 CC -1- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD

Query Match	Best Local Similarity	Matches 103;	Conservative	Score 412;	DB 1;	Length 246;	Pred. No. 3.7e-22;	Mismatches 84;	Indels 24;	Gaps 10;
4	LVLLVLLGLANGSPPLDNDKIRPSIC---	RGRPRGIPGRTGCHHSGSGSLPRDGRDGRDGA	60							
15	LVLLVLLAL---	PL-RSQASAGCYGIPGMPGAGCKGKHDLGPKSPGIPAVG	68							
61	APGKGGEGGRGRLGPRGDPGRGPA---	GAGPGTGPAGECSSVPR-----	SAFSAKRS	111						
69	TQGRKGQKGEGRGCMGRKKNPRGISGLR	GDPRGPRGEGVEGRYKOKIQSVTYTRQ	128							
112	ESRVPSPSDAPLPRDVLVNEQGHYDAVTGK	FTCOVPGVYVFAVHATVYRASLQFDLVKN	171							
129	TTQY-PEANALVYRESVYTNPGQHNPSTGK	FTCEVPLAYE-VYTSHTFANLCVHLMLN	186							
172	GESIASPFQFGCMKPRASLSGGAMVRLR	PEPDQVWVQVGDYIGTASIKTDSFTSGFL	231							

QY	232	VYSD	235	
Db	187	LARAFSCDHMFN-SKQVS-SGGLALLNLQKGDFTW--LSVNDYNGMGIIBGSNSVFSGFL	242	
QY	232	VYSD	235	
Db	243	LFPD	246	
RESULT 7				
ID	CALA_BOVIN	STANDARD:	PRT:	674 AA.
AC	P23206;			
DT	01-NOV-1991	(Rel. 20, Created)		
DT	01-NOV-1991	(Rel. 20, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Collagen alpha 1(X) chain precursor.			
GN	COL10A1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE:Collage;			
RX	MEDLINE=9111313; PubMed=1703407;			
RA	Thomas J.T., Kwan A.P.U., Grant M.E., Boot-Handford R.P.;			
RT	"Isolation of cDNAs encoding the complete sequence of bovine type X			
RT	collagen. Evidence for the condensed nature of mammalian type X			
RL	collagen genes.";			
RL	Biochem. J. 273:141-148(1991).			
CC	-1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC			
CC	CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE			
CC	MINERALIZATION ZONES OF HYALINE CARTILAGE.			
CC	-1- SUBUNIT: HOMOTRIMER.			
CC	-1- PM: PROLINS ARE AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING			
CC	UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.			
CC	-1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.			
CC	-1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.			
CC	-----			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	CC or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: X53556; CA37624.1; -.			
DR	PIR: S13301; S13301.			
DR	InterPro: IPR001073; C1q.			
DR	InterPro: IPR000087; Collagen.			
DR	Pfam: PF00386; C1q; 1.			
DR	Pfam: PF01391; Collagen; 9.			
DR	PRINTS: PR00007; COMPLEMENTC1Q.			
DR	ProDom: PD000007; Collagen; 1.			
DR	SMART: SM00110; C1Q; 1.			
DR	PROSITE: PS01113; C1Q; 1.			
KW	Extracellular matrix; Connective tissue; Repeat; Hydroxylation;			
KW	Cartilage; collagen; Signal; Glycoprotein.			
FT	SIGNAL	1	18	
FT	CHAIN	19	674	COLLAGEN ALPHA 1(X) CHAIN.
FT	DOMAIN	19	56	NONHELICAL REGION (NC2).
FT	DOMAIN	57	519	TRIPLE-HELICAL REGION.
FT	DOMAIN	520	674	NONHELICAL REGION (NC1).
FT	DOMAIN	539	674	C1Q.
FT	DISUFPID	194	197	BY SIMILARITY.
FT	MOD_RRS	460	460	HYDROXYLATION (BY SIMILARITY).
FT	MOD_RRS	463	463	HYDROXYLATION (BY SIMILARITY).
FT	CARBOHYD	611	611	N-LINKED (GLCNAc. . .) (POTENTIAL).
SO	SEQUENCE	674 AA;	65546 MM;	CD4CA73A03E0D04CA CRC64;
Query Match		31.18;	Score 411.5;	DB 1; Length 674;
Best Local Similarity		34.98;	Pred. NO. 1.1e-21;	

RT collagen mRNAs." Acta 1130:78-80(1992).

CC Blochm. Biophys. Acta 1130:78-80(1992).

CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC

CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE

CC MINERALIZATION ZONES OF HYALINE CARTILAGE.

CC -1- SUBUNIT: HOMOTRIMER.

CC -1- PFM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING

CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

CC -1- SIMILARITY: STRONG TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC -----

DR EMBL; X67348; CAA47763.1; -

DR EMBL; X65121; CAA46237.1; -

DR EMBL; X63013; CAA44741.1; -

DR EMBL; Z21610; CAA79736.1; -

DR PIR; S28807; S28807.

DR PIR; S31216; S31216.

DR PIR; S22215; S22215.

DR MGI; MGI:88445; Col10a1.

DR InterPro; IPR001073; C1q.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 9.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR ProDom; PD000007; Collagen; 2.

DR SMART; SM00110; C1Q; 1.

DR PROSITE; PS01113; C1Q; 1.

DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

KW Cartilage; Collagen; Signal.

FT SIGNAL 1 18

FT CHAIN 1 680

FT DOMAIN 19 56

FT DOMAIN 57 519

FT DOMAIN 520 680

FT DOMAIN 545 680

FT DOMAIN 248 248

FT CONFLICT 286 286

FT CONFLICT 306 306

FT CONFLICT 417 417

FT CONFLICT 451 451

FT CONFLICT 500 500

FT CONFLICT 567 567

FT CONFLICT 569 569

FT CONFLICT 571 572

FT CONFLICT 635 635

FT SEQUENCE 680 AA; 66775 MW; FE984CA99AF708E2 CRC64;

Query Match 30.8%; Score 408; DB 1; Length 680;

Best Local Similarity 33.4%; Pred. No. 1.9e-21;

Matches 99; Conservative 34; Mismatches 75; Indels 88; Gaps 9;

QY 15 GSPPLDNNKIPSLCPGHPGLP-----GRPGHH-----GSQ 44

DB 392 GEPGLNGPK-----GNFGLPGQKGDPPVGTPGLRGVPYGAKEGVGHNGEAGPRREP 445

QY 45 GLRGDGDGDGDGAPGARGEGEGRGRLPGPR-----GDPGRGKA----- 86

DB 446 GIPTRGPTGPPGVPGGFPGSKDPRNGAPGAPGATGKLGNGPTGPPGPPGPRGSGSPG 505

QY 87 --GPAGTPGAPGECVSP-----PRSAFSKRSRSPVP 117

DB 506 LRGPPGPPGPGGQAVMPDGFITKAGORPLSGMPLVSAHNGVTGMVSAFTVILSKAY--P 563

QY 118 PSDAPLPEDRLVNEQGHYDAVTKGFTCOVPGVYVFAVHATVYRASLOFDLVKNG-ESIA 176

DB 564 AVGAPIPDEILYNNQHYDPRSGIFTCKIPGIYFYFHVHVKGTHVMWGLYKNGPTMY 623

QY 177 SFQFFGMPPRPASISGAMWLEPEDVQVQVGYDYGITASKTSTSGFLV 232

DB 624 TYDEYSKGYLQDA--SGSAIMELTENDQWLOLPAESNGLYSSBYVHSSFGFLV 677

RESULT 10

ID CQT2_HUMAN STANDARD; PRT; 285 AA.

AC Q9BXJ5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Complement-c1q tumor necrosis factor-related protein 2 precursor.

GN C1QTNF2 OR C1RP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Piddington C.S., Bishop P.;

RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";

RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

CC -----

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CC -----

DR EMBL; AF329836; AAK17960.1; -

DR EMBL; BC011699; AAK11699.1; -

DR Gene; HGNC:14325; C1QTNF2.

DR InterPro; IPR001073; C1q.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 2.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR SMART; SM00110; C1Q; 1.

DR PROSITE; PS01113; C1Q; 1.

KW Collagen; Signal.

FT SIGNAL 1 15

FT CHAIN 1 285

FT DOMAIN 40 141

FT DOMAIN 143 285

FT SEQUENCE 285 AA; 29952 MW; 7E31F9868D4EDFA CRC64;

Query Match 30.4%; Score 403; DB 1; Length 285;

Best Local Similarity 36.3%; Pred. No. 1.8e-21;

Matches 98; Conservative 29; Mismatches 91; Indels 52; Gaps 8;

QY 9 LLGLAA-----GSPPLDNNKIPSLC-----PGHGLPRTGHHSGQLPGRDGDG 54

DB 18 LLGAFARDFRKGSPOL-----VCSLPDGPQGPAGAPGSPGSMRMGMPFGKDGDD 70

QY 55 RDGAPGARGEGEGGRP-----GLPGRDPPGRGEGAPGAP---TGPAGECVSPPSASNA 108

DB 71 HDGDRGDSGEGSPRGRTGNGRKPGRKAGAIGRAGPRGPGVNGTPGKHGTPGKKGPKG 130

QY 109 KRSESRVPPPSDA-----PLFEDRLVNEQGHYDAVTKGFTCO 146


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Db 13 LKLLLLLLLPLR-----GQANTGCGIGPMGDLPGAPGKDGIDLPGPKGPGIDA 64
OY 58 APGARKEGEGRRPGLPRGRDPRGRGAPRGPGRGECVPP-----RSASFA 108
Db 65 IPGIRPGQKGEPLPGHPRGNMGPPGMPGVGPGIGPEPEEGRYKOKFQSVTV 124
OY 109 KRSESRVPPSPDAPLPFDRVLVNEQGHDAVYKFTCOVPGVYFAVATVYRASLOPDL 168
Db 125 TR-QTHOPRPARSLRNFANVLNPGODYDTSTGKFTCAVPGIXYTVYHNS-HTANLCVIL 182
OY 169 VKNGESIASFPOFGGMPKPSL-SGAMVRLPEPDQVWVOYGVGYD--IGIVASIKTD 224
Db 183 YRSQGVYVY---FCGHTSKTNQVNSGVLLRLQVGEVW--LAVNDYDMVGIGQS---D 234
OY 225 STEFGEIYSD 235
Db 235 SVFSGELLPD 245

RESULT 12
CA18_RABIT STANDARD: PRT: 744 AA.
ID CA18_RABIT STANDARD: PRT: 744 AA.
AC P14282:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
GN COL8A1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8938019; PubMed=2476437;
RA Yamaguchi N., Benya P.D., Van der Rest M., Ninomiya Y.;
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
RT demonstrate that type VIII collagen is a short chain collagen and
RT contains triple-helical and carboxyl-terminal non-triple-helical
RT domains similar to those of type X collagen."
RL J. Biol. Chem. 264:16022-16029(1989).
CC -1- FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC -1- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC -1- PIV: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
CC AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE
CC HIGH THERMAL STABILITY OF THIS REGION OF THIS REGION.
CC -1- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC
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CC -----
CC EMBL: J05042; AAA31204.1;
CC PIR: A34246; A34246.
CC InterPro: IPR001073; C1q.
CC InterPro: IPR000087; Collagen.
CC Pfam: PF00386; C1q; 1.
CC Pfam: PF01391; Collagen; 8.
CC PRINTS: PR00007; COMPLEMENTC1Q.
CC SMART: SM00110; C1Q; 1.
CC PROSITE: PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Collagen; Signal.
FT SIGNAL 1 20

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FT CHAIN 21 744 COLLAGEN ALPHA 1(VIII) CHAIN.
FT DOMAIN 29 117 NONHELICAL REGION (NC).
FT DOMAIN 118 571 TRIPLE-HELICAL REGION.
FT DOMAIN 572 744 NONHELICAL REGION (NC1).
FT DOMAIN 609 744 C1Q.
SQ SEQUENCE 744 AA; 73358 MW; 2A8CEFE8274E99 CRC64;

Query Match 28.2%; Score 374; DB 1; Length 744;
Best Local Similarity 34.4%; Pred. No. 4.7e-19;
Matches 93; Conservative 36; Mismatches 79; Indels 62; Gaps 8;

OY 24 IPSLC--FGHPLPTPGHNSQGLPGRDGRGAGAPKEGEGRRPGLP----- 74
Db 475 VPGLGPRGEPRIPODGLQGPGLIGITGPGGPIRGPIRKPKEGLPGRPGPGVK 534
OY 75 -----GPRGP--GPRGE--AGAPGPGAGECVPPRS----- 104
Db 535 PGVAGLHGPGRKPGALGPQGPGLPGPGPPGPPAPVMPPTPAPGELYLPDMGLGIDG 594
OY 105 -----AFSAKRESKVP-----PPSDALPLPRVLVNEQGHDAVYKFT 144
Db 595 VKTPHAYAKKGNKNGPAPVEMPFTAEETAPPPGAPIKEDRLLYNGRONTNPQTGFT 654
OY 145 COVPGVYFAVATVYRASLOPDLVKNESIA-SFOFGGMPKPSLSCAMVRLPEPD 203
Db 655 CEVPGVYFAVATVYRASLOPDLVKNESIA-SFOFGGMPKPSLSCAMVRLPEPD 203
OY 204 QWVQVGVGYDYGIVASIKTDFSGFLVY 233
Db 713 RVFLQMPSEQAAGLVAGVYHSSFGYLTY 742

RESULT 13
ID COLE_LEPMA STANDARD: PRT: 419 AA.
AC P98085; Q91080;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inner ear-specific collagen precursor (Saccular collagen).
OS Lepomis macrochirus (Bluegill).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Centrarchidae; Lepomis.
OX NCBI_TaxID=13106;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95167486; PubMed=7863331;
RA Davis J.G., Oberholzer J.C., Burns F.R., Greene M.I.;
RT "Molecular cloning and characterization of an inner ear-specific
RT structural protein."
RT Science 267:1031-1034(1995).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Gibson T.;
RT Submitted (MAR-1995) to the SWISS-PROT data bank.
CC -1- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE OTOLITHIC
CC MEMBRANE (PROBABLY).
CC -1- TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING CELLS AT THE
CC OUTER PERIMETER OF THE SACCULAR EPITHELIUM.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO BE
CC INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE THE SIMILARITY
CC WITH OTHER SHORT-CHAIN COLLAGENS.
CC -----
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CC EMBL: U17431; AA69978.1; ALT_FRAME.
 DR InterPro: IPR001073; Clq.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; Clq; 1.
 DR Pfam: PF01391; Collagen; 3.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 DR Extracellular matrix; Repeat; Collagen; Signal.
 KW SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 419 INNER EAR-SPECIFIC COLLAGEN.
 FT DOMAIN 20 57 NONHELICAL REGION (NC2).
 FT DOMAIN 58 274 TRIPLE-HELICAL REGION (COL1).
 FT DOMAIN 275 419 NONHELICAL REGION (NC1).
 FT DOMAIN 272 419 C1Q.
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 419 AA; 43634 MW; 570CDB9675FC0F39 CRC64;

Query Match 28.2%; Score 373; DB 1; Length 419;
 Best Local Similarity 37.5%; Pred. No. 3.1e-19;
 Matches 96; Conservative 23; Mismatches 99; Indels 38; Gaps 6;

QY 15 GSPFLDUNK--IPSLCFGHPGLPTPGHSGQLPCR--DGRDGDGAPGAPGKGGGR 70
 DB 157 GEPGLNTGKSGIGREGPMPGLAGTKGLKGQGLKGLQEGKEKRGPPGLRGEMGLNGT 216
 QY 71 PGLPGRPDGP-----RGEAGPAGTPGAGGCSV 100
 DB 217 DGVGGERGEPPLGKDGKDTGAKRPPGPGGKMGALGKGLKGVKRGKRGKGGESVE 276
 QY 101 PPRSAFSAKRSSESVPPPSDAPLPDRVLVNEGHDYAVTGKTCQVPGVYFAVHAITY 160
 DB 277 QIRSAFSGVLSPRSKSPSPSLPVKFDYFVNGEGHMDPLTKFNVTYPGVYLFSYHILTVR 336
 QY 161 RASLOPFLVKNK--ESIASFQFPGGMPKRPASLSGAWRLPEPDQVQVGVGIGIYA 219
 DB 337 NRPVALVNVGVRKRLRDSLYGODIDQ--SNIALHLTDGQVWLET--LRDMNGKYS 393
 QY 220 SIKTSTFGFLVSD 235
 DB 394 SSEDDSTFGFLLPD 409

RESULT 14
 CA18_HUMAN STANDARD: PRT; 744 AA.

AC P27658; O96D07;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
 GN COL8A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91231001; PubMed=2029894.
 RA Muraguchi Y., Mattei M.-G., Yamaguchi N., Olsen B.R., Ntomiya Y.,
 RA "The complete primary structure of the human alpha 1 (VIII) chain and
 RA assignment of its gene (COL8A1) to chromosome 3.";
 RL Eur. J. Biochem. 197;615-622(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
 CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
 CC -1- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION

CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
 CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLETT REPEATING
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -1- MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
 CC AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE
 CC THE HIGH THERMAL STABILITY OF THIS REGION.
 CC -1- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@sib-sib.ch).

DR EMBL: X57527; CA40748.1; -.
 DR EMBL: BC013581; AAH13581.1; -.
 DR PIR: S15435; S15435.
 DR Genew: HGNC:2215; COL8A1.
 DR MIM: 120251; -.
 DR InterPro: IPR001073; Clq.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; Clq; 1.
 DR Pfam: PF01391; Collagen; 8.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR PRODOM: PD000007; Collagen; 1.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Glycoprotein; Cell adhesion; Collagen; Signal.
 FT SIGNAL 28
 FT CHAIN 29 744 COLLAGEN ALPHA 1(VIII) CHAIN.
 FT DOMAIN 29 117 NONHELICAL REGION (NC2).
 FT DOMAIN 118 571 TRIPLE-HELICAL REGION (COL1).
 FT DOMAIN 572 744 NONHELICAL REGION (NC1).
 FT DOMAIN 609 744 C1Q.
 FT CONFLICT 262 262 P -> L (IN REF. 1).
 FT CONFLICT 297 297 P -> R (IN REF. 1).
 FT CONFLICT 344 344 P -> A (IN REF. 1).
 FT CONFLICT 382 382 A -> S (IN REF. 1).
 FT CONFLICT 388 388 P -> S (IN REF. 1).
 FT CONFLICT 454 454 L -> F (IN REF. 1).
 FT CONFLICT 464 464 A -> H (IN REF. 1).
 FT CONFLICT 601 601 Y -> T (IN REF. 1).
 FT CONFLICT 631 631 A -> G (IN REF. 1).
 FT SEQUENCE 744 AA; 73364 MW; 28C1B0955DE2C9A3 CRC64;

Query Match 27.8%; Score 368; DB 1; Length 744;
 Best Local Similarity 33.3%; Pred. No. 1.2e-18;
 Matches 90; Conservative 34; Mismatches 84; Indels 62; Gaps 6;

QY 24 IPSLC--PGRHGLPGRGHHSGGLPRGRDGDGDAFGAPGEGGGRGLP----- 74
 DB 475 VPGLLGPKRGEPGLDGLGPPGLPGIGSGGIPGGLPGKGEGLPDPGPGIGK 534
 QY 75 -----GPRGDPGRGEAGPAGTPGP-----AGECS 99
 DB 535 PGVAGLGRPGKRPALGPGGGLPGRPPGPGPPRPAVMPPTPPGGEVLPDMGLGIDG 594
 QY 100 VPPRSAPSAKRSSESRV-----PPSDAPLPDRVLVNEGHDYAVTGKFT 144
 DB 595 VKRPHAYGAKKKGKGPAYEMPAFTALTPAPVGAPEVFNKLLYNGRONYNPOTGIFT 654
 QY 145 QVPGVYFAVHAITYAVASLQFDLVKNGESLA-SFQFPGGMPKRPASLSGAWRLPEPD 203
 DB 655 CEVPGVYFAVHCKKGGNVALEFKNNEPMVYIDYKKGFIDQA--SSAVILLRPGD 712
 QY 204 QVAVGVGVGVDIGIYASIKTDSFGFLVY 233
 DB 713 RVFLQMPSEDAAGLITAGQIYHSSFGYLL 742

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:50:06 ; Search time 32 Seconds

(without alignments)
1564.670 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325
Sequence: 1 MRPLVLLILGLAAGSPPLD.....DSTFGFLVYSDMHSPPYFA 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1254	94.6	243	11 Q8R002	Q8R002 mus musculu
2	425.5	32.1	240	6 Q95M04	Q95M04 bos taurus
3	422	31.8	243	6 Q95J07	Q95J07 macaca mula
4	415.5	31.4	675	6 Q9N178	Q9N178 sus scrofa
5	402	30.3	295	11 Q9Z1K4	Q9Z1K4 rattus norv
6	395	29.8	294	11 Q9D8U4	Q9D8U4 mus musculu
7	373.5	28.2	194	6 Q95J95	Q95J95 canis fam11
8	370.5	28.0	744	11 Q9D2V4	Q9D2V4 mus musculu
9	370.5	28.0	744	11 Q9Z1S8	Q9Z1S8 mus musculu
10	368	27.8	744	4 Q96D07	Q96D07 homo sapien
11	363.5	27.4	705	4 Q8EJ5	Q8EJ5 homo sapien
12	314	23.7	245	11 Q9DCM6	Q9DCM6 mus musculu
13	270.5	20.4	246	11 Q9ES30	Q9ES30 mus musculu
14	266.5	20.1	196	11 Q9Z0M0	Q9Z0M0 tamias sibi
15	252.5	19.1	246	13 Q91907	Q91907 carassius a
16	247.5	18.7	256	13 Q91909	Q91909 cyprinus ca

17	241.5	18.2	347	4 Q96I6	Q96I6 homo sapien
18	238.5	18.0	583	4 Q96G58	Q96G58 homo sapien
19	238.5	18.0	992	4 Q96G76	Q96G76 homo sapien
20	238.5	18.0	1016	4 Q96C2	Q96C2 homo sapien
21	237	17.9	890	5 Q77087	Q77087 alvinella p
22	235	17.7	1017	11 Q99K41	Q99K41 mus musculu
23	234.5	17.7	173	6 Q62789	Q62789 sus scrofa
24	225	17.0	325	5 Q17036	Q17036 caenorhabd1
25	223	16.8	281	11 Q90X7	Q90X7 mus musculu
26	222.5	16.8	322	5 Q01945	Q01945 meloidogyne
27	222	16.8	251	13 Q91908	Q91908 brachydanio
28	222	16.8	1378	5 Q97405	Q97405 halictus di
29	221.5	16.7	120	6 Q77782	Q77782 oryctolagus
30	221.5	16.7	248	6 Q9T706	Q9T706 ovis aries
31	220	16.6	341	5 Q20142	Q20142 caenorhabd1
32	219.5	16.6	205	11 Q9D0M2	Q9D0M2 mus musculu
33	219.5	16.6	326	11 Q8R066	Q8R066 mus musculu
34	219.5	16.6	381	5 Q94399	Q94399 caenorhabd1
35	219.5	16.6	589	11 Q99L6	Q99L6 mus musculu
36	219.5	16.6	1453	11 Q63079	Q63079 rattus norv
37	218	16.5	182	11 Q8R1P2	Q8R1P2 mus musculu
38	217	16.4	319	5 Q17038	Q17038 caenorhabd1
39	217	16.4	1160	4 Q14046	Q14046 homo sapien
40	217	16.4	1344	13 Q93419	Q93419 gallus gall
41	217	16.4	1418	6 Q28396	Q28396 equus caball
42	217	16.4	1442	11 Q62031	Q62031 mus musculu
43	217	16.4	1442	11 Q62033	Q62033 mus musculu
44	217	16.4	1450	13 Q9Y1B4	Q9Y1B4 cynops pyr
45	217	16.4	1459	11 Q62032	Q62032 mus musculu

ALIGNMENTS

RESULT 1

Q8R002

ID Q8R002 PRELIMINARY: PRT: 243 AA.

AC Q8R002: Q8R002: 01-JUN-2002 (TREMBL) 21, Created)

DT 01-JUN-2002 (TREMBL) 21, Last sequence update)

DE 01-JUN-2002 (TREMBL) 21, Last annotation update)

OS Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein).

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC023068; AAH23068.1; -

DR EMBL; BC025174; AAH25174.1; -

KW Hypothetical protein.

SQ SEQUENCE 243 AA: 25420 MW: 498129CD051DB97B CRC64;

Query Match 94.6%; Score 1254; DB 11; Length 243;

Best Local Similarity 93.4%; Pred. No. 5.1e-100;

Matches 227; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY	1	MRPLVLLILGLAAGSPPLDNRKIPSLCPGHPGLPCTPGHNGSGGLPGRDGRDGA	60
DB	1	MRPLVLLILGLAAGSPPLDNRKIPSLCPGHPGLPCTPGHNGSGGLPGRDGRDGA	60
QY	61	APGEGEGEGRGGLPGRDPPRGAGAGPAGPAGGCVPPRFAFAKRSERYPPSPD	120
DB	61	APGEGEGEGRGGLPGRDPPRGAGAGPAGPAGGCVPPRFAFAKRSERYPPSPD	120
QY	121	APLPDRVLYNQGQYDAVNTGKTCQYGVGYVYFANVAVYASLOFDLVKNCSTAS	180
DB	121	APLPDRVLYNQGQYDAVNTGKTCQYGVGYVYFANVAVYASLOFDLVKNCSTAS	180

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Db      121 TPLPFDVNLNEGCHPPTTGKTCQVPGVYFFAVHATVYRASLOFDLVKNGOSIASFFQ 180
QY      181 FFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGYIGIYASIKTSTFSGFLVYSDWHSSP 240
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 YFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVGYIGIYASIKTSTFSGFLVYSDWHSSP 240
QY      241 VFA 243
        |||
Db      241 VFA 243
        |||

RESULT 2
Q95M04  PRELIMINARY;      PRT;      240 AA.
ID      095M04;
AC      095M04;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Adipose tissue-specific protein adipo Q.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21369933; PubMed=11382781;
RA      Sato C., Yasukawa Z., Honda N., Matsuda T., Kitaajima K.;"
RT      "Identification and Adipocyte Differentiation-dependent Expression of
RT      the Unique Distal Residue in an Adipose Tissue-specific
RT      Glycoprotein, Adipo Q."
RL      J. Biol. Chem. 276:28849-28856(2001).
DR      EMBL; AF269230; AAK58902.1; -.
DR      InterPro; IPR001073; Clq.
DR      InterPro; IPR000087; Collagen.
DR      Pfam; PF00386; Clq; 1.
DR      Pfam; PF03391; Collagen; 1.
DR      Prodom; PD000007; Collagen; 1.
DR      Prosite; PS01113; Clq; UNKNOWN_1.
SQ      SEQUENCE 240 AA; 26091 MW; C6253BA803B9A668 CRC64;

Query Match      32.1%; Score 425.5; DB 6; Length 240;
Best Local Similarity 41.5%; Pred. No. 7.1e-29;
Matches 100; Conservative 35; Mismatches 81; Indels 25; Gaps 10;

QY      6 VLLILGLAA-GSPRLDNDKIP-SLCPG-HPGLPTPGHSGGLPGRGDRDGAAGAP 62
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      7 LLLILALPSHGEDNDMEPLPKGACAGMAGIPEGHNGT---PGRDGD-----GTP 57
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      63 GEKGEGRPLPGPRGD-----PGRGEAGPAGPTGPAECGCVPPRSATSAKRS 113
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      58 GEGKEKDAAGILGKGTGVDVMTGAGPRGFPETPRKGEPRGEAAVYRSASFV-GLET 116
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      114 RVPPSPDAPLPEDRVLVNEGCHYDAVTGKTCQVPGVYFFAVHATVYRASLOFDLVKNGE 173
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      117 RVVYVP-NVPIRFRTKIFYNQDNHDSGTGKTCYCNIGLYTSYHATVYMKDKVKSLEKKD 175
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      174 SIASFQFGGMPKPRASLSGGAMVRLPEPDQVWVQVGVCD-YIGIYASIKTSTFSGFLV 232
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      176 AVLETTYDQYE-KNVDAQSGSVLLHLEVDQVWLQVYEGERHNGNVADVNDSTFTGFL 234
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      233 Y 233
        |
Db      233 Y 233
        |

RESULT 3
Q95J07  PRELIMINARY;      PRT;      243 AA.
ID      095J07;
AC      095J07;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE      Adiponectin.
GN      APML.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2133234; PubMed=11334417;
RA      Horta K., Fumashanl T., Bodkin N.L., Ortmeier H.K., Arita Y.,
RA      Hansen B.C., Matsuzawa Y.;"
RT      "Circulating concentrations of the adipocyte protein adiponectin are
RT      decreased in parallel with reduced insulin sensitivity during the
RT      progression to type 2 diabetes in rhesus monkeys."
RL      Diabetes 50:1126-1133(2001).
DR      EMBL; AF404407; AAK92202.1; -.
DR      InterPro; IPR001073; Clq.
DR      InterPro; IPR000087; Collagen.
DR      Pfam; PF00386; Clq; 1.
DR      Pfam; PF03391; Collagen; 1.
DR      Prodom; PD000007; Collagen; 1.
DR      Prosite; PS01113; Clq; UNKNOWN_1.
SQ      SEQUENCE 243 AA; 26264 MW; 49A45DAF2B4613FD CRC64;

Query Match      31.8%; Score 422; DB 6; Length 243;
Best Local Similarity 42.3%; Pred. No. 1.4e-28;
Matches 104; Conservative 28; Mismatches 88; Indels 26; Gaps 8;

QY      6 VLLILGLAAGSPRLDNDKIRSLCPGNG-----LPRTFGHSGGLPGRGDRDGAAG 60
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      6 VLLILALPSHGODTTTGGPGVLLPLPKGACTGMAAGIPGPHGNGVGRDGRD-----G 59
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      61 APGEKGEGRPLPGPRGD-----PGRGEAGPAGPTGPAECGCVPPRSATSAKRS 111
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      60 TPGEKGEKDPGLGIPRGDGTGCTGACGPRGPGIQRKGEPRGEAAVYRSASFV-GT 118
        :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      112 ESRYVPPSDAPLPEDRVLVNEGCHYDAVTGKTCQVPGVYFFAVHATVYRASLOFDLVKN 171
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      119 ETVYVTP-NMPIRTKIFYNQDNHDSGTGKTCYCNIGLYTSYHATVYMKDKVKSLEKKD 177
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      172 GES-IAFQFGGMPKPRASLSGGAMVRLPEPDQVWVQV-GVGYITVYASIKTSTFSG 229
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      178 DKALFTYDQYQENNVDQA--SGSVLLHLEVDQVWLQVYGEGERNLGYADNDSTFTG 235
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      230 FLYYSD 235
        ||:|
Db      236 FLYYHD 241
        ||:|

RESULT 4
Q9N178  PRELIMINARY;      PRT;      675 AA.
ID      09N178;
AC      09N178;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Type x collagen.
GN      COL10A1.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21015405; PubMed=11130976;
RA      Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
RA      Skutki N.M., Thomsen B.;"
RT      "Abnormal growth plate function in pigs carrying a dominant mutation
RT      in type x collagen."
RL      Mamm. Genome 11:1087-1092(2000).
DR      EMBL; AF222861; AAF37271.1; -.

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OY 3 PLVLLVLLGLAAGSPPLDNNKIPSLCPGHPGLPCTPGHNGSOGLEPRDGRDGRGAPGAP 62
DB 41 POLYCSLPG-----PQGPBPAPGAPSSGVGRMGPPGKDGQGGDGRDSD 87
OY 63 GEKEGGR---GLPGRGDPGRGEGAPAP---TGRAGCSVPPRPAFAKSESSEVVP 116
DB 88 GEEBPPGKTGRNGKQGPGRKAGALGRAPRGPBGVSGTPGHNGTPPKGKGGKGPGLP 147
OY 117 PPSDA-----PLPDRVLVNEOGHYDAVTGKFTCOVPGVYFA 154
DB 148 GPGCGSSRAKSAFVAVTKSPRERLPKIKFDKILMNGGHYNNSSGKFTVCSVGIYFT 207
OY 155 VHAIVYRASLOFDLVKNGESIASFFQFGPWPKPAISGGAMVRLPEPDQVVOVGYDY 214
DB 208 YDITLANKHLAIGLVHNGQYRIRTFEDANTGNHDA--SGSTILAKEGDEVMQIFVSEQ 265
OY 215 IGI-YASIKIDSTFSGFLVSD 235
DB 266 NGLEYDPWYDLSLTGFLITAD 287

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RESULT 7

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ID 095J95 PRELIMINARY: PRT: 194 AA.
AC 095J95.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adiponectin (Fragment).
GN APM1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RA Kadir M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,
RA Dea M.K., Bergman R.N.;
RT "Regulation of Adiponectin gene expression in the fat-fed dog.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF417206; AL090702.1;
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR ProDom: PD000007; Collagen; 1.
DR PROSITE: PS01113; Clq; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;

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Query Match 28.2%; Score 373.5; DB 6; Length 194;
 Best Local Similarity 42.3%; Pred. No. 1.6e-24;
 Matches 90; Conservative 22; Mismatches 66; Indels 35; Gaps 9;

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OY 8 LLLGLAAGSPPLDNNKIPSLCPG-HPGLPCTPGHNGSOGLEPRDGRDGRGAPGAPGEG 66
DB 4 VLLPLPRGA-----CPGMAGIPGHPGHNGL---PGRGRD-----GTPEKG 43
OY 67 EGGRGGLPGRGD-----PGRGDAAGPAGTPAGGCSVPPRPAFAKSESSEVVP 117
DB 44 EKGPGGLVPRGDPGETGVTVGEGRPGFPGKRGPGESAVYHRSASFV-GLSEITV 102
OY 118 PSDAPLPDRVLVNEOGHYDAVTGKFTCOVGVYFAVHATVYRASLOFDLVKNGESIAS 177
DB 103 P-NPIFTKIFLYMLQNHHTGCTCKFCNPIGLTYFSYHITIVYLKDVKSILYKDK--AM 159
OY 178 FFOFGGMPKPA-SLGGAMVRLPEPDQVVOV 209
DB 160 LFTYDQYOEKNVDQAGSGSVLLHLEVGDQVNLQY 192

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RESULT 8

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ID 09D2V4 PRELIMINARY: PRT: 744 AA.
AC 09D2V4.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
EX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringuet M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK018742; BAB1383.1;
DR MGD: MGI:88463; Col8a1.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 7.
DR PRINTS: PR000007; COMPLEMENTC1Q.
DR SMART: SM00110; Clq; 1.
DR PROSITE: PS01113; Clq; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCEB99C CRC64;

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Query Match 28.0%; Score 370.5; DB 11; Length 744;
 Best Local Similarity 34.6%; Pred. No. 1.4e-23;
 Matches 93; Conservative 32; Mismatches 83; Indels 61; Gaps 7;

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OY 24 IPSLC--PGRHGLPCTPGHNGSOGLEPRDGRDGRGAPGAPGEGGRGRLP----- 74
DB 476 VFGILGPKGEGIPGDOGLOGPPTGIVPSGFTGPPGIPGPGEGGLPGEFFPGVVK 535
OY 75 -----GPRDPPGRGEGAGPAGTP-----AGCSV 100
DB 536 PGVAGLHPPGKKGALGPGQGLPGRGPGPRGPRPAVMPSPGSEYLPDMGLGIDGV 595
OY 101 PPRSAFSAKR-----SESRVP-PPSDAPLPDRVLVNEOGHYDAVTGKFTC 145
DB 596 KPRPAVYAGKKGKGGPAYEMPAPFAETLVPFPVPGVAGKDKLLYNQRQYNNQYTGFTC 655
OY 146 QVGVYFAVHATVYRASLOFDLVKNGESIA-SFFQFGGMPKPAISGGAMVRLPEPDQ 204
DB 656 EVPGVYFAVHCKGKNVAVLTKNNEPMYTYDEYKKGLDQA--SGSAVLLLRPGDQ 713
OY 205 VVVQVGVGDYIGIYASIKIDSTFSGFLVY 233
DB 714 VFLQMPSEQAAGLYAGGYVHSSFSGYLLY 742

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us-09-944-944-42.rsp

DR	PROSITE, PS000615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR	PROSITE, PSS00041; C_TYPE_LLECTIN_2; 1.
KW	LECTIN; Signal.
FT	NON_TER 1
FT	SIGNAL <1 13
FT	VARIANT 145 145
SO	SEQUENCE 246 AA; 25709 MW; AB692282D89D0D5 CRC64;
Query Match	19.1%; Score 252.5; DB 13; Length 246;
Best Local Similarity	31.9%; Pred. No. 5.2e-14;
Matches	80; Conservative 33; Mismatches 73; Indels 65; Gaps 14
QY	4 LVLVLLILGLAAGSPDLLDNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDGAPGAG 63
DB	2 LLLQFALQLLDGAPQNLN-----CPAAGVGPTGPHGN-----GLPGRDGRDGDGALGPKG 53
QY	64 EKGGG-----GRPLPGPRGDPCGRGEGAPGAPGPGEGCSVPYPSARSAKSSSESARVPP 118
DB	54 EKGGSGSVGGPPPKACAPPGTAGKEGEGRGPPGPGSPGSESVLESKEIIDLAKTI--- 110
QY	119 SDAFLPFDRLVLYNEQGHYDAVTGKTCQVPGSVYFAAHATVYRASLQFIDLKNGESIASF 178

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Db      111  -----ATPEK--VSSVCHFRKV-----GQKYYITDGWVG---NFD-----QGLKSC 146
QY      179  FQFFGGMFKPASLSGGMV--KLEPEDOVWQV-----GVGD---YIGIYASIKIDSTF-- 227
Db      147  MEF-----GGMVSPRTSAENALIKLVSSGLGSRKKPYIGV-TDRKTEGOFVD 194
QY      228  --SGFLVYSDW 236
Db      195  TEGKOLFTTNW 205

Search completed: June 13, 2003, 16:01:17
Job time : 34 secs

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Search completed: June 13, 2003, 16:01:17
Job time : 34 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 16:33:24 ; Search time 1719 Seconds

(without alignments)
2289,414 Million cell updates/sec

Title: US-09-944-944-42
Perfect score: 1325
Sequence: 1 MRPLVLLGLAAGSPPLD.....DSTFSGRLVYSDMHSSPVFA 243

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODELS-frame+_p2n_model -DEV-rlh
-O=/cgn2_1/USP10.spool/US09944944/runal_13062003_150047_24252/app_query.fasta.1.391
-DB-EST -QFMT=fastlap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-Biosum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09944944.ecgn.1.1.1306.6runat_13062003_150047_24252 -NCPU=6 -ICPU=3
-DEV TIMEOUT=120 -WARN SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO_MMAP -LARGESUBSTRY -NEG SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1164.5	87.9	844	10	BE309370 601094718
2	1138	85.9	1093	14	BM924569 AGENCOURT
3	1125	84.9	1045	14	BM920874 AGENCOURT
4	1062.5	80.2	778	12	BF098614
5	1034	78.0	1154	13	BM547549
6	1024.5	77.3	869	13	BF763193
7	1019	76.9	941	13	BF1821899
8	1006	75.9	879	13	BF1820945
9	984	74.3	887	13	BF1490062
10	982.5	74.2	842	13	BF1688017
11	917	69.2	846	13	BF1458455
12	895	67.3	1623	14	BM926477
13	873.5	65.9	567	13	BM021381
14	868.5	65.5	936	12	BF540263
15	827	62.4	870	9	AF451167
16	806	60.8	702	12	BF055285
17	754	56.9	649	13	BM427498
18	717	54.1	660	13	BM488918
19	713	53.8	630	12	BF706609
20	703	53.1	792	13	BF1770921
21	677	51.1	565	12	BF088379
22	674	50.9	801	13	BF1490880
23	673	50.8	628	13	BM426563
24	668.5	50.5	867	13	BF1818537
25	631	47.6	532	12	BF724241
26	623	47.0	664	14	BQ419058
27	612.5	46.2	564	14	BQ419213
28	609	46.0	655	14	BQ285731
29	593	44.8	410	12	BE861753
30	582	43.9	547	12	BE722922
31	575	43.4	735	14	BE208555
32	573	43.2	634	14	BQ449252
33	568	42.9	630	12	BF046067
34	567.5	42.8	418	9	AA510952
35	567	42.8	628	14	BF0285387
36	553.5	41.8	535	13	BF705095
37	549	41.4	613	13	BF1842952
38	545	41.1	613	13	BF1842844
39	530	40.0	517	14	BM966954
40	530	40.0	521	14	BM966810
41	520.5	39.3	606	14	BQ260266
42	520	39.2	962	12	BF340559
43	515	38.9	1349	14	BQ673882
44	502	37.9	325	9	A1070779
45	494	37.3	361	9	AF1614058

ALIGNMENTS

RESULT 1
LOCUS BE309370
DEFINITION BE309370 844 bp mRNA linear EST 26-OCT-2000
601094718P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489340 5',
LOCUS BE309370
ACCESSION BE309370
VERSION BE309370.1 GI:9167454
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 844)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

DB: 14 Gaps: 0

US-09-944-944-42 (1-243) x BM924569 (1-1093)

QY 36 GlyThrProGlyHisHisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArg 55
 DB 2 GGCACGGCGGGCCACCATGGACAGGAGGCGGCTTGGCGGGCGGATGGCGGACGGCGCCG 61

QY 56 AspGlyAlaProGlyAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 75
 DB 62 GACGGCGGGCGGGCGGCTCCGGGAGAGAAAGGCGAGGGGCGGAGCGGGAGCTGGCGGGA 121

QY 76 ProArgGlyAspProGlyProArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 95
 DB 122 CCTCAGGAGGAGACCGGGCGGCGGAGAGAGGCGGAGACCGGGCGGCCCGCGGCTGCC 181

QY 96 GlyGlyGlySerSerValProProArgSerAlaPheSerAlaLysArgSerGlySerArgVal 115
 DB 182 GGGGAGGTGCTCGGTCTCCGCGATCCGCTTCACGCGCCAGCGCTCCGAGAGCGGGGTG 241

QY 116 ProProProSerAspAlaProLeuProPheAspArgValLeuValAsnGlyGlnGlyHis 135
 DB 242 CTTCCGCGCGCTGACAGCACCTTCCCTTCGACCGCGCTGCTGTGACAGCAGGAGACT 301

QY 136 TyrAspAlaValThrGlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaVal 155
 DB 302 TACGACGCCGCTACCGGCAAGTTCACTCCAGGTGCTCGGGGTCTACTACTTCCGCGTC 361

QY 156 HisAlaThrValTyrArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIle 175
 DB 362 CATGCGACCGCTTACCGGGCGGCGCTGACGTTGATCTGGTAGAGATGGCAATCCATT 421

QY 176 AlaSerPhePheGlyPhePheGlyTyrTyrProLysProAlaSerLeuSerGlyGlyAla 195
 DB 422 GCTCTTTCTTCCATGTTTTCGGGGGAGTGGCCCAAGCGACCTCGCTCGGGGGGGGCG 481

QY 196 MetValArgLeuGlnProGlyLysAspGlnValTyrValGlnValGlyValGlyAspTyrIle 215
 DB 482 ATGGAGAGGCTGAGAGCTGAGAGCAAGTGGGTGGAGTGGGTGGTACTACAT 541

QY 216 GlyIleTyrAlaSerIleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAsp 235
 DB 542 GGCATCTATGCGAGATCAAGACAGACAGACACTTCTCGGATTTCTGGTGTACTCCGAC 601

QY 236 TrpHisSerSerProValPheAla 243
 DB 602 TGGCACAGCTCCCGACGTTTGTCT 625

RESULT 3
 BM920874 1045 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT_6706053 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752141
 DEFINITION 5', mRNA sequence.
 ACCESSION BM920874
 VERSION BM920874.1 GI:19371253
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1045)
 AUTHORS NIH-MGC http://mgi.nhlbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM12785 row: n column: 14
 High quality sequence stop: 415.
 Location/Qualifiers
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 /clone="IMAGE:5752141"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

BASE COUNT 176 a 343 c 341 g 183 t 2 others

ORIGIN

Alignment Scores:
 Pred. No.: 4,24e-72 Length: 1045
 Score: 1125.00 Matches: 217
 Percent Similarity: 90.98% Conservative: 5
 Best Local Similarity: 88.93% Mismatches: 18
 Query Match: 84.91% Indels: 4
 DB: 14 Gaps: 0

US-09-944-944-42 (1-243) x BM920874 (1-1045)

QY 1 MetArgProLeuLeuValLeuLeuLeuGlyLeuAlaGlySerProProLeuAsp 20
 DB 93 ATGAGGCGCCCT 152

QY 21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis 40
 DB 153 GACACAGATGCCAGCTCTGCGGGGAGCACCGGCGCTTCAGAGCGCGGGGCCAC 212

QY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
 DB 213 CATGCGACGACAGGCTTGGCGGGCGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGG 272

QY 61 AlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80
 DB 273 GCTCGGGAGATAAAGGCGAGGGCGGAGCGGCGGAGCTCCGGGACTTCGAGGGGACCC 332

QY 81 GlyProArgGlyGlyAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal 100
 DB 333 GGGCGCGAGAGAGGCGGAGCCCGCGGGCCACCGGCGCTCGGGGAGTGTCTGGTG 392

QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProSerAsp 120
 DB 393 CTTCCGCGATCCGCTTACGCGCAAGCGCTCGAGAGCGGCGGCTCTCCGCGACTGAC 452

QY 121 AlaProLeuProPheAspArgValLeuValAsnGlyGlnGlyHisTyrAspAlaValThr 140
 DB 453 GCACCTTGGCTTGGACCGCGCTGTGGTGAAGGAGGAGGAGCATTAGACCGCTCCAC 512

QY 141 GlyLysPheThrCysGlnValAlaProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
 DB 513 GGCAGAGATCACCTGCGAGGTGCTTGGGTCTACTCTTCCGCGCTCATGCCCTCTTAC 572

QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPhePheGln 180
 DB 573 CGGGCGAGCTCAGATTGATCTGGCGAAGATGGCATTCATTCCTTGTCTCAT 632

QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
 DB 633 GTTTTCGGGTGGTGGCCAAACACCTTCAGTCTGGGGGGGCGCATGTGTGTCTGGAG 692

QY 201 ProGlyAspGlnValTyrValGlnVal-GlyValGlyAspTyrIle-GlyIleTyr-Ala 219


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/lab1.host="DH0B"
/site1="Organ: ovary (pool of 3); Vector: pCMV-Sport6;
Site1: EcoRV (destroyed); Site2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
Tracking code 036."
BASE COUNT      178 a      382 c      401 g      193 t
ORIGIN

Alignment Scores:
Pred. No.:      1,79e-65      Length:      1154
Score:          1034.00      Matches:      202
Percent Similarity: 88.69%      Conservative: 6
Best Local Similarity: 86.32%      Mismatches: 23
Query Match:      78.04%      Indels:      4
DB:              13      Gaps:      1

US-09-944-944-42 (1-243) x BM547549 (1-1154)

QY      1 MetArgProLeuLeuValLeuLeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAsp 20
Db      188 ATGAGGCGACACTCTGCTGCTCTGCTCTGCTGAGGCGCGCGGCTGCCCGCCACTGTGAC 247

QY      21 AspAsnLysIleProSerLeuLeuCysProGlyHisProGlyLeuProGlyTyrHis 40
Db      248 GACACACAAAGATCCCAAGCTCTGCCCCGGGGGACACCCGGCCCTTCCACGACGACCGGGCCAC 307

QY      41 HisGlySerGlnGlyLeuProGlyIleArgAspGlyIleArgAspGlyIleArgAspGlyIle 60
Db      308 CATGGACACCGAGGGCTTCCGGGGCGCGATGGCGGACGGCCCGGAGAGGGCGCGCCGG 367

QY      61 AlaProGlyIleLysGlyGlyGlyGlyGlyIleArgProGlyLeuProGlyIleProArgGlyAspPro 80
Db      368 GCTCCCGGAGAGAAAGGCGAGGGCGGGGAGCGGAGACTGCCGGGACCTCGAGGGGACCC 427

QY      81 GlyProArgGlyGlyAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal 100
Db      428 GGGCGCGGAGAGAGCGCGGACCCGGCGGGCCACCGGGCTGCCGGGGAATGCTCGGTG 487

QY      101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProProSerAsp 120
Db      488 CCTCCGGGATCCCGCTTCAGCGCCAAAGCGCTCCGAGACCGGGGTGCTCCGCCGTGAC 547

QY      121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140
Db      548 GCACCCCTGCGCTTCGACCGCGGCTGTGTGAACGACGAGGACATTAAGACCGCGTCAC 607

QY      141 GlyLysPheThrCysGlnValAlaProGlyValTyrTyrPheAlaValAlaHisAlaThrValTyr 160
Db      608 GGCAGAGTTCACCTGCCAGGTGCTCGGGGTCTACTACTTCCGGCGTGCATGACGACCGTAC 667

QY      161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPhePheGln 180
Db      668 CGGGCCAGCCCGCAGTTTGATCCGCGGAGAGATGGCGATCTT- GCCCTCTTCTTCAGT 726

QY      181 PhePheGlyGlyTyrPProLysProAlaSerLeuSerGlyGlyIleAlaMetValArgLeuGln 200
Db      727 TTTTTCGGGGGGGGCCCAAGCCGCCCGCTGCTCTCGGGGGGGGACACTGTATAAGTGGAA 786

QY      201 -ProGlnAspGlnValTyrValGlnValGlyValGly--AspTyrIleGlyIleTyrAl 219
Db      787 CCCCGAGGACCAATGTGGGGGACCGGGGTGCGGAGGTGACCTCCCGGAGGACTTAATGC 846

QY      219 aser-IleLysThrAspSerThrPheSerGlyPheLeu 231
Db      847 CAGCGGTCCGAAACAAACAGACCTTTCCTGGGAATTGG 884

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LOCUS	BI7631193	869 bp	mRNA	linear	EST-25-SEP-2001
DEFINITION	603049929P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190222 5',				
ACCESSION	mRNA sequence.				
VERSION	BI7631193				
KEYWORDS	BI7631193.1	GI:15754771			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
JOURNAL	1 (bases 1 to 869)				
COMMENT	NIH-MGC http://mhc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapsb-remail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.llnl.gov				
	Plate: LRAM1475 row: 1 column: 07				
	High quality sequence stop: 777.				
FEATURES	Location/Qualifiers				
source	1..869				

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	/db_xref="taxon:9606"
	/clone="IMAGE:5190222"
	/clone_1lb="NIH_MGC_116"
	/lab_host="DH10B"
	/note="Organ: pooled colon, kidney, stomach; Vector: pCW-SPOF6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gubler (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT	133 a	277 c	339 g	120 t
ORIGIN				

Alignment Scores:	
Pred. No.:	6,74e-65
Score:	1024.50
Percent Similarity:	95.48%
Best Local Similarity:	94.12%
Query Match:	77.32%
DB:	13
Gaps:	0

US-09-944-944-42 (1-243) x B1763193 (1-869)

QY	1 MetArgProLeuLeuValLeuLeuLeuLeuGlyPheAlaAgiSerProProLeuAsp	20
Dd	217 ATGAGCGCAATCTCCTCGTCGTCGTCTCTGTGGCCGTGGCGGCGGCCACACTGGAC	276
QY	21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis	40
Dd	277 GACAACAAAGWCCCAGCCCTGCGCCCGGGCACCCCCCGGCTTCACAGGCACAGCCGGGCGAC	336
QY	41 HisGlySerIleIngLyLeuProGlyArgAspGlyYArgAspGlyYArgAspGlyAlaProGly	60
Dd	337 CATGGACGCCA-GGCTTGCCGGCGCGCGGATGCCGCACAGCGCCGACGGCGCCGGG	395
QY	61 AlaProGlyVgLiutysGlyIngLyYArgProGlyLeuProGlyProArGlyYAspPro	80
Dd	396 GCTCCGGAGAGAAGAGCGAGGGCGGGAGGCGGGAATGCTCGGGAACCTCCAGGGGACCCC	455
Y	81 GlyProArGlyGlyAlaInagLyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal	100

Dd	456	GGGCGGAGAGGAGCGCGGAGCCGCCGGGGCCACCGGGGCGTGGCGGTGGTG	515
Oy	101	ProPrOAHgSerAlaphSeSerAlAyaArSergUSeRAtAg-VAlProPrOProSeRs	120
Dd	516	CCTCGGCATCCTTCCTTAGCGCCAAAGCGCTCCGAGACC GGCGGCGCTCGCTCGA	575
Oy	120	pALAPrOleubProPhesApARgVAlLeuVal-ASnGLInGlYhIStYrAsPAlaVal-	139
Dd	576	CGACACCTTCGCCCTTCGACCGCGTCTGTGTGAACAGACAGGACATTACGACGCCCTTC	635
Oy	140	ThrgILyLSpherhChysGlnValPrOGlyValYTrYPheAlaValHIsAlathVal	159
Dd	636	ACCGCAAGTTCCACTCGCCAGGTGGCTGGGCTCTACTTCCTCGCGTCCATGCCACCTGC	695
Oy	160	TyrAlgaLaseRleuGlnPhasPreuValLySaAnGIvGUseRlIeAlaseRphEhe	179
Dd	696	TACGGGGAGCGCTGACAGTTGATGTGTGAAGAATGGCGCATTCATTGGCTC-TTCCTTC	754
Oy	180	GlnPhepHeplgyLYTrPProlYSProAlaseRleuseRsglyGlyAlameValArgLeu	199
Dd	755	CAGTTTACGGGGGGGTGGCCAAGCC--AGCTGCGCTCGGGGGGGGCCATGTGAGCGTG	812
Oy	200	GUprOGluApBgInValITryValGlnValGlyVal-glyAspyrTlleGlylle	217
Dd	813	GAGCCTGAGGACCAAGTGTGGTGTGAGGTGTGTGGTGTGACTAGCTTGGGCATC	867
RESULT 7	B1821899	941 bp mRNA linear EST 04-OCT-2001	
LOCUS	B1821899	6030357996P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176967 5'	
DEFINITION		mRNA sequence.	
ACCESSION	B1821899		
VERSION	B1821899.1	GI:15933449	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens .		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 941)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: gcgsb@femail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LLMML1440 row: p column: 24 High quality sequence stop: 779. Location/Qualifiers 1..941 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5176967" /clone_id="NIH_MGC_115" /lab_host="DH10B" /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 65. Library is o1y0-or primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."		
FEATURES	source		
BASE COUNT	130 a 320 c 329 g 162 t		
ORIGIN			

Alignment Scores:					
Pred. No.:	1,81e-64	Length:	941		
Score:	1019.00	Matches:	223		
Percent Similarity:	90.40%	Conservative:	3		
Best Local Similarity:	89.20%	Mismatches:	13		
Query Match:	76.91%	Indels:	14		
DB:	13	Gaps:	0		
US-09-944-944-42 (1-243) x B1821899 (1-941)					
OY	3	ProLeuLeuValIleuLeuLeuLeuLysAlaIaglySerProProLeuAspaspasn	22		
Dd	179	CCACGCTCCHGTCTGCTGTCCTCGTGGGCCGCGGGCCGGGTGCCTCCCCCACTGGACAGACAAC	238		
OY	23	LysLIleProserLeuCysProglyHisProglyLeuProglyThrProglyHisIshgLy	42		
Dd	239	AAGATCCCAGACTCTTGCCCGGGGGCACCCGGCCCTTCCAGGCACCCCGGGCCCATATGCG	298		
OY	43	Ser-GlnIleLeuProglyArgAspGIArgAspGLyArgAspGLyAlaIaprogly-Alap	62		
Dd	239	AGCATGGGCTTGGCCGGGGCCGGAGATGGCGGACGGCCGCGGGGGCCGGGGGGCTC	358		
OY	62	roglYglULysglYglUglYglYArgPProglyLeuProglyProArnglYaspproglyP	82		
Dd	359	CGGGAGAAAGGCGAGGGCGGGAGACCGGGACTCGGAGACTCGAAGGGGACC CGGGGC	418		
OY	82	roArnglYglULaIaglyProAIaglyProThr-GlyProAla-GlyGlucYsserValPr	101		
Dd	419	CGCGGAGAGAGCGGGACCCGGGGGGCCACCGGGGCTCGCGGGGAGTGTCTCGGTCC	478		
OY	101	oProArngSerAlaPheSerAlaLYsArgSergIusEr--ArgValIProProserAsp	120		
Dd	479	TCCGGGATCCGGCTTCACGGCCAGCGCTCGAGAGCCTGGGTGCTCTCCGCGCTGCAC	538		
OY	121	AlApProLeu-ProPheAspArgValLeuValAsnGLInglInglYHISTYRAspAlaValTh	140		
Dd	539	GCACCCCTTGGCCCTTCGACCGCGTCTGTGTGAACAGAGAGGACATTACGAGCCGCTAC	598		
OY	140	rGLYspPheThrCys-GlnValProglyValTYrPheAlaValHis-AlatharVal	159		
Dd	559	CGGCAAGTTCACTCCGCGAGGTGCTGGGGCTTACTACTTGGCCCTCCATTGCCACCGTC	658		
OY	160	TYrArGalaserLeuGlnPheAspLeuValLYsAsnGLYglusErTIIalasErfephe	179		
Dd	659	TACGGGGCCAGCTGCACTTGTGATCTGGTAAGAATGGCAATCATTCATTCCTTCTTC	718		
OY	180	GlnPhePheglYglTYrProlYSProAlaserLeuserGLYglYAlaMetValArgLeu	199		
Dd	719	CAGTT-TTCGGGGCACTGGCCCAAGCAACCTCGCTCGGGGGGGCCATGTGTAGGCTG	777		
OY	200	GLU-ProILyspGlnValITrPvalGlnVal-GlyValGLYAspTYrTIIleglyIleTYra	219		
Dd	778	GAGCCCTTAGGACCAAGTGTGGGTCCGGTGGGGTGTGGTGTACTACTTGGCTTCTATG	837		
OY	219	IasErTIIeLYsThrAspSerThrPheSergLYPheLeuValTYrsAsprTHIsers	239		
Dd	838	CCAGATAGGCA-GACAGAGACTTCTCGGATTCTG-CTGTACTCCGACTGGCACAATC	895		
OY	239	erProval 241			
Dd	896	CCGAGTTC 903			
RESULT 8 B1820945 879 bp mRNA linear EST 04-OCT-2001 LOCUS 60303398P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175070 5', DEFINITION mRNA sequence. ACCESSION B1820945 VERSION B1820945.1 GI:15932495 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens					

[illegible]

JOURNAL
COMMENT

Published (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rsfemail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.nih.gov
Plate: L1M11904 row: k column: 22
High quality sequence stop: 795.

FEATURES
source
location/Qualifiers

1.842
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5355789"
/clone_1ib="NCL CGAP Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_note="H108"
/host="Organ: mammary; Vector: PCMV-SPORT6; Site:1: Saliv site:2: Notti; Cloned unidirectionally. Primer: Oligo dr library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT
ORIGIN
161 a 256 c 265 g 160 t

Alignment Scores:
Pred. NO.: 7.18e-62 Length: 842
Score: 982.50 Matches: 197
Percent Similarity: 88.03% Conservative: 9
Best Local Similarity: 84.19% Mismatches: 22
Query Match: 74.15% Indels: 7
DB: 13 Gaps: 1

US-09-944-944-42 (1-243) x B1688017 (1-842)

OY 1 MetArgProleuLeuValLeuLeuLeuLeuValAlaGlySerProProleuasp 20
|||||
Db 152 ATGAGGCCATTCTTCCCTTCTGCTTCTGGGTCTGGTCAAGCTCTCTCTCTGGAC 211
|||||
OY 21 AspAsnLysIleProSerLeuLysProGlyHisProGlyLeuProGlyTyrProGlyHis 40
|||||
Db 212 GACCAACAAGTCCCCAGCCTGTGTCTCCGGGAGCCGGGCTTCAGGACACAGAGTAC 273
|||||
OY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
|||||
Db 272 CATGGCAGCCCAAGCCCTGCTGCTGCTGAGCCGCGCTGATGGCGGAGCGGACCCGGA 331
|||||
OY 61 AlaProGlyGluLysGlyGluGlyGlyAlaGlyProGlyLeuProGlyProArgGlyAspPro 80
|||||
Db 332 GCTCCGGGAGAGAAAGGCGAGGGCGGAGACCGGAGCTACCTGGGCCACGTGGGAGCC 393
|||||
OY 81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGlyLysSerVal 100
|||||
Db 392 GGGCGCGTGGAGAGGACGAGGCGCATTACGGGCGTGGGGGAGTGGCTGGTA 451
|||||
OY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProProSerAsp 122
|||||
Db 452 CCCCCAGATCAGCCCTTCACTGATCCCAAGCATCCGAGAGCCGGGTACCTCCCGACCGCAC 511
|||||
OY 121 AlaProLeuProPheAspArgValLeuVal-AsnGluGlnGlyHisTyrAspAlaValTh 140
|||||
Db 512 ACACCCCTTACCTTTCACCGCTGTGCTGCTAAATAGCAGGGCCATTTCGACCCCACTAC 571
|||||
OY 140 rGlyLysPheThrCysGln-ValProGlyValTyrTyrPheAlaValHisAlaThrValT 160
|||||
Db 572 TGGCAAGTTCACCTGCGCAAGGTGCTGGGTCTACTACTTGTCTGTGACCGCACTGTCT 631
|||||
OY 160 yrrArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerTlleAlaSerPhePheg 180

AUTHORS Sharma,S., Chang,J.T., Della,N.G., Campochiaro,P.A. and Zack,D.J.
TITLE Identification of novel bovine RPE and retinal genes by subtractive
hybridization
JOURNAL Mol. Vis. 8, 251-258 (2002)
COMMENT Contact: Sharma S
Ophthalmology
Flinders University
Flinders Drive, Bedford Park, SA 5042, Australia
Email: shivani.sharma@flinders.edu.au

FEATURES
SOURCE 1. 870
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="Bos taurus retinal pigment epithelium"
/tissue_type="retinal pigment epithelium"
/note="Heterologous primer from porcine were used to
amplify bovine target cDNA"

BASE COUNT 171 a 251 c 265 g 183 t
ORIGIN

Alignment Scores:
Pred. No.: 1,33e-50 Length: 870
Score: 827.00 Matches: 154
Percent Similarity: 98.73% Conservative: 1
Best Local Similarity: 98.09% Mismatches: 2
Query Match: 62.42% Indels: 0
DB: Gaps: 9

US-09-944-944-42 (1-243) x AF451167 (1-870)

```
QY 87 G1PProAlaGlyProThrGlyProAlaGlyGluCysSerValProProArgSerAlaPhe 106
Db 2 GGACCCATGGGGGCAACCGGGCGCGGAGAGTCGCGCTCCGCGCTCCGCTTC 61
QY 107 SerAlaLysArgSerGluSerArgValProProProSerAspAlaProLeuProPheAsp 126
Db 62 AGCGCTAAGCGCTCTTGAGAGCGGGTCCCGCGCGTGGAGCGGCCCTACCTTCGAC 121
QY 127 ArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThrGlyLysPheThrCysGln 146
Db 122 CCGGTGCTGGTGAACGAGCAGGAGCACTACGACCGCTCAACCGGCAAGTTCACCTGCCAG 181
QY 147 ValProGlyValTyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeuGlnPhe 166
Db 182 GTGCCCGGGGCTACTACTCTGCGCTCCACGCCACCGCTACCGGCTAGCCTGCAGTTT 241
QY 167 AspLeuValLysAsnGlyGluSerIleAlaSerPhePheGlnPhePheGlyTyrPro 186
Db 242 GATCTGCTCAAGAAATGGCGAGCTATCGCCTTTCTTCAGTTCTTGAGAGGTGGCCC 301
QY 187 LysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGlnValTyr 206
Db 302 AAGCGACGCTCGCTCTCCGGGGGGCCATGTGAGGCTGGAGCCTGAAGACAGGTGTGG 361
QY 207 ValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAspSerThr 226
Db 362 GTACAGGTGGCGTGGGAGTATATGTGCACTACGCCAGCATCAAGACAGACAGCACC 421
QY 227 PheSerGlyPheLeuValTyrSerAspTyrHisSerSerProValPheAla 243
Db 422 TTCTCTGATTTTCTAGTGTATTTCTGACTGGACACACTCCCTGTCTTGCT 472
```

Search completed: June 21, 2003, 18:00:05
Job time: 1733 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:58:21 ; Search time 41 Seconds
(without alignments)
569.772 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSTFGFLVSDMHSSPVFA 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	91.1	219	2 T14782	hypothetical prote
2	424	32.0	244	2 JG4708	gelatin-binding 28
3	418.5	31.6	680	1 CGHUIB	collagen alpha 1(X
4	416.5	31.4	674	2 S23297	collagen alpha 1(X
5	412	31.1	246	2 S29328	collagen subcomp
6	411.5	31.1	674	2 S13301	collagen alpha 1(X
7	408	30.8	680	2 S31216	collagen alpha 1(X
8	399	30.1	245	1 C1HUOC	collagen alpha 1(X
9	374	28.2	744	1 A34246	collagen alpha 1(X
10	370	27.9	744	1 S23298	collagen alpha 1(X
11	363.5	27.4	743	1 S23779	collagen alpha 1(X
12	363	27.4	635	2 A57131	collagen alpha 2(V
13	362	27.3	253	1 C1HUOB	collagen subcomp
14	360.5	27.2	253	2 S49158	collagen subcomp
15	359	27.1	744	2 S15435	collagen alpha 1(X
16	351	26.5	253	2 A5797	collagen precursor
17	316	23.8	423	2 A5797	collagen precursor
18	314	23.7	245	1 C1HUOA	collagen precursor
19	314	23.7	245	2 S19018	collagen precursor
20	280.5	21.2	215	2 B48150	collagen precursor
21	277.5	20.9	215	2 C48150	collagen precursor
22	261.5	19.7	196	2 A48150	collagen precursor
23	238.5	18.0	992	2 T08772	collagen precursor
24	230.5	17.4	1049	1 CG8075	collagen precursor
25	227.5	17.2	248	2 S1921	collagen precursor
26	225	17.0	248	1 LNHUP1	collagen precursor
27	225	17.0	325	2 T32248	collagen precursor
28	224	16.9	636	2 S41067	collagen precursor
29	223	16.8	1464	2 S59856	collagen precursor

30	222.5	16.8	1758	2 T29350	hypothetical prote
31	222.5	16.8	1759	2 T29351	collagen alpha 2(I
32	222	16.8	360	2 T37285	collagen dpy-2 - C
33	221.5	16.7	170	2 B57131	collagen alpha 2(V
34	221	16.7	886	2 I50694	collagen alpha 1(I
35	221	16.7	1019	1 A32856	collagen alpha 1(V
36	220	16.6	248	1 LNDGPS	collagen alpha 1(I
37	220	16.6	341	2 T16296	collagen alpha 1(I
38	220	16.6	380	2 T28888	collagen alpha 1(I
39	219.5	16.6	247	1 LNRBP5	collagen alpha 1(I
40	219.5	16.6	381	2 T27806	collagen alpha 1(I
41	219.5	16.6	673	1 CG806C	collagen alpha 1(I
42	219.5	16.6	1466	1 CGHUTL	collagen alpha 1(I
43	219	16.5	671	1 CG8WT5	collagen alpha 1(I
44	218.5	16.5	1453	1 S21626	collagen alpha 1(I
45	217	16.4	283	2 T29980	hypothetical prote

ALIGNMENTS

RESULT 1
T14782
hypothetical protein DKFZp586B0621.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C:Accession: T14782
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wilmann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: 218184
A:Accession: T14782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <OT>
A:Cross-references: EMBL:AL110261
A:Experimental source: adult uterus; clone DKFZp586B0621
A:Genetics:
A:Note: DKFZp586B0621.1
C:Superfamily: complement C1q carboxyl-terminal homology

Query Match 91.1%; Score 1207; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.3e-77;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	25	PSLCGHNGLPTEPHHSGSLGPGDGDGAGAGGEGGEGGPGPGRG	84
DB	1	PSLCGHNGLPTEPHHSGSLGPGDGDGAGAGGEGGEGGPGPGRG	60
QY	85	EAGPAGTPGAGGECVPPRSAPSAKRSRVPDPDAPLPDRLVYNQGHYDAYTGKT	144
DB	61	EAGPAGTPGAGGECVPPRSAPSAKRSRVPDPDAPLPDRLVYNQGHYDAYTGKT	120
QY	145	QVPGVYVFAVHATYRASLQFDLVKNESIASFPQFGMPKPSLSGAMVRLPEPDQ	204
DB	121	QVPGVYVFAVHATYRASLQFDLVKNESIASFPQFGMPKPSLSGAMVRLPEPDQ	180
QY	205	VWVGVDYDYGITASITDSTFGFLVSDMHSSPVFA	243
DB	181	VWVGVDYDYGITASITDSTFGFLVSDMHSSPVFA	219

RESULT 2
JG4708
gelatin-binding 28k protein precursor - human
N:Alternate names: adipose specific collagen-like factor
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999
C:Accession: JG4708; JG4944
R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochem. Biophys. Res. Commun. 221, 286-289, 1996
A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor
A:Reference number: JG4708; MUID:96224171; PMID:8619847
A:Accession: JG4708

A:Molecule type: mRNA
 A:Residues: 1-244 <MAE>
 A:Cross-references: DDBJ:D45371; NID:9871886; PIDN:BA08227.1; PID:9871887
 A:Experimental source: adipose tissue
 R:Nakano, Y.; Tobé, T.; Choi-Miyura, N.H.; Mazda, T.; Tomita, M.
 J. Biochem. 120, 803-812, 1996
 A:Title: Isolation and characterization of GBP28, a novel gelatin-binding protein purified from sheep adipose tissue
 A:Reference number: J04944; MUID:97103474; PMID:8947845
 A:Accession: J04944
 A:Molecule type: protein
 A:Residues: 19-38/93-100/101-112/135-149/173-178 <NAK>
 C:Comment: This protein is an endogenous factor that binds with a collagen-like domain.
 C:Genetics:
 A:Gene: apm1
 C:Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology
 C:Keywords: adipose tissue; glycoprotein; hydroxyproline
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>
 F:42-107/Region: collagen-like
 F:114-241/Domain: complement C1q carboxyl-terminal homology <C1Q>
 F:95/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.08; Score 424; DB 2; Length 244;
 Best Local Similarity 40.58; Pred. No. 7.7e-23;
 Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

QY 6 VLLILGLAAGSPDDNKRIPSLCPGH-----PG-----LPGTPGHHSQ 44
 Db 7 VLLILGLA-----PGHDETTTQGPVLLPRLPKAGACGMAIGRHHGN 50
 QY 45 GLPGRGRDGRDAGAPAGEKEGGRGLPGRGD-----PGRGAPGAPGPA 95
 Db 51 GAPRGRDGRD-----GTPGEKEGKDPGLGPKGDIETGVPAGEGPFPGIGRKEP 104
 QY 96 GEGCVPRRASFASAKRSRPPPSDAPLPFRVLYNQGHDAATGKFTQVPRVYFAY 155
 Db 105 GEGVYVRSASFV-GLETTYITP-NMPIRFKIITYNQGNHMDSTGKFRHCPILYFYAY 162
 QY 156 HATYVRASLPFDLVKNEES-IASFQFEGGMPKPSASGAMVRLPEDDQVWVQV-GVGD 213
 Db 163 HITVYMDVKSLEFKKAKMLFTYDQYQENNVDAA--SGSVLLHLEVDQVWLQVYGE 220
 QY 214 YIGIVASIKTDSIFSGFLVSD 235
 Db 221 RRGILYADNDNDSTFTGFLYHD 242

RESULT 3
 CGRUID
 collagen alpha 1(X) chain precursor - human
 N:Alternate names: procollagen alpha 1(X) chain
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
 C:Accession: S26396; S30086; S18249; A43901; I51870; S21856
 R:Reichenberger, E.; Beyer, F.; Luvallie, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
 FEBS Lett. 311, 305-310, 1992
 A:Title: Genomic organization and full-length cDNA sequence of human collagen X.
 A:Reference number: S26396; MUID:93012005; PMID:1397333
 A:Accession: S26396
 A:Molecule type: DNA
 A:Residues: 1-680 <REI>
 A:Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB:S47715
 R:Apfe, S.S.
 Submitted to the EMBL Data Library, March 1992
 A:Reference number: S30085
 A:Accession: S30086
 A:Molecule type: DNA
 A:Residues: 71PTFGWVCWCLT, 52-680 <APT>
 A:Cross-references: EMBL:X65120; NID:823129
 R:Apfe, S.; Mattei, M.G.; Olsen, B.R.
 FEBS Lett. 282, 393-396, 1991

A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene
 A:Reference number: S18249; MUID:91243838; PMID:2037056
 A:Accession: S18249
 A:Molecule type: DNA
 A:Residues: 361-647, G', 649-666 <AP2>
 A:Cross-references: EMBL:X58879; NID:930013; PIDN:CAA41686.1; PID:930014
 R:Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant
 Biochem. J. 280, 617-623, 1991
 A:Title: The human collagen X gene. Complete primary translated sequence and chromoso
 A:Reference number: S18249; MUID:92109659; PMID:1764025
 A:Accession: S18249
 A:Molecule type: DNA
 A:Residues: 1-26, T', 28-680 <THO>
 A:Cross-references: EMBL:X60382; NID:930094; PIDN:CAA42933.1; PID:930095
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-
 R:Reichenberger, E.; Aligned, T.; von der Mark, K.; Stoss, H.; Bertling, W.
 Dev. Biol. 148, 562-572, 1991
 A:Title: In situ hybridization studies on the expression of type X collagen in fetal
 A:Reference number: A43901; MUID:92077285; PMID:1743401
 A:Accession: A43901
 A:Molecule type: mRNA
 A:Residues: 547-656 <RE2>
 A:Cross-references: GB:M74050; GB:D57494; NID:9339884; PIDN:AA6121.1; PID:9553796
 A:Note: sequence extracted from NCBI backbone (NCBI:65012, NCBI:65014)
 R:Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant,
 Am. J. Hum. Genet. 54, 169-178, 1994
 A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal doma
 pe Schmid.
 A:Reference number: I51870; MUID:94136476; PMID:8304336
 A:Accession: I51870
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 520-597, D', 599-680 <NAL>
 A:Cross-references: GB:S68531; NID:9545180; PIDN:AA60615.1; PID:9545181
 A:Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
 A:Comment: a second mutant sequence with 614-Pro is also described
 C:Note: Prolines and lysines at the third position of the tripeptide repeating unit
 ed and subsequently O-glycosylated.
 C:Genetics:
 A:Gene: GDB:COL10A1
 A:Cross-references: GDB:128635; OMIM:120110
 A:Map position: 6q21-6q22
 A:Introns: 52/1
 A:Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
 C:Complex: type X collagen may be a homotrimer
 C:Function:
 A:Description: structural component of extracellular fibrous polymer specifically and
 be important for skeletogenesis
 C:Superfamily: collagen alpha 1(VII) chain; complement C1q carboxyl-terminal homology
 C:Keywords: collid coll; extracellular matrix; glycoprotein; homotrimer; hydroxylysin
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
 F:19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
 F:57-519/Region: interrupted helical
 F:520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
 F:535-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
 F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.68; Score 418.5; DB 1; Length 680;
 Best Local Similarity 34.98; Pred. No. 5.4e-22;
 Matches 98; Conservative 34; Mismatches 82; Indels 67; Gaps 6;

QY 15 GSPPLDNNKIPSLCPGRHGLPGRGHGSGGLPGRDGRDAGAPAGEKEGGRGLP 74
 Db 401 GNPGLPGRKDPGRGPGGLPGRGAPGAKMPGHNGBAGRGAPGIPGRPGIP 460
 QY 75 -----GPRGPPGRGPA-----GPRGPPGRGPA-----GPRGPPGRGPA 99
 Db 461 GPRGSKDPPGPPGPPGAGIATKGLNGPGRGPPGPPGPPGPPGPPGPPGPPGPP 520
 QY 100 VP-----PSSAFSARSRVPPPSDAPLPFRVLYNE 132
 Db 521 MPGEFIRAGORPSLGPPLVANSOGVTGMPVSAFTVILSKAY--PAIGTPIPEFKILYNR 578

collagen alpha 1(X) chain precursor - chicken
N:Alternate names: type X collagen
C:Species: Gallus gallus (chicken)
C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C:Accession: S23297, A31896; S65594; S77711; I50218
R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jaceenko, O.; LuValle, P.; McC
maguchi, N.; Olsen, B.R.
A>Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23297
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-674 <NIN>
R:LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A>Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
A:Reference number: A31896; MUID:89054019; PMID:2461368
A:Accession: A31896
A:Molecule type: mRNA
A:Residues: 1-75 <LDV>
R:Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.
J. Biol. Chem. 261, 5041-5050, 1986
A>Title: The developmentally regulated type X collagen gene contains a long open reading
A:Reference number: I50218; MUID:86168227; PMID:3082876
A:Accession: S65594
A:Molecule type: DNA
A:Residues: 'T', 9 'D', 11-12, 'EDOMKIXLFTW', 30-31, 'CKSGRAATTYMIQONWADLVSSH', 48-89, 'L',
629, 'POAVLSIKRTKCCSSCOIOPMVSIPLMFLLSOSYLKSNITPLMS' <NIN>
A:Cross-references: EMBL:M13496; NID:9211699; PIDN:AAA48736.1; PID:9211700
A:Accession: S77711
A:Molecule type: protein
A:Residues: 104-112, 'X', 114-117:453-466 <NIN>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline,
F:1-18/Domin: signal sequence #status predicted <SIG>
F:347-673/Domin: complement C1q carboxyl-terminal homology <C1Q>
F:453,456/Modified site: hydroxyproline (Pro) #status experimental
F:611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.48; Score 416.5; DB 2; Length 674;
Best Local Similarity 36.08; Pred. No. 7.3e-22;
Matches 96; Conservative 34; Mismatches 84; Indels 53; Gaps 6;

Dy 14 AGSPPLDDNNKIPSLCPGHPGLPRPGHNGSGULPGRGRGRGRCAGAPAREKEGGAPGL 73
Db 408 AGPPGLGCPVPQGVKVPINGEPGRGSGIGTGIRGPMPPEAPPAKKGABAPGL 467

Dy 74 PGPR-----GDPTGRGEA-----GPAPTGPAGECSTP----- 101
Db 468 PGAGIATKTGLRGPMGPGRPKNGSGEGELPPCPPPGPGGSTIREGYVGESNELS 527

Dy 102 -----PRSASFSAKRSESRPPPSDALPLPDRLVLVNEQGHYDAVTGFTTC 145
Db 528 GMSEFMKAGNOALTGMVSAFWYILSKAY--PGATVPYIKRKDKILLYNQOQHVDRTGTGFTC 585

Dy 146 QVPEGVYFAVAHYATYRASIQFDLYKNGESIA-SFFQFGCGMPASISGAMARLEPEDQ 204
Db 586 RIEQLYFYFSYHVAAKGINWVALYKKNSPYMYTYIDEYOKRYLDOA--SGSAVIDIMENDQ 643

Dy 205 VWOVGVDYIGIYASTIKDTSFSGFL 231

```

Db          644  VWIQLPNSGSLYSSEYVHSSFSQFL 670
               |||:|:|  |:|:|  |:|:|:|
RESULT 5
S29328
complement subcomponent C1q chain C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S29328
R:Petrey, F.; Reid, K.B.M.; Loos, M.
R:J. Biochem. 209, 129-134, 1992
A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for
eCecrbellin.
A:Reference number: S29328; MUID:93011118; PMID:139691
A:Accession: S29328
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <PEP>
A:Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950229
C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal
F:122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match          31.1%; Score 412; DB 2; Length 246;
Best Local Similarity 42.2%; Pred. No. 5.4e-22;
Matches 103; Conservative 33; Mismatches 84; Indels 24; Gaps 10;

4  LTVLLLLGLAGSPRLDNRKTPSLC---PGHRLGPGTRGCHHGSGGLDGRGDRGDAGP 60
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
15  LLLFLFLML-----PL-RSQASAGCYGIGPHRFGMGAPGKGDHGLQGPKEPIPAVPG 68
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
61  APGEKGEGRPLDGPRLDGPGRGEA--GPAGPTGPAGECVPPR-----SAFSAKRS 111
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
69  TQGRKGQGEPMGMRHCKNGPRGTSGLPDRPGRPGREGVGGRYKQKHQSVFTYRQ 128
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
112  ESRVPRPDAFLPRDRLVNLQGHYDAVTGKFTQGVGVYVFNVAHNAVYRASLDPLVKN 171
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
129  TTQY-PEKNAVLVRNSVNTNPGHYNBTGKFTCEVPELTYE-VYYSHTNLVLVHLNL 186
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
172  GESIASFPQFPGGPRKASLSGAMVRLERPEDDQVGVGVGYIGIYASITDSTFSQFL 231
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
187  LARVASFCDHMFN-SKQVS-SGGALLRLQGRDEW--LSVNDYGMVGIGESNSVFSQFL 242
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
232  VYSD 235
|||:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|  |:|:|
243  LFPD 246

RESULT 6
S13301
collagen alpha 1(X) chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C:Accession: S13301
R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
R:Biochem. J. 273, 141-148, 1991
A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen
A:Reference number: S13301; MUID:91113131; PMID:1703407
A:Accession: S13301
A:Molecule type: mRNA
A:Residues: 1-674 <TTH>
A:Cross-references: EMBL:X53556; NID:9263; PIDN:CAA37624.1; PID:9264
A:Gene: COL10A1
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coll1; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match          31.1%; Score 411.5; DB 2; Length 674;
Best Local Similarity 34.9%; Pred. No. 1.6e-21;
Matches 96; Conservative 34; Mismatches 84; Indels 61; Gaps 6;

```


Qy 15 GSPPLDNNKIPSLCPHGLPCTPGHHGSGQLPGRDGRDGDGAPGAGEKEGGRCPLP 74
 Db 401 GNPGLPGPKDGPAGSGPLGPGVAGAKGVPGHNGAGPRGVGIRGTGPIGPGCIP 460
 Qy 75 -----GPRGDPGPRGEA-----GPAETPGAGECS 99
 Db 461 GPGSGKDVGTGPPGPGAGIAVKGLNGPTGPPGPGNGEPGLPQPGPPGPGQVA 520
 Qy 100 VP-----PRSAFSAKRSERVPSPDAPLPFRVLVNGQGHDA 138
 Db 521 LPDEFVAGAGRPVSAQGVGMVSAFTYLSKAY--PAIGTPIPFEDKILYKQGHDP 578
 Qy 139 VTGFTGQVPGVYFAVAVATYRASLQFDLVKNGESIA-SFQEPFGMPKPSLSGAMV 197
 Db 579 RTGIFTCKIPGIYFESHVHKGTAWGLYKNGPVMVYTDYKYLQDA--SGSAVI 636
 Qy 198 RLPEPDQVWVGVDYIGIYASIKTDSFSGFLV 232
 Db 637 DLTEPDQVWVQLPNAAGSLXSPYVHSSFSGLV 671

RESULT 7

S31216
 collagen alpha 1(X) chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C:Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830

C:Keywords: R.Y.C.; Kkan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; C

Eur. J. Biochem. 213, 99-111, 1993

A:Title: Intron-exon structure, alternative use of promoter and expression of the mouse

A:Reference number: S31216; MUID:93238750; PMID:8477738

A:Accession: S31216

A:Molecule type: DNA

A:Residues: 1-680 <KON>

A:Cross-references: EMBL:X67348; NID:950480; PIDN:CAA7763.1; PID:949794

R:Elima, K.; Eerola, I.; Rosatti, R.; Mettaeranta, M.; Garofalo, S.; Pettaelae, M.; de Crc

Biochem. J. 283, 247-253, 1993

A:Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp

A:Reference number: S28807; MUID:93143676; PMID:8424763

A:Accession: S28807

A:Molecule type: DNA

A:Residues: 1-285, 'A', 287-680 <ELT>

A:Cross-references: EMBL:X67348; NID:950480; PIDN:CAA7763.1; PID:950481

R:Elima, K.; Mettaeranta, M.; Kallio, J.; Pettaelae, M.; Eerola, I.; Garofalo, S.; de Crc

Biochim. Biophys. Acta 1130, 78-80, 1992

A:Title: Specific hybridization probes for mouse alpha-2(I) and alpha-1(X) collagen mRN

A:Reference number: S22215; MUID:92182017; PMID:1543751

A:Accession: S22215

A:Molecule type: Preliminary

A:Status: Preliminary

A:Residues: 385-450, 'K', 452-627 <ELA>

A:Cross-references: EMBL:X63013; NID:949795; PIDN:CAA44741.1; PID:949796

A:Accession: S30127

A:Molecule type: Preliminary

A:Status: Preliminary

A:Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L

R:Appe, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.

Eur. J. Biochem. 206, 217-224, 1992

A:Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse t

A:Reference number: I48299; MUID:92267014; PMID:1587271

A:Accession: I48299

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'J

A:Cross-references: EMBL:X65121; NID:950482; PIDN:CAA46237.1; PID:9667031

R:Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.

J. Biol. Chem. 263, 581-587, 1988

A:Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibod

A:Reference number: S26397; MUID:88087150; PMID:2826450

A:Accession: S26397

A:Molecule type: Protein

A:Residues: 'SDGYFSQ', 24-26, 'KQ' <SUM>

C:Genetics:

A:Gene: Col10a-1

A:Map position: 10

A:Introns: 51/3

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog

C:Keywords: coll; extracellular matrix; glycoprotein; homotrimer

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-68/Domain: signal sequence #status predicted <SIG>

F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 30.8%, Score 408; DB 2; Length 680;

Best Local Similarity 33.4%, Pred. No. 2.9e-21;

Matches 99; Conservative 34; Mismatches 75; Indels 88; Gaps 9;

Qy 15 GSPPLDNNKIPSLCPHGLPCTPGHHGSGQLPGRDGRDGDGAPGAGEKEGGRCPLP 74

Db 392 GEPGLNGPK-----GNGLPGQKGDGPGVGTGTPGLRGPVPGVAGAKGVPGHNGEAGPRGEP 445

Qy 45 GLPGRDGRDGRDGAAGAPGAGEKEGGRCPLPGR-----GDPGPRGEA----- 86

Db 446 GIPGTGPTGPPGPGVPGFPGSKGDPCNFCAPGAPAGIATKGLNGPTGPPGPPGPRGSGEPG 505

Qy 87 --GPAETPGAGECSVP-----PRSAFSAKRSERVP 117

Db 506 LPGPGRPGPGGQVAVPDGFIKAGQRPRLSGMPLVSAHGVGMVSAFTYLSKAY--P 563

Qy 118 PDSAPLPDPDRVLVNEQGHYDAVTKFTQVGVYFAVAVATYRASLQFDLVKNG-ESIA 176

Db 564 AVGAPIPPEDELIVNRQOHYDPRSGIFTCCKIPGIYFESHVHKGTAWGLYKNGTPMXY 623

Qy 177 SFQFPGGMPKPSLSGAMVRLPEPDQVWVGVDYIGIYASIKTDSFSGFLV 232

Db 624 TYDEYSKGYLQDA--SGSAIHELTENDQVWQLPNAESNGLSSEYVHSSFSGLV 677

RESULT 8
 C1HUC
 Complement subcomponent C1q chain C precursor - human

N:Alternate names: complement subcomponent C1q gamma chain

C:Species: Homo sapiens (man)

C:Date: 22-May-1991 #sequence_revision 31-May-1996 #text_change 22-May-1998

C:Accession: S14351; A03207

R:Sellar, G.C.; Blake, D.J.; Reid, K.B.M.

Biochem. J. 274, 481-490, 1991

A:Title: Characterization and organization of the genes encoding the A-, B- and C-cha

A:Reference number: S14350; MUID:91174759; PMID:1706597

A:Accession: S14351

A:Molecule type: DNA

A:Status: not compared with conceptual translation

A:Residues: 1-245 <SEL>

R:Reid, K.B.M.

Biochem. J. 179, 367-371, 1979

A:Title: Complete amino acid sequences of the three collagen-like regions present in

A:Reference number: A90304; MUID:80020137; PMID:486087

A:Accession: A03207

A:Molecule type: Protein

A:Residues: 25-56, 'P', 58-65, 'K', 67-71, 'P', 73-83, 'K', 85-86, 'D', 88-89, 'N', 91-122 <REI>

C:Comment: The first component of complement is a calcium-dependent complex of the ch

ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complemen

C:Comment: The C1q subcomponent is composed of nine subunits, six of which are disulf

dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after r

C:Genetics:

A:Gene: GDB:C1QG

A:Cross-references: GDB:128132; OMIM:120575

A:Map position: 1p36.3-1p34.1

A:Introns: 60/3

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal

C:Keywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyprolin

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-245/Product: complement subcomponent C1q chain B #status predicted <MAT>
F:31-114/Domain: collagenous, triple helix <COL>
F:121-244/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:32/Disulfide bonds: Interchain #status experimental
F:36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experimental
F:57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
F:75/Binding site: carbohydrate (Lys) (covalent) #status experimental

Query Match 30.1%; Score 399; DB 1; Length 245;

Best Local Similarity 39.8%; Pred. No. 4.3e-21;

Matches 100; Conservative 33; Mismatches 84; Indels 34; Gaps 10;

QY 1 MRPLVLLILGLAASPLDDKRTSLC---PGHGLPCTPGHSGSLGPGDGRGRG 57
DB 13 LKLLILLLLALR-----GQANTGCGITGMPGLPAPAGKDGIDGLPKRGEGLTA 64
QY 58 APGARKEGEGRPLPGPRGDPGRGEPAGPTGPAECSSVPP-----RSAPSA 108
DB 65 IPGIRGPKGQKGEPLPGHKGKNGPMGPGMGVPMGIDPGEPEGKTKKQKFGSVFTV 124
QY 109 KRSESRVPPSPAPLPDRVLYNBOGHDAVTGKTCOVPGYTVFVAVATVTRASIQEDL 168
DB 125 TR-QTHPPAPNSLIRFNAVLINPGQDDVTFSTGKTKVPGGLYFVTHAS-HTANLCVLL 182
QY 169 VKNGESIASFEQFGMPKPAEL-SGAMVRLPEDDQVWVGVGDY---IGIYASIKTD 224
DB 183 YRSQVKKVY---FCHHTSTKTNVNSGVLRLQVGEHW--LAANDYIMVGIQGS---D 234
QY 225 STFGSFLVYSD 235
DB 235 SVFSGFLLEPDD 245

RESULT 9

A34246

collagen alpha 1(VIII) chain precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A34246

R.Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Nlinomiya, Y.

J. Biol. Chem. 264, 16022-16029, 1989

A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type

omains similar to those of type X collagen.

A:Reference number: A34246; MUID:89380199; PMID:2476437

A:Accession: A34246

A:Molecule type: mRNA

A:Residues: 1-744 <YAM>

A:Cross-references: GB:J05042; NID:G164895; PIDN:AAA31204.1; PID:G164896

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>

F:21-117/Region: amino-terminal nonhelical

F:118-571/Region: interrupted helical

F:572-744/Region: carboxyl-terminal nonhelical

F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 28.2%; Score 374; DB 1; Length 744;

Best Local Similarity 34.4%; Pred. No. 7.6e-19;

Matches 93; Conservative 36; Mismatches 79; Indels 62; Gaps 8;

QY 24 IPSLC--PGHGLPCTPGHSGSLGPGDGRGRGAPARKEGGRGRLP----- 74
DB 475 VPGLLGPKRGEPLPGDQGLGPRGIGITGPGSGIPGPRGKPEGLPGPRPGVCK 534
QY 75 -----GPRGP---GPRGE---AGPAGPTGPAECSSVPPS----- 104
DB 535 PGVAGLHGPCKPGALGPGQGLGPRGPPPPPPAPVMPPTPAPOGEYLPDMGLGIDG 594
QY 105 -----AFSAKRESRNP-----PPSDAPLPDRVLYNBOGHDAVTGKRT 144
DB 595 VTPHAYAAKKKNGKNGPRAYEMPAFTALTPPPGAPKTFKRLYNGQNPNPOTGIT 654
QY 145 CQVPGVYFAVHATVYRASLQFDLVKNESIA-SFQFGGMPKPAISGAMVRLPEPD 203

DB 655 CEVPGYTVFVAVHCKGKGVWVWALFKNNRPVATVTEYKKGFLDQA--SGSAVLLLRPDD 712

QY 204 QVWVGVGDYIGITASIKTDSTFGSEFLY 233

DB 713 RVFLQMPSEQAAGLVAGQYVHSSFGSYLLY 742

RESULT 10

S23298

collagen alpha 1(VIII) chain - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S23298

R.Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jasenko, O.; Luvalle, P.;

maguchi, N.; Olsen, B.R.

In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic

A:Title: The molecular biology of collagens with short triple-helical domains.

A:Reference number: S22243

A:Accession: S23298

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-744 <NIN>

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 27.9%; Score 370; DB 1; Length 744;

Best Local Similarity 34.4%; Pred. No. 1.4e-18;

Matches 93; Conservative 35; Mismatches 80; Indels 62; Gaps 8;

QY 24 IPSLC--PGHGLPCTPGHSGSLGPGDGRGRGAPARKEGGRGRLP----- 74
DB 475 VPGLLGPKRGEPLPGDQGLGPRGIGITGPGSGIPGPRGKPEGLPGPRPGVCK 534
QY 75 -----GPRGP---GPRGE---AGPAGPTGPAECSSVPPS----- 104
DB 535 PGVAGLHGPCKPGALGPGQGLGPRGPPPPPPAPVMPPTPAPOGEYLPDMGLGIDG 594
QY 105 -----AFSAKRESRNP-----PPSDAPLPDRVLYNBOGHDAVTGKRT 144
DB 595 VTPHAYAAKKKNGKNGPRAYEMPAFTALTPPPGAPKTFKRLYNGQNPNPOTGIT 654
QY 204 QVWVGVGDYIGITASIKTDSTFGSEFLY 233
DB 713 RVFLQMPSEQAAGLVAGQYVHSSFGSYLLY 742

RESULT 11

S23779

collagen alpha 1(VIII) chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: S23779

R.Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.

Eur. J. Biochem. 207, 895-902, 1992

A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polype

A:Reference number: S23779; MUID:92362626; PMID:1499564

A:Accession: S23779

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-743 <MUR>

A:Cross-references: EMBL:X66976; NID:G50493; PIDN:CAA47387.1; PID:G1359953

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

F:616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 27.4%; Score 363.5; DB 1; Length 743;

Best Local Similarity 32.8%; Pred. No. 4.1e-18;

Matches 90; Conservative 35; Mismatches 78; Indels 71; Gaps 7;

Db 132 VPLRRDQITREDVITNNMNNPEPSGKFTCKVPLLYTYTHAS-SRGLTCVNLKGRGR 190
QY 174 --SIASFQFPGGKPKASLSGGMVRLPEDDQVQVGVSDYIGIVASIKTDSFSGFL 231
Db 191 AOKVVTFCDD--AYMTFQVTTGGVNLKLEQGENVFLO--ATDKNSILGMEGANSJFSGL 246
QY 232 VYSD 235
Db 247 LFDP 250

RESULT 14

549158
complement protein C1q beta chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
C:Accession: S49158
R:Schwaeble, W.; Petry, F.; Loos, M.
submitted to the EMBL Data Library, March 1993
A:Description: cDNA cloning and expression of the mRNA encoding the B-chain of rat C1q.
A:Reference number: S49158
A:Accession: S49158
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <SCH>
C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom
F:121-249/Domain: complement C1q carboxyl-terminal homology <C1q>

Query Match 27.2%; Score 360.5; DB 2; Length 253;
Best Local Similarity 36.1%; Pred. No. 2, 2e-18;
Matches 95; Conservative 43; Mismatches 76; Indels 49; Gaps 13;

QY 1 MRPLVLLILGLAAGSPPLDNKIPSLC---PGHPLPDPETHHSGQLPGRDGNDG 57
Db 9 LTPPL-LILLGL-----LHWSMAQSCSTGSPGIPGVDPGIPGSDKPGPIKGEKG 61
QY 58 APGAP-----GEGEGGRPLP---GPRGDPGRGEAGPAGPTP---AGCSVPPRSA 105
Db 62 LPGLAGDHGELGEGKDGAGIPGPKVGRPGVGRPGPRGPKGSGDYKATOKVA 121
QY 106 FSAKRSERVPSPDAPLPFRVLYNEQHYDAVTGFTCOVPGVYFAVNAHTVYRASIQ 165
Db 122 FSALETVNSALRPNA-IRFEKIVTNDNVEPRSGKFTCKVGLYTYTHAS-SRGNIC 179
QY 166 FDLVKNK-----ESIASF-----FQFFGGMKPKASLSGGMVRLPEDDQVQVQ-VGVG 212
Db 180 VNIVGRDRDRMQKVLTFCDYAQNPFQV-----TTGGVVLKLEQEEVNLQATDKN 230
QY 213 DYIGIVASIKTDSFSGFLVYSD 235
Db 231 SLGVEGA---NSITGFLFDP 250

RESULT 15

S15435
collagen alpha 1(VIII) chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S15435
R:Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Nimmiya, Y.
Eur. J. Biochem. 197, 615-622, 1991
A:Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
A:Reference number: S15435; MUID:91231001; PMID:2029894
A:Accession: S15435
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-744 <MUR>
A:Cross-references: EMBL:X57527; NID:g30081; PIDN:CAA40748.1; PID:g30082
C:Genetics:
A:Gene: GDB:COL8A1
A:Cross-references: GDB:128104; OMIM:120251

A:Map position: 3q11.1-3q13.2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1q>

Query Match 27.1%; Score 359; DB 2; Length 744;
Best Local Similarity 33.0%; Pred. No. 8, 5e-18;
Matches 89; Conservative 33; Mismatches 86; Indels 62; Gaps 6;

QY 24 IPSLC--PQHPLPDPETHHSGQLPGRDGNDGAPGEGEGGRPLP----- 74
Db 475 VPLGLPKGPEIPDIOGIPGIPGIGSPGIPGPKGPEGLPGRPGPIGK 534
QY 75 -----GPRGDPGRGEAGPAGPTP-----AGCS 99
Db 535 PGVAGLHPPPKPKALGFGOGDLPGRPPGPPGPPPAVMPPTPPPGSEYLPDMGLGIDG 594
QY 100 VPPRSAPFAKRSSEHP-----PPSDAPLPDRLVLYNEQHYDAVTGFT 144
Db 595 VKPPHATGAKKKNCGPAPVEMPAPFTAEITAPPPVGVKFNKILYNGRONYNPQTGIT 654
QY 145 QVPGVYFAVNAHTVYRASLDPLVKNESIR-SFQFFGGMKPKASLSGGMVRLPEDD 203
Db 655 CEVPGVYFAVHVCCKGNVWVALPKNNEPVYTYDEYKGLDQA--SGSAVLLLRPD 712
QY 204 QVWVGVGVSDYIGIVASIKTDSFSGFLVY 233
Db 713 RYFLQMPSEQAAGLYAGQYVHSSFSGYLLY 742

Search completed: June 13, 2003, 16:02:34
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:59:26 ; Search time 15 Seconds

(without alignments)
476.651 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSTFGFLVSDWHSPPVFA 243

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1325	100.0	243	4	US-09-140-804-2
2	1325	100.0	243	4	US-09-336-536-3
3	1271	95.9	243	4	US-09-188-930-295
4	1258	94.9	243	4	US-09-336-536-10
5	1256	94.8	228	4	US-09-336-536-4
6	1200	90.6	228	4	US-09-336-536-11
7	675	50.9	128	4	US-09-336-536-7
8	650	49.1	128	4	US-09-336-536-14
9	433.5	32.7	247	2	US-08-463-911-2
10	428.5	32.3	247	4	US-09-140-804-8
11	428.5	32.3	247	4	US-09-118-408-3
12	428.5	32.3	247	4	US-09-506-853-3
13	424	32.0	244	2	US-08-463-911-7
14	424	32.0	244	4	US-09-140-804-3
15	424	32.0	244	4	US-09-336-536-20
16	424	32.0	244	4	US-09-530-423-1
17	417	31.5	231	4	US-09-530-423-2
18	412	31.1	246	2	US-08-463-911-4
19	399	30.1	294	4	US-09-188-930-294
20	347	26.2	60	4	US-09-336-536-6
21	324	23.8	60	4	US-09-336-536-13
22	316	23.8	423	1	US-08-383-744-2
23	316	23.8	423	5	US-08-999-336-2
24	316	23.8	423	5	PCT-US96-01427-2
25	314	23.7	245	4	US-09-140-804-4
26	280.5	21.2	215	4	US-09-140-804-5
27	277.5	20.9	185	2	US-08-463-911-3

28	276	20.8	236	4	US-09-140-804-6	Sequence 6, Appl1
29	266.5	20.1	198	4	US-09-188-930-138	Sequence 138, App
30	257.5	19.4	130	4	US-09-485-316A-13	Sequence 13, Appl
31	251.5	19.0	130	4	US-09-485-316A-12	Sequence 12, Appl
32	243.5	18.4	130	4	US-09-485-316A-11	Sequence 11, Appl
33	240	18.1	161	4	US-09-415-551-3	Sequence 3, Appl
34	229.5	17.3	280	4	US-09-247-155-178	Sequence 178, App
35	229.5	17.3	281	4	US-09-118-408-2	Sequence 2, Appl1
36	229.5	17.3	281	4	US-09-506-855-2	Sequence 12, Appl
37	228	17.2	684	1	US-08-555-663-12	Sequence 12, Appl
38	228	17.2	684	3	US-09-073-663-12	Sequence 38, Appl
39	224	16.9	228	4	US-09-219-849-38	Sequence 44, Appl
40	223	16.8	281	4	US-09-118-408-44	Sequence 44, Appl
41	223	16.8	281	4	US-09-506-855-44	Sequence 44, Appl
42	221	16.7	124	4	US-09-485-316A-9	Sequence 9, Appl1
43	219.5	16.6	1057	3	US-08-931-820-4	Sequence 4, Appl1
44	219.5	16.6	1078	3	US-08-963-825-21	Sequence 21, Appl
45	219.5	16.6	1078	4	US-09-500-811-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1	US-09-140-804-2	
Sequence 2, Application US/09140804		
Patent No. 6197930		
GENERAL INFORMATION:		
APPLICANT: Sheppard, Paul O.		
APPLICANT: Humes, Jacqueline M.		
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS		
FILE REFERENCE: 97-49		
CURRENT FILING DATE: 1998-08-26		
EARLIER FILING DATE: 1997-08-26		
NUMBER OF SEQ ID NOS: 47		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 2		
LENGTH: 243		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-140-804-2		
Query Match	100.0%	Score 1325; DB 4; Length 243;
Best Local Similarity	100.0%	Pred. No. 9.5e-114;
Matches 243; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MRPLVLLLLGLAAGSPPLDNDKIPSLCPGHHGSLPGDRGDRGAPG 60
DB	1	MRPLVLLLLGLAAGSPPLDNDKIPSLCPGHHGSLPGDRGDRGAPG 60
QY	61	APGEGEGRGPLPGPRGDPGPRGAGPAGPTGPAEGSVPRSAFSAKRSESVPPSD 120
DB	61	APGEGEGRGPLPGPRGDPGPRGAGPAGPTGPAEGSVPRSAFSAKRSESVPPSD 120
QY	121	APLPDRVLYNQGHTDAVTKFTQVGVYFYFAHAYYRASLQFDLYKNGESTASFEQ 180
DB	121	APLPDRVLYNQGHTDAVTKFTQVGVYFYFAHAYYRASLQFDLYKNGESTASFEQ 180
QY	181	FFGGMPKPRASLSGAMVRLPEPDQVWVGVDYIGYASITDSTFGFLVSPWHSPP 240
DB	181	FFGGMPKPRASLSGAMVRLPEPDQVWVGVDYIGYASITDSTFGFLVSPWHSPP 240
QY	241	VFA 243
DB	241	VFA 243
RESULT 2	US-09-336-536-3	
Sequence 3, Application US/09336536		
Patent No. 6406884		

```
GENERAL INFORMATION:
: APPLICANT: Leidy, K.
: APPLICANT: Bosson, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 3
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-336-536-3
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Query Match          100.0%; Score 1325; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.5e-114;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
DB 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
QY 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
DB 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
DB 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
DB 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
DB 241 VFA 243
```

```
RESULT 3
: US-09-188-930-295
: Sequence 295, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188, 930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 295
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Rat
: US-09-188-930-295
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Query Match          95.9%; Score 1271; DB 4; Length 243;
Best Local Similarity 95.1%; Pred. No. 8.2e-109;
Matches 231; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
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QY 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
DB 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
QY 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
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```
DB 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
DB 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
DB 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
DB 241 VFA 243
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```
RESULT 4
: US-09-336-536-10
: Sequence 10, Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leidy, K.
: APPLICANT: Bosson, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 10
: LENGTH: 243
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-336-536-10
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Query Match          94.9%; Score 1258; DB 4; Length 243;
Best Local Similarity 93.8%; Pred. No. 1.3e-107;
Matches 228; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
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QY 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
DB 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAGP 60
QY 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
DB 61 APGEKGSGRGLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
DB 121 APLEPDRVLVNEOGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
DB 181 FFGGMPKPRASISGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
DB 241 VFA 243
```

```
RESULT 5
: US-09-336-536-4
: Sequence 4, Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leidy, K.
: APPLICANT: Bosson, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
```

NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-4

Query Match
Best Local Similarity 100.0%; Score 1256; DB 4; Length 228;
Pred. No. 1.8e-107;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SPPLDNNKIPSLCPGHPGLPTGPHHSGSLGRDGRDGDAPGAPGEGGGRPLPG 75
DB 1 SPPLDNNKIPSLCPGHPGLPTGPHHSGSLGRDGRDGDAPGAPGEGGGRPLPG 60
QY 76 PGDGPGRGEGAPGAPGTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 135
DB 61 PGDGPGRGEGAPGAPGTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 120
QY 136 YDAVVGKFTCOVPGYVFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 195
DB 121 YDAVVGKFTCOVPGYVFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 180
QY 186 MYRLPEPDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 243
DB 181 MYRLPEPDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 228

RESULT 6
US-09-336-536-11
Sequence 11, Application US/09336536
Patent No. 6406884

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 11
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-336-536-11

Query Match
Best Local Similarity 94.7%; Score 1200; DB 4; Length 228;
Pred. No. 2.4e-102;
Matches 216; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 SPPLDNNKIPSLCPGHPGLPTGPHHSGSLGRDGRDGDAPGAPGEGGGRPLPG 75
DB 1 SPPLDNNKIPSLCPGHPGLPTGPHHSGSLGRDGRDGDAPGAPGEGGGRPLPG 60
QY 76 PGDGPGRGEGAPGAPGTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 135
DB 61 PGDGPGRGEGAPGAPGTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 120
QY 136 YDAVVGKFTCOVPGYVFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 195
DB 121 YDAVVGKFTCOVPGYVFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 180
QY 186 MYRLPEPDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 243
DB 181 MYRLPEPDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 228

RESULT 7
US-09-336-536-7
Sequence 7, Application US/09336536

Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-7

Query Match
Best Local Similarity 100.0%; Score 675; DB 4; Length 128;
Pred. No. 1.2e-54;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVYTGKTCOVPGYVFAVHATYVRASL 164
DB 1 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVYTGKTCOVPGYVFAVHATYVRASL 60
QY 165 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDYIGIYASIKTD 224
DB 61 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDYIGIYASIKTD 120
QY 225 STFSGFLV 232
DB 121 STFSGFLV 128

RESULT 8
US-09-336-536-14
Sequence 14, Application US/09336536
Patent No. 6406884

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 14
LENGTH: 128
TYPE: PRT
ORGANISM: Mus musculus
US-09-336-536-14

Query Match
Best Local Similarity 94.1%; Score 650; DB 4; Length 128;
Pred. No. 2.3e-52;
Matches 121; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 105 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVYTGKTCOVPGYVFAVHATYVRASL 164
DB 1 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVYTGKTCOVPGYVFAVHATYVRASL 60
QY 165 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDYIGIYASIKTD 224
DB 61 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDYIGIYASIKTD 120
QY 225 STFSGFLV 232
DB 121 STFSGFLV 128

RESULT 9
US-08-463-911-2

Sequence 2, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Miltia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-911-2

Query Match 32.7%; Score 433.5; DB 2; Length 247;
Best Local Similarity 40.6%; Pred. No. 3.4e-32;
Matches 102; Conservative 32; Mismatches 92; Indels 25; Gaps 8;

QY 1 MRPLVLL-L-GLAAGSPPLDNNKIPSLCPGHPG-----LPGTGHHGSGGLPGRDGRD 54
DB 4 LQALLFLILLPSHAEDDVTTEELAPALVPPPKTCAGMMAGIPGHGHNCTPGRDGRD- 62
QY 55 RDGAPGAPGEGEGRGPLGPRDGPGRGAGPAGP-----TGPAGECSVPPRSA 105
DB 63 -----GTPGEGEGGAGLGLPKGTGDTGVTGAGRGPRGPRGPRGPRGPRGPRGPRSA 117
QY 106 FSAKRSRVPSPDAPLPEDRVLVNEGHYDAVTGKFTQCPGVYFAVAHYRASLQ 165
DB 118 FSV-GLETRVTV-NVPIRFTKIFYNOONHYDSTGKFCYCNIPGLYFYSHIITYMMDVK 175
QY 166 FDLVKNESIASFFQFGGPKRPSLSGAMVRLPEPDQWVQV-GVGDYIGIYASIKTD 224
DB 176 VSLFKKRAVLFTYDQOE-KNVDAQSGSVLLHLEVGDQWLVQYGGDHNGLTADVND 234
QY 225 STFGFLVYSD 235
DB 235 STFGFLVYHD 245

RESULT 10
US-09-140-804-8
Sequence 8, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-804-8

Query Match 32.3%; Score 428.5; DB 4; Length 247;
Best Local Similarity 40.2%; Pred. No. 9.7e-32;
Matches 101; Conservative 32; Mismatches 93; Indels 25; Gaps 8;

QY 1 MRPLVLL-L-GLAAGSPPLDNNKIPSLCPGHPG-----LPGTGHHGSGGLPGRDGRD 54
DB 4 LQALLFLILLPSHAEDDVTTEELAPALVPPPKTCAGMMAGIPGHGHNCTPGRDGRD- 62
QY 55 RDGAPGAPGEGEGRGPLGPRDGPGRGAGPAGP-----TGPAGECSVPPRSA 105
DB 63 -----GTPGEGEGGAGLGLPKGTGDTGVTGAGRGPRGPRGPRGPRGPRGPRSA 117
QY 106 FSAKRSRVPSPDAPLPEDRVLVNEGHYDAVTGKFTQCPGVYFAVAHYRASLQ 165
DB 118 FSV-GLETRVTV-NVPIRFTKIFYNOONHYDSTGKFCYCNIPGLYFYSHIITYMMDVK 175
QY 166 FDLVKNESIASFFQFGGPKRPSLSGAMVRLPEPDQWVQV-GVGDYIGIYASIKTD 224
DB 176 VSLFKKRAVLFTYDQOE-KNVDAQSGSVLLHLEVGDQWLVQYGGDHNGLTADVND 234
QY 225 STFGFLVYSD 235
DB 235 STFGFLVYHD 245

RESULT 11
US-09-118-408-3
Sequence 3, Application US/09118408A
Patent No. 6265544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-118-408-3

Query Match 32.3%; Score 428.5; DB 4; Length 247;
Best Local Similarity 40.2%; Pred. No. 9.7e-32;
Matches 101; Conservative 32; Mismatches 93; Indels 25; Gaps 8;

QY 1 MRPLVLL-L-GLAAGSPPLDNNKIPSLCPGHPG-----LPGTGHHGSGGLPGRDGRD 54
DB 4 LQALLFLILLPSHAEDDVTTEELAPALVPPPKTCAGMMAGIPGHGHNCTPGRDGRD- 62
QY 55 RDGAPGAPGEGEGRGPLGPRDGPGRGAGPAGP-----TGPAGECSVPPRSA 105
DB 63 -----GTPGEGEGGAGLGLPKGTGDTGVTGAGRGPRGPRGPRGPRGPRGPRSA 117
QY 106 FSAKRSRVPSPDAPLPEDRVLVNEGHYDAVTGKFTQCPGVYFAVAHYRASLQ 165
DB 118 FSV-GLETRVTV-NVPIRFTKIFYNOONHYDSTGKFCYCNIPGLYFYSHIITYMMDVK 175

OY 166 FDLYKNGESIASFQFGGMPKPSLGSAMVRLPEDDQVWVOY-GVGDYIGIYASIKTD 224
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 176 VSLRKKDKAVLFTTDQYOE-KNVDAQSGSVLLHLEVGQVWLQYVGGDGHNGLYADNVND 234
OY 225 STFGFLYSD 235
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 235 STFGFLYHD 245

RESULT 12
US-09-506-855-3
Sequence 3, Application US/09506855
Patent No. 6448221
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-506-855-3

Query Match
Best Local Similarity 40.2%; Score 428.5; DB 4; Length 247;
Matches 101; Conservative 32; Mismatches 93; Indels 25; Gaps 8;

OY 1 MRPLVLLLL-GLAAGSPPLDNDKIPSLCPGHPG-----LPQTPGHHSQGLPGRDGDG 54
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 4 LQALLFLILPSHAEDVYTTTEELAPALVPPPKGICACWMAIGIPGHNCPGRDGD- 62
OY 55 RDGAPGAGEGEGGRRLPGRDPRGRGAPGAPG-----TPAGECSTPPPSA 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 63 -----GTPGEGEGGADALLGPKGTGDMTGAGGPGFPOTPRKGEPEAAVMTSA 117
OY 106 FSAKRSRVPSPDAPLPFDRLVNEQGHDAVTKFTCOVPGVYVAVATVYRASLO 165
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 118 FSV-GLETRYVTP-NVPIRTFKIFYNQNHIDGSGKRYCAIPGLYIYHYIMAKYK 175
OY 166 FDLYKNGESIASFQFGGMPKPSLGSAMVRLPEDDQVWVOY-GVGDYIGIYASIKTD 224
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 176 VSLRKKDKAVLFTTDQYOE-KNVDAQSGSVLLHLEVGQVWLQYVGGDGHNGLYADNVND 234
OY 225 STFGFLYSD 235
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 235 STFGFLYHD 245

RESULT 13
US-08-463-911-7
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-911-7

Query Match
Best Local Similarity 40.5%; Score 424; DB 2; Length 244;
Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

OY 6 VLLIGLAAAGSPPLDNDKIPSLCPGHPG-----LPQTPGHHSQGL 44
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 7 VLLILAL-----PCHDEYTTQGGVLLPLPKGACGTGMAIGIPGHPHN 50
OY 45 GLPGRDGDGDGAPGAPGAGEGEGGRRLPGRD-----PGRGEGAPGAPGPA 95
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 51 GAPGRDGD-----GTPGEGEGGDPDLGPKDIGETGYVPAAGPGRPGIGRKEP 104
OY 96 GECSTPPRSASAKRSRVPSPDAPLPFDRLVNEQGHDAVTKFTCOVPGVYVAV 155
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 105 GEGAVVYSATSV-GLETRYVTP-NVPIRTFKIFYNQNHIDGSGKRYCAIPGLYIY 162
OY 156 HATVYRASLOFDLYKNGES-IASFQFGGMPKPSLGSAMVRLPEDDQVWVOY-GVGD 213
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 163 HITVYMKVYKSLFEKKDAMLFTTDQYQENNVDQ--SGSVLLHLEVGQVWLQYVGG 220
OY 214 YIGIYASIKTDSTFGFLYSD 235
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 221 RNLGYADNDSTFGFLYHD 242

RESULT 14
US-09-140-804-3
Sequence 3, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-804-3

Query Match
Best Local Similarity 40.5%; Score 424; DB 4; Length 244;
Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

```
OY 6 VLLLLGLAAGSPPLDNNKIPSLCPGH-----PG-----LPDTPGHHSQ 44
    ||||| |
Db 7 VLLLLAL-----PGHDETTTQGPVLLPLPKGACTGMMAGITPGHPGN 50
OY 45 GLPGRDGRDGDAPGAPGEGGGRPLPGPRGD-----PGPRGEGAPGPTGPA 95
    ||||| |
Db 51 GAPGRDGD-----GTPGEGKEGKDPGLIGPKDIDGETGVPAGEGPRGPGIQRKGP 104
OY 96 GECVPPRPSAFSAKRSESRVPPSDAPLPFDRLVNEQGHYDAVTKFTCOVPGVYFAY 155
    ||: ||||| |
Db 105 GEGAYVYRSANFV-GLETYYTIP-NMPIRFTKIIFYNOQNHVDGSGTKFHCNIPGLYFAY 162
OY 156 HATVYRASLOFDLVKNES-IASFQFPGGMPKASLSGAMVRLPEPDQVYQV-GVGD 213
    ||||| |
Db 163 HITVYMDVKVSLFKKDKAMLFYDQYQENNVDQ--SGSVLLHLEVGDQVWLQVYGE 220
OY 214 YIGIYASIKTDSFTSGFLYSD 235
    ||: ||||| |
Db 221 RNLGYADNDNDSTFTGFLYHD 242
```

RESULT 15

```
US-09-336-536-20
: Sequence 20 Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leidy, K.
: APPLICANT: McKay, C.
: APPLICANT: Bossone, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 244
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-336-536-20
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Query Match

37.0%; Score 424; DB 4; Length 244;

Best Local Similarity 40.5%; Pred. No. 2.5e-31;

Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

```
OY 6 VLLLLGLAAGSPPLDNNKIPSLCPGH-----PG-----LPDTPGHHSQ 44
    ||||| |
Db 7 VLLLLAL-----PGHDETTTQGPVLLPLPKGACTGMMAGITPGHPGN 50
OY 45 GLPGRDGRDGDAPGAPGEGGGRPLPGPRGD-----PGPRGEGAPGPTGPA 95
    ||||| |
Db 51 GAPGRDGD-----GTPGEGKEGKDPGLIGPKDIDGETGVPAGEGPRGPGIQRKGP 104
OY 96 GECVPPRPSAFSAKRSESRVPPSDAPLPFDRLVNEQGHYDAVTKFTCOVPGVYFAY 155
    ||: ||||| |
Db 105 GEGAYVYRSANFV-GLETYYTIP-NMPIRFTKIIFYNOQNHVDGSGTKFHCNIPGLYFAY 162
OY 156 HATVYRASLOFDLVKNES-IASFQFPGGMPKASLSGAMVRLPEPDQVYQV-GVGD 213
    ||||| |
Db 163 HITVYMDVKVSLFKKDKAMLFYDQYQENNVDQ--SGSVLLHLEVGDQVWLQVYGE 220
OY 214 YIGIYASIKTDSFTSGFLYSD 235
    ||: ||||| |
Db 221 RNLGYADNDNDSTFTGFLYHD 242
```

Search completed: June 13, 2003, 16:02:56
Job time : 17 secs

Db 315 CACCANTGGACGAGGGCTTCCGGGCGCGGATGGCCGAGACGGCCGCGAGCGCCGCGCC 374
 QY 404 GGGGCTCCGGAGAGAAAGCGAGAGGGCGGAGGCGCGGAGCTGCCGGGACCTCGAGGGAC 463
 Db 375 GGGGCTCCGGAGAGAAAGCGAGAGGGCGGAGGCGCGGAGCTGCCGGGACCTCGAGGGAC 434
 QY 464 CCCGGGCGGAGAGAGGGCGGAGCCCGGGGGCCCAACCGGGCTGCCGGGAGTGTCTCG 523
 Db 435 CCCGGGCGGAGAGAGGGCGGAGCCCGGGGGCCCAACCGGGCTGCCGGGAGTGTCTCG 494
 QY 524 GTGGCTCCGGAGATCCGGCTTCAGGCGGCAACGCTCCGAGAGCGGGGTGCTCGCGCTCT 583
 Db 495 GTGGCTCCGGAGATCCGGCTTCAGGCGGCAACGCTCCGAGAGCGGGGTGCTCGCGCTCT 554
 QY 584 GAGCAGACCTTGGCTTCGAGACCGGCTGTGTGAACAGAGAGGAGATTTAGAGCGCGTC 643
 Db 555 GAGCAGACCTTGGCTTCGAGACCGGCTGTGTGAACAGAGAGGAGATTTAGAGCGCGTC 614
 QY 644 ACCGGGCAAGTTCACTGCGAGGTGCTGGGGTCTACTACTTCCGCTCATGCCACCGTC 703
 Db 615 ACCGGGCAAGTTCACTGCGAGGTGCTGGGGTCTACTACTTCCGCTCATGCCACCGTC 674
 QY 704 TACCGGGCCAGCTGCGAGTTTGATCTGTGAAGATGGCGAATCCATTCGCTCTTCTTC 763
 Db 675 TACCGGGCCAGCTGCGAGTTTGATCTGTGAAGATGGCGAATCCATTCGCTCTTCTTC 734
 QY 764 CAGTTTTTCGGGGGTGGCCCAAGCCAGCTCGCTCGGGGGGGGCGCATGTGTAGAGCTG 823
 Db 735 CAGTTTTTCGGGGGTGGCCCAAGCCAGCTCGCTCGGGGGGGGCGCATGTGTAGAGCTG 794
 QY 824 GAGCCTTGAAGACCAAGT 883
 Db 795 GAGCCTTGAAGACCAAGT 854
 QY 884 AGCATCAAGACAGACAGACACTTCTCCGAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 943
 Db 855 AGCATCAAGACAGACAGACACTTCTCCGAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 914
 QY 944 CCAAGTCTTCTAGTCCCACTGCAAGAGAGCTCAATGTCTCACTCTAGAGAGAGG 1003
 Db 915 CCAAGTCTTCTAGTCCCACTGCAAGAGAGCTCAATGTCTCACTCTAGAGAGAGG 974
 QY 1004 TGTGAGGCTTACAAACAGGTATTCAGAGAGGGCTGGCCCTGTGAATATTGTGTATGAC 1063
 Db 975 TGTGAGGCTTACAAACAGGTATTCAGAGAGGGCTGGCCCTGTGAATATTGTGTATGAC 1034
 QY 1064 TAGGAGAGTGGGTAGAGACACTTCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123
 Db 1035 TAGGAGAGTGGGTAGAGACACTTCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1094
 QY 1124 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1183
 Db 1095 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1154
 QY 1184 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1243
 Db 1155 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1214
 QY 1244 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1303
 Db 1215 GTCTGCATGAGTCTGGGAGCATGGGGAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1274
 QY 1304 CCGGCGCTTTTTCAGAGATCACTCATTAACCTAAGAACCTCA 1348
 Db 1275 CCGGCGCTTTTTCAGAGATCACTCATTAACCTAAGAACCTCA 1319

RESULT 2
 US-09-336-536-1
 ; Sequence 1, Application us/09336536
 ; Patent No. 6406884
 ; GENERAL INFORMATION:
 ; APPLICANT: Leibny, K.

; APPLICANT: McKay, C.
 ; APPLICANT: Bosson, S.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 7853-144
 ; CURRENT APPLICATION NUMBER: US/09/336.536
 ; CURRENT FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 1338
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-336-536-1
 Query Match 81.3%; Score 1119; DB 4; Length 1338;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1289; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 57 GGAATGGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 116
 Db 18 GGAATGGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 77
 QY 117 ACCACCACTGAGAGGCTCCGAGTACGAGAGCGCCCGAAGAGAGGAGGAGGAGGAGGAGGAGG 176
 Db 78 ACCACCACTGAGAGGCTCCGAGTACGAGAGCGCCCGAAGAGAGGAGGAGGAGGAGGAGGAGG 137
 QY 177 AGGGGGAGCTGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
 Db 138 AGGGGGAGCTGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 197
 QY 237 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296
 Db 198 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
 QY 297 TCCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
 Db 258 TCCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
 QY 357 AGGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
 Db 318 AGGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 377
 QY 417 AGAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
 Db 378 AGAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 436
 QY 477 GAGAG 536
 Db 437 GAGAG 496
 QY 537 CCGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 596
 Db 497 CCGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 556
 QY 597 CTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656
 Db 557 CTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 616
 QY 657 CTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
 Db 617 CTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 676
 QY 717 TGCAGTTTGAATCTGTGTGAAGATGGGAGATTCATTCGCTTCTTCTTCTTCTTCTTCTTCTTCT 776
 Db 677 TGCAGTTTGAATCTGTGTGAAGATGGGAGATTCATTCGCTTCTTCTTCTTCTTCTTCTTCTTCT 736
 QY 777 GGTGGCCCAAGCAGCCTGCTCTCGGGGGGGGAGCATGTGAGCTGTGAGAGCTGTGAGAGAC 836
 Db 737 GGTGGCCCAAGCAGCCTGCTCTCGGGGGGGGAGCATGTGAGAGCTGTGAGAGAC 796
 QY 837 AAGTGTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 896
 Db 797 AAGTGTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 856

QY	897	ACAGACCTTCCTCCGGATTTCTTCGGGTACTCCGACTGGACACGTCCTCCCAAGTCCTTGGT	956
Db	857	ACAGACCTTCCTCCGGATTTCTTCGGGTACTCCGACTGGACACGTCCTCCCAAGTCCTTGGT	916
QY	957	AGTGGCCACTGC CA AAAGTAGAGCTCAATGCTCTCACTCCTAGAAAGAGGGGTGTAGAGCTGACA	1011
Db	917	AGTGGCCACTGC CA AAAGTAGAGCTCAATGCTCTCACTCCTAGAAAGAGGGGTGTAGAGCTGACA	976
QY	1017	ACCAAGTATATCCAGGAGGGCTTGGCCCCCTGGATATTTGTGAATGACTATAGGAGAGTGGGG	1077
Db	977	ACCGGTGATATCCAGGAGGGCTTGGCCCCCTGGATATTTGTGAATGACTATAGGAGAGTGGGG	1037
QY	1077	TAGAGCACTCTCCGCTGTGCTGTGGCAAGAAATGGGAAACAGTGGCTGTCTCGATCAGG	1137
Db	1037	TAGAGCACTCTCCGCTGTGCTGTGGCAAGAAATGGGAAACAGTGGCTGTCTCGATCAGG	1097
QY	1137	TCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCCAAGACCAAGAGAGTGTCTGTGCTG	1197
Db	1097	TCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCCAAGACCAAGAGAGTGTCTGTGCTG	1157
QY	1197	GCAAGTGAAGCCCCCGAAGTGCCTGTGGTCCAGAGAGCCACAGGTGGGGGTGCTGTCTCT	1257
Db	1157	GCAAGTGAAGTCCCCCGAAGTGTCTGTGGTCCAGAGAGCCACAGGTGGGGGTGCTGTCTCTCT	1217
QY	1257	GGTCCCTGCTCTCTGTGATCCTCCCAACCCCTCTGTCTCTGTGGGGCGGGCCCTTTTCT	1317
Db	1217	GGTCCCTGCTCTCTGTGATCCTCCCAACCCCTCTGTCTCTGTGGGGCGGGCCCTTTTCT	1277
QY	1317	CAGAGATCACTCAATAACTTAAGAAACCTC	1347
Db	1277	CAGAGATCACTCAATAACTTAAGAAACCTC	1307

OY		227	ATGAGGCCACMCCTCCTCGTCTGTCCTGGGCGCCGCGGCCTCGCCCTCCACTGTGAC	286
Dd		1	ATTGAGGCCACTCTCTCTCTCTCTCTGTTCTGCGGGCTGGGGCGCGGCTCGCCCTCACTGTGAC	60
OY		287	GACAACAAGATCCCAGGCTCTGACCAGGGGACCCCCGGGCTTCCAGGCAAGCCGGGGCAC	346
Dd		61	GACAACAAGATCCCAGGCTCTGCGCCGGGGACACCCCGGCTTCCAGGCAAGCCGGGGCAC	120
OY		347	CATGGACGCCAGGGGCTTGCCGGGCGCGCATGGCCGCGAAGCGCCGAGACGGCCGGCGG	406
Dd		121	CATGGACGCCAGGGGCTTGCCGGGCGCGCATGGCCGCGAAGCGCCGAGACGGCCGGCGG	180
OY		407	GCTCCGGGAGAAGAGGAGGCGGAGGCGGGAGCCGGGACATCTGCGGAGCTTGAGAGGAGCC	466
Dd		181	GCTCCGGGAGAAGAGGAGGCGGAGGCGGGAGG-CGGGACATCTGCGGAGCTTGAGAGGAGCC	239

Query Match 44.2% Score 608; DB 4; Length 728;
Best Local Similarity 99.9%; Pred. No. 4, 9e-236;
Matches 728; Conservative 0; Mismatches 0; Indels 1; Gaps 1

RESULT 3
US-09-336-536-2
Sequence 2, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536-2

QY	467	GGGCGCGAGAGAGAGGCGGGGAGACCCGCGGGGGCCACCAGGCGCTGCGGGGAGAGTCTGGGTTG	526
Db	240	GGGCGCGAGGAGAGGCGGGAGCCGCGGGGCCACCGGGCCCTGCGGGGAGAGTCTGGGTTG	299
QY	527	CCTCGCGATCGGCTTCAGCGCGCAAGGCGCTCCGAGAGCGGGGTGCTCGCGCGCTGAG	586
Db	300	CCTCGCGATCGGCTTCAGCGCGCAAGGCGCTCCGAGAGCGGGGTGCTCGCGCGCTGAG	359
QY	587	GCACCCCTTGCCCTTCGACCGCGCGTGTGTGGAACAGAGCAGGAGCATTTACGACGCGCTAC	646
Db	360	GCACCCCTTGCCCTTCGACCGCGCGTGTGTGGAACAGAGCAGGAGCATTTACGACGCGCTAC	419
QY	647	GGCAAGTTACCTGCGAGGTGCTGTGGGGTCTACTACTTGCCTCCATGCCACGCTTAC	706
Db	420	GGCAAGTTACCTGCGAGGTGCTGTGGGGTCTACTACTTGCCTCCATGCCACGCTTAC	479
QY	707	CGGGCGACCTGCGAATTGTGATCTGGTGAAGAAATGGCGAATCCATTGCTCTTCTCCAG	766
Db	480	CGGGCGACCTGCGAATTGTGATCTGGTGAAGAAATGGCGAATCCATTGCTCTTCTCCAG	539
QY	767	TTTTTGGGGGGTGGCCCCAAGCGCAGCTGCGTCTCGGGGGGGGCCATTGGAGAGCTGGAG	826
Db	540	TTTTTGGGGGGTGGCCCCAAGCGCAGCTGCGTCTCGGGGGGGGCCATTGGAGAGCTGGAG	599
QY	827	CCTGAGGACCAAGTGTGGGTGCGAGGTGGGTGTGGGTGATCTACATTGGCATTTATGCCAC	886
Db	600	CCTGAGGACCAAGTGTGGGTGCGAGGTGGGTGTGGGTGATCTACATTGGCATTTATGCCAC	659
QY	887	ATCAAGACAGACAGCACCTTCTCGGATTTCTGTTGTACTCCGACTGSCAGACTGCCCA	946
Db	660	ATCAAGACAGACAGCACCTTCTCGGATTTCTGTTGTACTCCGACTGSCAGACTGCCCA	719
QY	947	GTCCTTGCT 955	
Db	720	GTCCTTGCT 728	

```

RESULT 4
US-09-140-804-28
; Sequence 28, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminal untagged linker
US-09-140-804-28

Query Match
5.3%; Score 73; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 280 ACTGAGACGACAACAAGATCCCGAGCTCTGCCCCGGGGGACACCCCGGCTTCCAGGACAGCC 339
Db 72 ACTGAGACGACAACAAGATCCCGAGCTCTGCCCCGGGGGACACCCCGGCTTCCAGGACAGCC 131
OY 340 GGGCCACCATGGC 352
Db 132 GGGCCACCATGGC 144

```

RESULT 5
US-09-140-804-29
; Sequence 29, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminal Glu-Glu tag linker
US-09-140-804-29

Query Match 5.28; Score 72; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 281 CTGAGCAGACAAGATCCAGCCTGCGCGGGGACCCGGGCTTCCAGGACGCCG 340
DB 73 CTGAGCAGACAAGATCCAGCCTGCGCGGGGACCCGGGCTTCCAGGACGCCG 132

OY 341 GGGCACCATTGGC 352
DB 133 GGGCACCATTGGC 144

RESULT 6
US-09-140-804-31
; Sequence 31, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminal Glu-Glu tag linker
US-09-140-804-31

Query Match 5.28; Score 72; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 884 AGCATCAGACAGACAGACCTTCGCGATTCTGTGTAAGTCCGACGTGGACAGCTCC 943
DB 1 AGCATCAGACAGACAGACCTTCGCGATTCTGTGTAAGTCCGACGTGGACAGCTCC 60
OY 944 CCAGCTTTGCT 955
DB 61 CCAGCTTTGCT 72

RESULT 7
US-09-140-804-30
; Sequence 30, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminal untagged linker
US-09-140-804-30

Query Match 3.98; Score 54; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 905 TTCTCCGATTCTGTGTAAGTCCGACTGGCAGACAGTCCAGTCTTGTAG 958
DB 22 TTCTCCGATTCTGTGTAAGTCCGACTGGCAGACAGTCCAGTCTTGTAG 75

RESULT 8
US-09-140-804-35/c
; Sequence 35, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15273
US-09-140-804-35

Query Match 3.78; Score 51; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 CCAGCTTCGCGGACCCGCGCTTCCAGCAGCCGGGCGCCAGCATG 350
DB 51 CCAGCTTCGCGGACCCGCGCTTCCAGCAGCCGGGCGCCAGCATG 1

RESULT 9
US-09-140-804-43/c
; Sequence 43, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49

;; CURRENT APPLICATION NUMBER: US/09/140,804
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: 60/056,983
;; EARLIER FILING DATE: 1997-08-26
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 43
;; LENGTH: 51
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide ZC15274
US-09-140-804-43

Query Match 3.7%; Score 51; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGACGCGGACCATG 350
|||||
Db 51 CCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGACGCGGACCATG 1

RESULT 10
US-09-140-804-36
;; Sequence 36, Application US/09140804
;; Patent No. 6197930
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Humes, Jacqueline M.
;; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
;; FILE REFERENCE: 97-49
;; CURRENT APPLICATION NUMBER: US/09/140,804
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: 60/056,983
;; EARLIER FILING DATE: 1997-08-26
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 36
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide ZC15273
US-09-140-804-36

Query Match 3.6%; Score 50; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 CATCAGACAGACAGACCTTCTCGGATTTCTGSGTGACTCCGACTGGC 935
|||||
Db 1 CATCAGACAGACAGACCTTCTCGGATTTCTGSGTGACTCCGACTGGC 50

RESULT 11
US-09-140-804-44
;; Sequence 44, Application US/09140804
;; Patent No. 6197930
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Humes, Jacqueline M.
;; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
;; FILE REFERENCE: 97-49
;; CURRENT APPLICATION NUMBER: US/09/140,804
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: 60/056,983
;; EARLIER FILING DATE: 1997-08-26
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 44
;; LENGTH: 50
;; TYPE: DNA

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide ZC15273
US-09-140-804-44

Query Match 3.6%; Score 50; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 CATCAGACAGACAGACCTTCTCGGATTTCTGSGTGACTCCGACTGGC 935
|||||
Db 1 CATCAGACAGACAGACCTTCTCGGATTTCTGSGTGACTCCGACTGGC 50

RESULT 12
US-09-140-804-37
;; Sequence 37, Application US/09140804
;; Patent No. 6197930
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Humes, Jacqueline M.
;; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
;; FILE REFERENCE: 97-49
;; CURRENT APPLICATION NUMBER: US/09/140,804
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: 60/056,983
;; EARLIER FILING DATE: 1997-08-26
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 37
;; LENGTH: 65
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide ZC15724
US-09-140-804-37

Query Match 3.3%; Score 45; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 TTCTGTGTACTCCGACTGGACAGCTCCGAGTCTTGTGTTAG 958
|||||
Db 1 TTCTGTGTACTCCGACTGGACAGCTCCGAGTCTTGTGTTAG 45

RESULT 13
US-09-140-804-45
;; Sequence 45, Application US/09140804
;; Patent No. 6197930
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Humes, Jacqueline M.
;; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
;; FILE REFERENCE: 97-49
;; CURRENT APPLICATION NUMBER: US/09/140,804
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: 60/056,983
;; EARLIER FILING DATE: 1997-08-26
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 45
;; LENGTH: 68
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide ZC15267
US-09-140-804-45

Query Match 3.1%; Score 43; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 913 ATTTCTGTGTAATCCGATCGACAGCTCCCACTCTTGCT 955
|||||
Db 1 ATTTCTGTGTAATCCGATCGACAGCTCCCACTCTTGCT 43

RESULT 14
US-09-140-804-42/C
; Sequence 42, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ. ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15269
US-09-140-804-42

Query Match 2.8%; Score 39; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 ACTGAGACACACAGATCCCGACCTCTGCGGGGCA 318
|||||
Db 39 ACTGAGACACACAGATCCCGACCTCTGCGGGGCA 1

RESULT 15
US-09-140-804-33/C
; Sequence 33, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ. ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Oligonucleotide ZCARTificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15268
US-09-140-804-33

Query Match 2.8%; Score 38; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 CTGAGACACACAGATCCCGACCTCTGCGGGGCA 318
|||||
Db 38 CTGAGACACACAGATCCCGACCTCTGCGGGGCA 1

Search completed: June 21, 2003, 14:34:08
Job time : 82 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 08:08:59 ; Search time 2191 Seconds
(without alignments)
10178.542 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1 gactagctctcttgagctct.....aaaaaaaaaaaaaaaaa 1377

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estov:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767.8	55.8	869	13	BM763193 603049929
2	750.6	54.5	1154	13	BM547549 AGENCOURT
3	732.8	53.2	1093	14	BM924569 AGENCOURT
4	730.2	53.0	846	13	BM458455 AGENCOURT
5	712.6	51.8	801	13	BM490880 603031867
6	672.2	48.8	724	13	BM71879 603055280

Result 1	LOCUS	DEFINITION	ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
7	671	48.7	1045	14	BM920874	BM920874	AGENCOURT			
8	660.4	48.0	792	13	BM770921	BM770921	603059737			
9	641.8	46.6	887	13	BM490062	BM490062	603031867			
10	631	45.8	1623	14	BM926477	BM926477	AGENCOURT			
11	607.2	44.1	630	12	BM706609	BM706609	602672994			
12	596	43.3	596	14	BM893587	BM893587	1126910.x			
13	586.4	42.6	541	13	BM544255	BM544255	AGENCOURT			
14	583.2	42.4	941	13	BM181899	BM181899	603035796			
15	578	42.0	878	14	BM893691	BM893691	1128608.x			
16	577.2	41.9	879	13	BM820945	BM820945	603033989			
17	572.4	41.6	574	13	BM021127	BM021127	1e76e01.x			
18	554	40.2	850	9	AF451167	AF451167	AF451167			
19	551.4	40.0	532	12	BF882978	BF882978	IL3-EF011			
20	532	38.6	532	12	BF724241	BF724241	bx02e11.y			
21	521	37.8	521	14	BM966810	BM966810	1126910.y			
22	517	37.5	517	14	BM966954	BM966954	1126910.y			
23	507.6	36.9	574	10	AM150070	AM150070	xg48b05.x			
24	507.6	36.9	844	10	BE309370	BE309370	601094718			
25	489.4	35.5	567	13	BM021381	BM021381	1e76e01.y			
26	479	34.8	778	12	BF098614	BF098614	601750614			
27	463.4	33.7	867	13	BM18537	BM18537	603033057			
28	457.4	33.2	1349	14	BM067382	BM067382	AGENCOURT			
29	453.2	32.9	702	12	BF055285	BF055285	7177902.x			
30	452.4	32.9	454	9	AI805087	AI805087	tuc3905.x			
31	448.4	32.6	462	10	AM070344	AM070344	xal0d10.x			
32	440.2	32.0	445	14	BM673416	BM673416	UI-E-CR1-			
33	438.4	31.8	842	13	BM688017	BM688017	60315786			
34	426.4	31.0	449	13	BM668611	BM668611	UI-E-CR1-			
35	424.4	30.8	442	14	BM693336	BM693336	UI-E-CR1-			
36	423.4	30.7	548	12	BF906443	BF906443	IL0-OT012			
37	421.6	30.6	630	12	BF046067	BF046067	BP250014A			
38	409.8	29.8	413	9	AI083823	AI083823	qf18c08.x			
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43	394.6	28.7	936	12	BF540263	BF540263	602052317			
44	392	28.5	392	10	BE138819	BE138819	xw95h11.x			
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RESULT 1
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DEFINITION 603049929F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190222 5',
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ACCESSION BM763193
KEYWORDS BM763193.1 GI:15754771
SOURCE EST.
ORGANISM human.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11475 row: 1 column: 07
High quality sequence stop: 777.
Location/Qualifiers
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/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sports; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb.
Insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber. (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

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Query Match	55.8%	Score 767.8	DB 13	Length 869	
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				Gaps	7
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QY	71	GCAGGGCAGGGGGCGCTGGCCGGGGAGAACCGCGGGGGCTGGAGACACCACTGGAG	130		
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QY	191	GAGAGACCCGAGCTCCGGGCTCCCGGTCCACAGCGCTATGAGAGCCACTCGTCCGTGCG	250		
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QY	251	CTCTGGGAGCTGGGGCGCGGCTCGCCCCACTGGACGACAACAGATCCCAAGCTCTGCG	310		
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QY	311	CCGGGGGACCCCGGCGCTTCCAGAGCACGCGGGGCCACATGGCAGCGCAGGGCTTGGCGGC	370		
Db	301	CCGGGGGACCCCGGCGCTTCCAGAGCACGCGGGGCCACATGGCAGCGCA-GGCTTGGCGGCGC	359		
QY	371	CGCATATGCGCGACGCGCGCGAGCGCGCGCCGGGGGCTCGGGGAGCAAAAGCGCAGGCG	430		
Db	360	CGCATATGCGCGCGACGCGCGCGAGCGCGCGCGCGGGGCTCGGGGAGCAAAAGCGCAGGCG	419		
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QY	491	GCGGGGCGCCACCGGGGCTGCCGGGAGTGTCTGGTCTCGCGATCGGCTTACGCGCC	550		
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QY	668	CTGGGGGTACTACTTTCGCGGTCCATGCCACGCTTACCGGGCAGCGCTCAGTTTGAT	727		
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QY	728	CTGGTGAAGATGGCGAATCCATTGGCTCTTCTTCCAGTTTTCGGGGGTGGCCCAAG	787		

DB	720	CTGCGAAGAAATGCGGAATTCATATGGGCTC-TTCCTTCAGTTTATACGGGGGCGGGCC--AA	776
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DB	777	GCCACCTGCTCTCGGGGGGGGCCCATATGTGAGCCTGTGAGAGCACAATGTGGGTG	836
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ACCESSION	5' mRNA sequence.		
VERSION	BM547549		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1154)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Invitrogen		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
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	(EcoRV site is destroyed upon cloning). Average insert		
	size 2.1 kb, insert size range 1-3.5 kb. Library is		
	normalized and enriched for full-length clones and was		
	constructed by C. Gruber (Invitrogen). Research Genetics		
	tracking code 036."		
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QY	100	AGGCGGGGGGCTGGAGACCAACCACTGTGAGGGTTCGGAGTATGAGGAGGCGCCCGAAGAG	159
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QY	160	GCCATCGGGGAGCCGGGAGGGGGAGATCCGAGAGAGACCCGGGCGTCCGGCTCCCGGATG	219
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OY		880	TGCCAGATCAACGACAGACACCCTTCCTCCGAATTCTGGTACTGTGTAATCCGACTGGCACG	939
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OY		940	CTCCCCAGCTTTTGCTTAGTGCCCACTGCACAAGAATGAGCTCATGCTCTACTCTAGAAAG	999
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OY		1000	AGGCTGTGAGGCTGACAAACAGATCATCCAGAGAGGGCGGCCCCCTGGAATATTGCGAA	1059
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VERSION	Bm920874.1			
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 1045)			
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distance information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM12785 row: n column: 14 High quality sequence stop: 415. Location/Qualifiers 1..1045			

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37	GCTGTGTCCACAGACTGTGGAAGAGACCCCGGCTCCCGTGTCCAGCGGTATGA	96				
231	GAGCACTCTCTGCTGTCTGCTCCGAGGAGCGGCGGCGGCTCCGCTACATGACGACA	290				
97	GAGCACTCTCTGCTGTCTGCTCTGCTCTGCGGCGCTGCGGCGGCGCTCCGCTACATGACGACA	156				
291	ACAAGATCCCAAGCTCTGCTCCCGGGGACCCCGGCTTCCAGAGCACGCGGGGACACATG	350				
157	ACAAGATCCCAAGCTCTGCTCCCGGGGACCCCGGCTTCCAGAGCACGCGGGGACACATG	216				
351	GCAGCAGAGGCTGTGCGGGGCGGCGATGAGCGGAGAGGCGGAGCGGCGCGCGCGGCGCTC	410				
217	GCAGCAGAGGCTGTGCGGGGCGGCGATGAGCGGAGAGGCGGAGCGGCGCGCGCGGCGCTC	276				
411	CGGAGAGAAAGCGAGGCGGAGCGGAGCCGAGACTCCCGGACCTTGAGAGGAGACCCCGGCG	470				
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591	CCTTGCGCTTTCAGCGCGCTGCTGTGAGACGAGGAGGACATTTAGACCGCGCTCACCGGACA	650				
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711	CGAGCTGCGAGTTGATGTGTTGAAGAAATGGCGAATCCATTGGCTCTTTCTTCCAGTTT	770				
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637	TCGGGGGTTGGCCCAAGCGCAGCGTGTGATCTGCGGGGGGGCCATGATGATGAGGCGCTG	696				
831	AGAGCAAGTGTGGGTGAGGAGTG-GGTGTGGGTGACTACA-TTGGCATCTATGCCA-GCA	887				
697	ATGACCAAGTGTGNOTGATGTGNGGTGTGCGTGTGACTACATTTGATGTGATGACATTC	756				
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 version B1770921.1
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 source human.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 792)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH MGC Library."

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Query Match 48.0%; Score 660.4; DB 13; Length 792;
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 version EST.
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 source human.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 887)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.

ORIGIN	BASE COUNT	93 a	215 c	257 g	65 t
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OY	67	GACGCGAGAGGCGAGGGGGGCGCTTGGCCCGGGAGAGAGCGGGGGGCTGGAGCACACCACT	126		
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OY	127	GGAGGGTCCGAGATAGCAGAGCGCCGCCGAGAGAGGCCATCTGGGGAGACCCGGAGGGGGAGCT	186		
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OY	307	CTGGCCCGGGGACACCCCGGCTTTCAGAGCAGCAGCGGGCCACCATGGAGCAGCAGGCGTTTGC	366		
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SOURCE	EST.				
ORGANISM	Homo sapiens				
	human.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 596)				
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,				
	Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,				
	Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,				
	Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas				
	,M., Gibbons,M., Mcann,R., Cole,R., Tsagarishvili,R., Williams,T.,				
	Jackson,Y. and Bowers,Y.				
TITLE	Endocrine Pancreas Consortium				

**JOURNAL
COMMENT**

Unpublished (2000)
Contract: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brownefas.harvard.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 441.
Location/Qualifiers

FEATURES
source

BASE COUNT	139 a	183 c	169 g	105 t
ORIGIN				

Query Match	43.38;	Score 596;	DB 14;	Length 596;
Best Local Similarity	100.08;	Pred. NO. 2.5e-72;		
Matches 596;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	752	GCCTCTTTCCTCCAGTTTTCCTGGGGGGGGGCCAAGCCAGCTGCTCTCGGGGGGGGGCC	811
Db	596	GCCCTCTTCTCCAGTTTTTCCTGGGGGGGGGGCCCAAGCCAGCTCTCGGGGGGGGGCC	537
QY	812	ATGGTGAAGGCTGAGGAGCCCTGAGGACCAAGTGGGTGTCAGGTGGGTGGGTGATACATT	871
Db	536	ATGGTGAAGGCTGAGGAGCCCTGAGGACCAAGTGGGTGTCAGGTGGGTGGGTGATACATT	477
QY	872	GGCATCTATGCGACATCTAGACACAGACAGACACTTCTCCGGATTTCTGGTACTCCGAC	931
Db	476	GGCATCTATGCGACATCTAGACACAGACAGACACTTCTCCGGATTTCTGGTACTCCGAC	417
QY	932	TGGACAGAGCTCCCGAGTCTTGTGCTTAGAGGCCACGCAAGGAGAGCTATGCTCAGTC	991
Db	416	TGGACAGAGCTCCCGAGTCTTGTGCTTAGAGGCCACGCAAGTGAAGTATGCTCTCAGTC	357
QY	992	CTAGAAGAGGGGTGAGGCTGAGACCAACGAGTCTATCCAGGAGGGGTGGCCCCCTCGAAT	1051
Db	356	CTAGAAGAGGGGTGAGGCTGAGACCAACGAGTCTATCCAGGAGGGGTGGCCCCCTCGAAT	297
QY	1052	ATTGTGAATGACTTGGGAGGTGGGGGTAGAGCACTCTCCGTCTGCTGTGGCAAGAAATG	1111
Db	296	ATTGTGAATGACTTGGGAGGTGGGGGTAGAGCACTCTCCGTCTGCTGTGGCAAGAAATG	237
QY	1112	GGAAACAGTGGGTGCTGGATCCAGTCTGGAGATGGGGGAGAGAGCTGGAATTCAGGCC	1171
Db	236	GGAAACAGTGGGTGCTGGATCCAGTCTGGAGATGGGGGAGAGAGCTGGAATTCAGGCC	177

0Y 1172 AAGACCAAGAGAGTGTGCTGTGCGAGCAAGGTAAATGCCCAAGTGTGCTGTGCTGCACAGA 1231
 |||||
 Db 176 AAGACCAAGAGAGTGTGCTGTGCTGTGCGCAAGGTAAATGCCCAAGTGTGCTGTGCTGCACAGA 117
 0Y 1232 GCCCACGGTGGGGGAGCTCTCTCCGCGAGCTCTGTGCTCTGTGAGATCTCCACACCCCTC 1291
 |||||
 Db 116 GCCCACGGTGGGGGAGCTCTCTCTCCGAGTCTGTGCTCTGTGAGATCTCTCCACACCCCTC 57
 0Y 1292 CTGTCTCCGTGGGGGAGCCCTTTTCTCACAAGATCACTCAATAAACCCTAAGAACCCTC 1347
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 Db 56 CTGTCTCCGTGGGGGAGCCCTTTTCTCACAAGATCACTCAATAAACCCTAAGAACCCTC 1

RESULT	13				
LOCUS	BM544255				
DEFINITION	BM544255	596 bp	mrna	linear	EST 20-FEB-2002
ACCESSION	AGNCOCIRT 6490655	NIH_MGC_125	Hom sapiens	CDNA clone	IMAGE:5587759
VERSION	5', mRNA sequence.				
KEYWORDS	BM544255				
SOURCE	BM544255.1	GI:18775356			
ORGANISM	EST.				
REFERENCE	human.				

REFERENCE	1 (bases 1 to 596)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES

BASE COUNT	138 a	158 c	172 g	127 t	1 others
ORIGIN					

Query Match	42.68;	Score 586.4;	DB 13;	Length 596;
Best Local Similarity	99.78;	Pred. No. 5e-71;		
Matches 587; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

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Db      121  CGGATTTCTGGTACTCCGACGTCCGACAGCTCCCGAGTCTTTCTAGTGCACAGTGC 180
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Db      181  AAAGTACATCTGCTCTCACCCTCAGAGAGGCTGTAGAGCTACACACAGGTCTATCC 240
OY      1029  AGGAGGCTGCCCCCTGGAATATTGTAATGATAGAGAGGCTGTAGAGCTATCC 1088
Db      241  AGGAGGCTGCCCCCTGGAATATTGTAATGATAGAGAGGCTGTAGAGCTATCC 300
OY      1089  GCTCTGCTGCTGAGCAAGGAATGGAGACAGTGTCTGTGATCAGTGTGAGCAATG 1148
Db      301  GCTCTGCTGCTGAGCAAGGAATGGAGACAGTGTCTGTGATCAGTGTGAGCAATG 360
OY      1149  GGGCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
Db      361  GGGCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
OY      1209  CCCCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1268
Db      421  CCCCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
OY      1269  CTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1328
Db      481  CTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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RESULT 14
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DEFINITION B1821899.1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176967 5',
mRNA sequence.
ACCESSION B1821899
VERSION B1821899.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE: NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 941)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: csapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1440 row: P column: 24
High quality sequence stop: 779.
Location/Qualifiers
1. 941
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/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and

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enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

Query Match 42.4%; Score 583.2; DB 13; Length 941;
Best Local Similarity 94.3%; Pred. No. 1e-70;
Matches 758; Conservative 0; Mismatches 28; Indels 18; Gaps 14;

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Db      136  GAGGACCCCGGCGTCCGAGCTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCC 195
OY      250  GCTCTGCTGCTGAGCAAGGAATGGAGACAGTGTCTGTGATCAGTGTGAGCAATG 309
Db      196  GCTCTGCTGCTGAGCAAGGAATGGAGACAGTGTCTGTGATCAGTGTGAGCAATG 255
OY      310  CCGGCGGACCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
Db      256  CCGGCGGACCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
OY      369  GCCGCGATGCGCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
Db      316  GCCGCGATGCGCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 375
OY      428  GCGGCGGAGCGCGGAGCTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 487
Db      376  GCGGCGGAGCGCGGAGCTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 435
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Db      496  GCGGCGGAGCGCGGAGCTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 555
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Db      616  GAGTGCGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 675
OY      721  GTTATATCTGCTGAGCAAGGAATGGAGACAGTGTCTGTGATCAGTGTGAGCAATG 780
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OY      840  TGTGCGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 898
Db      795  TGTGCGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 853
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Db      854  AGCACTCTCTCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCC 912
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RESULT 15
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DEFINITION BM893691.1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136046 3' similar to TR:Q9UFY4 Q9UFY4
HYPOTHETICAL 22.8 KD PROTEIN ; mRNA sequence.

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ACCESSION BM893691
VERSION BM893691.1 GI:19349159
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarsa,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,K., Tsagarelisvill,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Juliana Brown
(brown@efas.harvard.edu)
Seq primer: -40UP from Glibco
High quality sequence stop: 408.
Location/Qualifiers
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Site:2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dt priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT 130 a 181 c 163 g 104 t
ORIGIN
Query Match 42.0%; Score 578; DB 14; Length 578;
Best Local Similarity 100.0%; Pred. No. 7.1e-70;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 770 TTGCGGGGGTGGCCCAAGCCAGCCTCGCTCGGGGGGGCCATGTGAGGCTGGAGCCT 829
DB 578 TTGCGGGGGTGGCCCAAGCCAGCCTCGCTCGGGGGGGCCATGTGAGGCTGGAGCCT 519
QY 830 GAGGACCAAGTGGGCGAGGCGGTGGGTGACATACATTTGGCATCTATGCCAGATC 889
DB 518 GAGGACCAAGTGGGCGAGGCGGTGGGTGACATACATTTGGCATCTATGCCAGATC 459
QY 890 AAGACAGACAGACCTTCTCCGATTTCTGTGTACTCCAGCTGGACAGCTCCCAAGTC 949
DB 458 AAGACAGACAGACCTTCTCCGATTTCTGTGTACTCCAGCTGGACAGCTCCCAAGTC 399

QY 950 TTGCTTAGTCCCACTGCAAAAGTACGCTATGCTCTGACTCTAGAGAAGAGGCTGTAG 1009
DB 398 TTGCTTAGTCCCACTGCAAAAGTACGCTATGCTCTGACTCTAGAGAAGAGGCTGTAG 339
QY 1010 GCTGACAAACAGGTCATCCAGAGGAGGCTGGCCCCCGGGAATATTGGAATGACTAGGA 1069
DB 338 GCTGACAAACAGGTCATCCAGAGGAGGCTGGCCCCCGGGAATATTGGAATGACTAGGA 279
QY 1070 GGTGGGTAGAGACACTCTCCCTGCTGTGCGAAGGAATGGAAGAGTGGCTGTGCG 1129
DB 278 GGTGGGTAGAGACACTCTCCCTGCTGTGCGAAGGAATGGAAGAGTGGCTGTGCG 219
QY 1130 GATCAGCTCTGCGACATGCGGCGAGTGGCTGGAATTTGCCCCAAGACAGAGAGTGTGC 1189
DB 218 GATCAGCTCTGCGACATGCGGCGAGTGGCTGGAATTTGCCCCAAGACAGAGAGTGTGC 159
QY 1190 TGTGCTGGAAGTGTAGTCCCGAGTGGCTGTGCTGCGAAGGCCACAGGCTGGCTC 1249
DB 158 TGTGCTGGAAGTGTAGTCCCGAGTGGCTGTGCTGCGAAGGCCACAGGCTGGCTC 99
QY 1250 TCTTCTGATCCCTGCTGCTGCTGATGCTCCCAAGGCTGCTGCTGCTGCTGCTGCTG 1309
DB 98 TCTTCTGATCCCTGCTGCTGCTGATGCTCCCAAGGCTGCTGCTGCTGCTGCTGCTG 39
QY 1310 CTTTCTCAGAGATCACTCAATAAAGCTAAGACCTTC 1347
DB 38 CTTTCTCAGAGATCACTCAATAAAGCTAAGACCTTC 1

Search completed: June 21, 2003, 11:25:26
Job time : 2203 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_n2p model

Run on: June 21, 2003, 14:34:16 ; Search time 19.5 seconds

(without alignments)
5857.734 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 2540

Sequence: 1 gactagctctcttgagctc.....aaaaaaaaaaaaaaaaaa 1377

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -LARGEOUTERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1325	52.2	243	1	Q9BXJ0 homo sapien
2	458	18.0	680	1	CA1A_HUMAN
3	454	17.9	674	1	CA1A_BOVIN
4	451	17.8	674	1	CA1A_CHICK
5	448	17.6	680	1	CA1A_MOUSE
6	433.5	17.1	247	1	APM1_MOUSE
7	426.5	16.8	744	1	CA18_RABIT
8	424	16.7	244	1	APM1_HUMAN
9	417.5	16.4	635	1	CA28_HUMAN
10	417	16.4	289	1	Q9BXJ2 homo sapien
11	417	16.4	743	1	CA18_HUMAN
12	415.5	16.4	744	1	CA18_MOUSE
13	412	16.2	246	1	CA18_HUMAN
14	407	16.0	419	1	COLE_MOUSE
15	403	15.9	285	1	COLE_MOUSE
16	397	15.6	245	1	Q9BXJ5 homo sapien
17	362	14.3	251	1	CA10B_HUMAN
18	360.5	14.2	253	1	CA10B_RAT

19	350	13.8	253	1	CA10B_MOUSE	P14106 mus musculu
20	328	12.9	1049	1	CA13_BOVIN	P04258 bos taurus
21	322	12.7	1464	1	CA11_HUMAN	P02452 homo sapien
22	318.5	12.5	1453	1	CA11_CHICK	P02457 gallus galli
23	314	12.4	245	1	CA10A_HUMAN	P02457 gallus galli
24	314	12.4	245	1	CA10A_MOUSE	P02457 gallus galli
25	313.5	12.3	1460	1	CA11_MOUSE	P02457 gallus galli
26	310.5	12.2	1459	1	CA12_MOUSE	P02457 gallus galli
27	309	12.2	1670	1	CA34_HUMAN	P02457 gallus galli
28	306.5	12.1	1262	1	CA13_CHICK	P02457 gallus galli
29	303.5	11.9	255	1	CA13_MOUSE	P02457 gallus galli
30	302	11.9	636	1	CA13_RAT	P02457 gallus galli
31	302	11.9	1464	1	CA13_MOUSE	P02457 gallus galli
32	301.5	11.8	1418	1	CA12_HUMAN	P02457 gallus galli
33	300	11.8	747	1	CA12_BOVIN	P02457 gallus galli
34	300	11.8	1466	1	CA13_HUMAN	P02457 gallus galli
35	298.5	11.8	258	1	CA13_MOUSE	P02457 gallus galli
36	298.5	11.8	258	1	CA13_MOUSE	P02457 gallus galli
37	298.5	11.8	779	1	CA11_BOVIN	P02457 gallus galli
38	298	11.7	1453	1	CA11_MOUSE	P02457 gallus galli
39	297.5	11.7	1366	1	CA21_MOUSE	P02457 gallus galli
40	297	11.7	1364	1	CA21_BOVIN	P02457 gallus galli
41	296	11.7	1355	1	CA21_RANCA	P02457 gallus galli
42	295.5	11.6	671	1	CA11_RAT	P02457 gallus galli
43	294	11.6	1372	1	CA21_MOUSE	P02457 gallus galli
44	294	11.6	1838	1	CA15_HUMAN	P20908 homo sapien
45	293	11.5	1806	1	CA1B_HUMAN	P12107 homo sapien

ALIGNMENTS

RESULT 1

CDT5_HUMAN STANDARD: PRT: 243 AA.

AC Q9BXJ0: Q9BXJ0; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement-c1q tumor necrosis factor-related protein 5 precursor.
GN C1QTNF5 OR C1QTNF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SHEPPARD P.O., Humes J.M.;
RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 25-243 FROM N.A.
RC TISSUE=uterus;
RA Ottenwelder B., Obermayer B., Mewes H.-W., Gassenhuber J.,
RA Wilmann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
CC EMBL: AF329841; AA317965.1;
CC EMBL: AL110261; CAB53702.1;
CC Genew, HGNC:14344; C1QTNF5.
CC InterPro: IPR001073; C1q.
CC InterPro: IPR000087; Collagen.
CC Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 1.

RT occur in two unrelated families with metaphyseal chondrodysplasia
RT type Schmid.";
RL Am. J. Hum. Genet. 54:169-178(1994).
RN [10]
RP VARIANT SMCD ARG-591.
RX MEDLINE-94272470; PubMed-8004099;
RA McIntosh I., Abbott M.H., Merman M.L., Olsen B.R., Francimano C.A.;
RT "Additional mutations of type X collagen confirm COL10A1 as the
RT Schmid metaphyseal chondrodysplasia locus.";
RL Hum. Mol. Genet. 3:303-307(1994).
RN [11]
RP VARIANT SMCD VAL-618.
RX MEDLINE-95181449; PubMed-7876225;
RA Chan D., Cole W.G., Rogers J.G., Bateman J.F.;
RT "Type X collagen multimer assembly in vitro, is prevented by a Gly618
RT to Val mutation in the alpha 1(X) NC1 domain resulting in Schmid
RT metaphyseal chondrodysplasia.";
RL J. Biol. Chem. 270:4558-4562(1995).
RN [12]
RP VARIANTS SMCD ARG-545; GLU-595; HIS-597; LYS-617; ARG-644 AND GLY-648
RX MEDLINE-95331767; PubMed-7607655;
RA Bonaventure J., Chamaïade F., Marcoteaux P.;
RT "Mutations in three subdomains of the carboxy-terminal region of
RT collagen type X account for most of the Schmid metaphyseal
RT dysplasias.";
RL Hum. Genet. 96:58-64(1995).
RN [13]
RP VARIANT SMCD PRO-600.
RX MEDLINE-96375754; PubMed-8782043;
RA Wells G.A., Rash B., Sykes B., Bonaventure J., Marcoteaux P.,
RT Zabel B., Wynne-Davies R., Grant M.E., Boot-Handford R.P.;
RT "Mutations within the gene encoding the alpha 1 (X) chain of type X
RT collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid but
RT not several other forms of metaphyseal chondrodysplasia.";
RL J. Med. Genet. 33:450-457(1996).
RN [14]
RP VARIANTS SMCD GLU-18 AND ARG-18.
RX MEDLINE-97220591; PubMed-9067753;
RA Ikegawa S., Nakamura K., Nagano A., Haga N., Nakamura Y.;
RT "Mutations in the N-terminal globular domain of the type X collagen
RT gene (COL10A1) in patients with schmid metaphyseal
RT chondrodysplasia.";
RL Hum. Mutat. 9:131-135(1997).
RN [15]
RP VARIANTS SMD GLU-595.
RX MEDLINE-99057503; PubMed-9837818;
RA Ikegawa S., Nishimura G., Negai T., Hasegawa T., Ohashi H.,
RA Nakamura Y.;
RT "Mutation of the type X collagen gene 'COL10A1' causes
RT spondylometaphyseal dysplasia.";
RL Am. J. Hum. Genet. 63:1659-1662(1998).
RN [16]
RP VARIANT SMCD CYS-597.
RX MEDLINE-99069781; PubMed-9852679;
RA Sawai H., Ida A., Nakata Y., Koyama K.;
RT "Novel missense mutation resulting in the substitution of tyrosine by
RT cysteine at codon 597 of the type X collagen gene associated with
RT Schmid metaphyseal chondrodysplasia.";
RL J. Hum. Genet. 43:259-261(1998).
RN [17]
RP FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
RX CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC [18]
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PPM: PROLINS ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- DISEASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SCHMID TYPE
CC METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED
CC DISORDER OF THE OSSEOUS SKELETON. THE CARDINAL FEATURES OF THE
CC PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT.
CC RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE
CC METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE, ESPECIALLY OF THE
CC KNEES.
CC -1- DISEASE DEFECTS IN COL10A1 ARE THE CAUSE OF SPONDYLOMETAPHYSEAL

```

CC      DYSPLASIA (SMD) : SMD COMPRISES A HETEROGENEOUS GROUP OF HERITABLE
CC      SKELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE
CC      VERTEBRAL BODIES OF THE SPINE AND METAPHASES OF THE TUBULAR BONES.
CC      -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC      -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X60382; CAA42933.1; -.
CC      EMBL; X65120; CAA46236.1; -.
CC      EMBL; X98568; CAA67178.1; -.
CC      EMBL; A1121963; CAA87590.1; -.
CC      EMBL; S68531; AAC60615.1; -.
CC      EMBL; X58879; CAA41686.1; -.
CC      EMBL; M74050; AAA61221.1; -.
CC      EMBL; X72579; CAA51170.1; -.
CC      EMBL; X72580; CAA51170.1; JOINED.
CC      PIR; S15826; S15826.
CC      PIR; S30086; S30086.
CC      PIR; A43901; A43901.
CC      PIR; S18249; S18249.
CC      PIR; S21856; S21856.
CC      PIR; S26396; S26396.
CC      Genew; HGNC:2185; COL10A1.
CC      MIM; 120110; -.
CC      MIM; 156500; -.
CC      DR MIM; 184250; -.
CC      DR InterPro: IPR001073; C1q.
CC      DR InterPro: IPR000087; Collagen.
CC      DR Pfam; PF00386; C1q; 1.
CC      DR Pfam; PF01391; Collagen; 8.
CC      DR PRINTS; PR00007; COMPLEMNTC1Q.
CC      DR SMART; SMO0110; C1Q; 1.
CC      DR PROSITE; PS0113; C1Q; 1.
CC      KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC      Cartilage; Collagen; Signal; Disease mutation; Polymorphism.
CC      FT SIGNAL 1 18
CC      FT CHAIN 19 680
CC      FT DOMAIN 19 56
CC      FT DOMAIN 57 519
CC      FT DOMAIN 520 680
CC      FT DOMAIN 545 680
CC      FT VARIANT 18 18
CC      FT VARIANT 18 18
CC      FT VARIANT 545 545
CC      FT VARIANT 591 591
CC      FT VARIANT 591 591
CC      FT FTID=VAR_001838.
CC      FT FTID=VAR_001839.
CC      FT G->R.
CC      FT FTID=VAR_001840.
CC      FT C->R (IN SMD).
CC      FT FTID=VAR_001841.
CC      -----
CC      Alignment Scores:
CC      Pred. No.: 2.24e-14
CC      Score: 458.00
CC      Percent Similarity: 42.78%
CC      Best local Similarity: 32.47%
CC      Query Match: 18.03%
CC      DB: 1
CC      Length: 680
CC      Matches: 126
CC      Conservative: 40
CC      Mismatches: 123
CC      Indels: 99
CC      Gaps: 13

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Db	323	gTuglUGInGInGlyProAlaGlyLeuProGlyLysProGlyLysIleuThGlyProProGlyLysP	34.2
QY	121	-----CCAGCTGGAGAGGCTCCGAGCA-----	14.1
Db	343	MetGlyProGInGInGlyProLysGlyIleProGlySerIleGlyLeuProGlyProLysGly	36.2
QY	142	GGAGAGCGCCCGCAGAGAGAGGCAATCGGAGAGAGCGGAGAGGGAGGAGCTCGAGAGAGCGCCG	20.1
Db	363	GIuThInGlyProAlaGlyProAlaGlyLysProGlyAlaLysLysLysLysLysLysLysLysLys	38.0
QY	202	CGTCCGGGCTCCCGGCTGCCAGCGCTATGAGGCCACTGCT-----CGTCCGCT	24.9
Db	381	SerProGlySer-----AspGlyLysProGlyLysIleProGlyLysProGly	39.5
QY	250	GCTCGTGGGCGCGGCGCGGCTCGCGCCCGCAGCTGAGCGAGCAACAAATCCCGCGGCTCG	30.9
Db	356	LeuAerGlyProLysGlyLysAsnProGlyLeuProGlyProLysGlyAsp-ProGlyVal--	41.4
QY	310	CCCGGGGACACCCGGGCTTTCCAGGACAGCGGGGCGCCACATGCGAGCGAGGCTTGGCGGG	36.9
Db	415	-GlyLysProGlyLeuProGlyProAlaGlyProAlaGlyAlaLysLysLysLysLysLysLys	43.4
QY	370	CCGGATGGCCCGCAGAGCGCGGAGAGCGCGCGCGCGGCTCCGGGAGAGAAAGCGAGGG	42.9
Db	434	YHISnGInGlyAlaGlyProAlaGlyLysProGlyLysLysLysLysLysLysLysLysLysLys	45.4
QY	430	CGGAGAGCCCGGAGAGCTGCCG-----	44.8
Db	454	eGlyProProGlyIleProGlyLysIleProGlySerLysGlyLysAspProGlySerProGlyLys	47.4
QY	449	-----GAGCTCGAGAGGGA	46.2
Db	474	oProGlyProAlaGlyLysLysLysLysGlyLysAsnGlyProThGlyProThGlyProProGlyLys	49.4
QY	463	CCCGCGGCGCGCGAGGAGAGCG-----GAGCGCGGAGGCGCCACCGG	50.4
Db	494	oProGlyProAlaGlyLysSerGlyLysProGlyLysProGlyLysProGlyLysProGlyLys	51.4
QY	505	GCCTCCCGGAGAGTCTCGTGCTT-----	52.9
Db	514	YProGlyLysAlaLysAlaLysMetProGlyLysIleLysLysAlaGlyLysAspProGlyLys	53.4
QY	530	-----CCGCGAGCTCGGCTT	54.3
Db	534	uSerGlyLysProLeuValSerAlaLysnGInGlyAlaLysIleGlyLysMetProValSerLysLys	55.4
QY	544	CAGCGCCAGAGCGCTCCGAGAGCGCGGCTCTCGCGCTGAGAGCAACCGTCCGCTTGA	60.3
Db	554	eThValLysLeuSerLysLysAlaLysLys-----ProAlaLysGlyLysProLysProLysPheAs	57.2
QY	604	CCGGCTGCTGGTGAAGAGAGGAGGAGCATATGACAGCGCGCTCACCGGAGAGTATGACCGCA	66.3
Db	572	PLysIleLeuTYrAsnAlaGInGInHisTYrAsnProAlaGInGlyLysIleTherTYrSGL	59.2
QY	664	GGTGCCTGGGCTACTACTTTCGCGCGATGCGACGACGCTACCGCGGAGCGAGCTGCAGATT	72.3
Db	592	nIleProGlyLysIleTYrLysSerTYrHisValHisValLysGlyLysIleHisValIlePrya	61.2
QY	724	TGATCTGGTGAAGATGGCGAATTCATTTGCC-----TCTTCTCTCCAGTCTTTTGGGGGGTG	78.0
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QY	781	GGCCAAAGCGAGCTGCTTCGGGGGGGCGCATGGAGAGCGTGGAGCGTGGAGCACAAGT	84.0
Db	632	rLeuAspGlnAla-----SerGlySerLysLysLysLysLysLysLysLysLysLysLysLys	65.0
QY	841	GTGGGTGAGGTGGGTGGGTGCTACTATCTGATCTTATGCGAGCATGACAGACAGAG	90.0
Db	650	IYrPrenGInLeuProAsnAlaGlyLysAsnGlyLeuTYrSerSerGlyLysIleValHisSe	67.0
QY	901	CACCTTTCGGGATTTCTGGTG	92.2
Db	670	rSerPheSerGlyPheLeuVal	67.7

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RESULT 3
CALA_BOVIN
ID CALA_BOVIN STANDARD: PRT: 674 AA.
AC P23206:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE collagen alpha 1(x) chain precursor.
GN COL10A1.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=911131; PubMed=1703407;
RX Thomas J.T., Kwan A.P.D., Grant M.E., Boot-Handford R.P.;
RT "Isolation of cDNAs encoding the complete sequence of bovine type X
RT collagen. Evidence for the condensed nature of mammalian type X
RT collagen genes".
RT Blochem. J. 273:141-148(1991).
RL B1ochem. J. 273:141-148(1991).
CC -1 FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1 SUBUNIT: HOMOTRIMER.
CC -1 PPT: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1 SIMILARITY: STRONG TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1 SIMILARITY: CONTAINS 1 C10 DOMAIN.
CC -----
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CC -----
DR EMBL; X53556; CAA37624.1; -.
DR PIR; S13301; S13301.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; C1q; 1.
DR Pfam; PF01391; Collagen; 9.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR ProDom; PD000007; Collagen; 1.
DR SMART; SM00110; C1q; 1.
DR SMART; SM00110; C1q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Cartilage; Collagen; Signal; Glycoprotein.
KW SIGNAL
FT CHAIN 1 18 COLLAGEN ALPHA 1(X) CHAIN.
FT CHAIN 19 674 NONHEMELICAL REGION (NC2).
FT DOMAIN 19 56 TRIPLE-HELICAL REGION.
FT DOMAIN 57 519 TRIPLE-HELICAL REGION.
FT DOMAIN 520 674 NONHEMELICAL REGION (NC1).
FT DOMAIN 539 674 C1Q.
FT DISULFID 194 197 BY SIMILARITY.
FT MOD_RES 460 460 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 463 463 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 674 AA; 65546 MW; CD4CA73A03ED004CA CMC64;

Alignment Scores:
Pred. NO.: 3.4e-14 Length: 674
Score: 454.00 Matches: 122
Percent Similarity: 44.93% Conservative: 42
Best Local Similarity: 33.42% Mismatches: 116
Query Match: 17.87% Indels: 85
DB: 1 Gaps: 13

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US-09-944-944-41 (1-1377) x CALA_BOVIN (1-674)
OY 46 GGAGGACGAGGACTGGGT-----GAGGCGAGGCGAGGGGGCGCTGGCGG 93
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Db 320 G1yAlAlAylsGlyGlInGlyProAlaGlyHisProGlyGlyAlaGly-----LeuPro 337
OY 94 GGGAGAGACGGGGGGCTGGAGACACCACTGAGGTCGGAGTAGCGAGCGGCCCG 153
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 338 G1yProSerGlyAsnMetGly-----ProGlnGlyProGlyGlyLeuProGlyAsnPro 355
OY 154 AAGGAGCCATCGGGGAGCGGGAGGGGAGCTCGAGAGGACCC-----CGG 201
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Db 356 -----GlyLeuProGlyProGlyGlyGlyMetGlyGlyAlaGlyProAlaGly 371
OY 202 CGTCGGGCTCCCGGCTGCGAGGCTATGAGGCC-----ACGCCGTCGCTGCTCTCT 255
   |||||  :|||  |||  |||  |||  |||  |||  |||  |||  |||
Db 372 AsnProGlyAlaGlyGlyGlyGlyGlyGlySerGlyLeuAspGlyLysProGlyTyrPro 391
OY 256 GGGCGCTGGCGCGCGCTCGCCCGACCTGAGCAGACAAAGATCCCGACCT----- 306
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Db 392 GlyGluProGlyLeuAsnGlyProGlyGlyAsnProGlyLeuProGlyProGlyGlyLysP 411
OY 307 -----CTGCCCGGGGACCCCGGCTTCAGAGCAGCGCGGCCACCATGCGAGCGAGG 360
   :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 412 ProGlyLeuAlaGlySer-ProGlyLeuProGlyProAlaGlyAlaGlyAlaGly 431
OY 361 CTGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGAA 420
   |||||  :|||  |||  |||  |||||  |||||  |||||  :|||
Db 431 yValProGlyHisAsnGlyAlaGlyProGlyGlyAlaGlyProGlyLeuProGlyTyrThr 451
OY 421 AGCGGAGGCGGGAGGCGCGGAGCTGCGC----- 448
   |||  |||  |||||  :|||  |||  |||  |||  |||  |||  |||
Db 451 gGlyProGlyLeuProGlyLeuProGlyLeuProGlyPheProGlySerGlyAspValGlyTh 471
OY 449 -----GAGC 453
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 471 rProGlyProProGlyProAlaGlyLeuAlaValLysGlyLeuAsnGlyProThrGlyP 491
OY 454 TCGAGGAGGACCGCGCGCGCGAGGAGGCG-----GAGCGCGCGGG 495
   |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 491 oProGlyProProGlyProAlaGlyAsnAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 511
OY 496 GCCCAGCGCGCGCGCGCGAGTGTCTCGTGGCT----- 529
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Db 511 yProProGlyProProGlyGlyGlyAlaLeuProGlyAsnAspPheValLysAlaGlyGlnAr 531
OY 530 -----CCGCGATCCGCTTCAGCGCAA 552
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Db 531 gProPheValSerAlaAsnGlyValThrGlyMetProValSerAlaPheThrValIl 551
OY 553 GCGCTCCGAGCGCGGTGCTCGCGCTGAGCGACCTTCGCGCGCGGTGCT 612
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Db 551 eleuSerLysAlaTyr-----ProAlaIlleGlyThrProIleProPheAspLysIlle 569
OY 613 GGTGAAGCAGGAGGACATTAAGACGCGCGCGAGTTCACCTCCAGGTGCTG 672
   |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 569 uTyAsnLysGlnGlnHisTyrAspProArgThrGlyLeuPheThrCysLysIlleProG 589
OY 673 GGTCTACTACTTCGCGCGCGCGACCGCTACCGCGCGCGCGCGAGTTGATCTG 732
   |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 589 yIleLysTyrPheSerTyrHisLysValLysGlyThrHisAlaTyrValGlyLeuTy 609
OY 733 GAGAGATGCGCATTCATGCGC-----TCTTCTTCAGTTTTCGGGGGTGGCCCAACC 789
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 609 rLysAsnGlyThrProAlaMetTyrThrTyrAspGlyTyrLysGlyTyrLeuAspG 629
OY 790 AGCTCGCTTCGCGGGGGCGCATAGTGGAGCTGAGCGCAAGTGGGGTCA 849
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Db 629 nAla-----SerGlySerAlaValIlleAspLeuThrLysAsnAspGlnValTyrPleuG 647
OY 850 GGTGGGTGGTGGTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTC 909
   |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 647 nLeuProAsnAlaGlySerAsnGlyLeuTyrSerProGlyTyrValHisSerPheSe 667

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OY 910 CGGATTCGCGTG 922
Db 667 rGlyPheLeuVal 671

RESULT 4
CALA_CHICK
ID CALA_CHICK STANDARD: PRT: 674 AA.
AC P08125:
DT 01-AUG-1988 (rel. 08, Created)
DT 01-NOV-1991 (rel. 20, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Collagen alpha 1(x) chain precursor.
GN COL10A1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP MEDLINE-86168227, PubMed-3082876;
RX MEDLINE-86168227, PubMed-3082876;
RA Nimmiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,
RA Olsen B.R.;
RT "The developmentally regulated type X collagen gene contains a long
RT open reading frame without introns."
RL J. Biol. Chem. 261:5041-5050(1986).
RN [2]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE-89054019; PubMed-2461368;
RA Luvall P., Nimmiya Y., Rosenblum N.D., Olsen B.R.;
RT "The type X collagen gene. Intron sequences split the 5'-untranslated
RT region and separate the coding regions for the non-collagenous amino-
RT terminal and triple-helical domains."
RL J. Biol. Chem. 263:18378-18385(1988).
RN [3]
RP REVISIONS TO C-TERMINUS.
RX MEDLINE-89380199; PubMed-2476437;
RA Yamaguchi N., Benya P.D., van der Rest M., Nimmiya Y.;
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
RT demonstrate that type VIII collagen is a short chain collagen and
RT contains triple-helical and carboxyl-terminal non-triple-helical
RT domains similar to those of type X collagen."
RL J. Biol. Chem. 264:16022-16029(1989).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1- SIMILARITY: CONTRAINS 1 C1Q DOMAIN.
CC -----
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CC -----
DR EMBL: M13496; AAA48736.1; ALT_SEQ.
DR EMBL: J04194; AAA48634.1; -.
DR PIR: A31896; A31896.
DR InterPro: IPR01073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; collagen; 8.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Cartilage; Collagen; Signal.

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ID	APML_MOUSE	STANDARD:	PRT:	247 AA.
AC	060994:	0622400; Q9DC68:		
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Adiponectin precursor (30 kDa adipocyte complement-related protein)			
DE	(ACRP30) (Adipocyte specific protein AdipoQ).			
GN	APM1 OR ACRP30 OR ADIPOQ.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Adipocyte.			
RX	MEDLINE=96070757; PubMed=7592907;			
RA	Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;			
RT	"A novel serum protein similar to Ctg, produced exclusively in			
RL	adipocytes."			
RL	J. Biol. Chem. 270:26746-26749(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fibroadip.			
RX	MEDLINE=9620999; PubMed=8631877;			
RA	Hu E., Liang P., Spiegelman B.M.;			
RT	"AdipoQ is a novel adipose-specific gene dysregulated in obesity."			
RL	J. Biol. Chem. 271:10697-10703(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=1162643;			
RA	Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;			
RT	"Chromosomal localization, expression pattern, and promoter analysis			
RT	of the mouse gene encoding adipocyte-specific secretory protein			
RL	Acip30."			
RL	Biochem. Biophys. Res. Commun. 280:1120-1129(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Heart;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,			
RA	Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,			
RA	Schirrali L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakomura N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,			
RA	Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
RL	[5]			
RP	FUNCTION.			
RX	MEDLINE=21372498; PubMed=11479627;			
RA	Yamauchi T., Kamon J., Maki H., Teranishi Y., Kubota N., Hara K.,			
RA	Mori Y., Ide T., Murakami K., Isuboyama-Kasaka N., Ezaki O.,			
RA	Akanuma Y., Gavrilova O., Vlasov C., Reitman M.L., Kagechika H.,			
RA	Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,			
RA	Froguel P., Kadwaki T.;			
RT	"The fat-derived hormone adiponectin reverses insulin resistance			
RT	associated with both lipodystrophy and obesity."			
RL	Nat. Med. 7:941-946(2001).			
RN	[6]			
RP	FUNCTION.			

```

RX MEDLINE=21372499; PubMed=11479628;
RA Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;
RI "The adipocyte-secreted protein Acrp30 enhances hepatic insulin
RL action."
RL Nat. Med. 7:947-953(2001).
CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
CC SYSTEMS: MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING
CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE
CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
CC -1- SUBUNIT: HOMODIGOMER.
CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND
CC SECRETED INTO SERUM.
CC -1- INDUCTION: DURING HORMONE-INDUCED ADIPOSE DIFFERENTIATION AND
CC ACTIVATED BY INSULIN.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sb.ch).
CC -----
DR EMBL: U37222; AAA80543.1; -.
DR EMBL: U49915; AAB06706.1; -.
DR EMBL: AF304456; AAK33417.1; -.
DR EMBL: AK003138; BAB22597.1; -.
DR MGI: 106675; Acrp30.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRINTS: PRO0007; COMPLETEC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
KW Polymorphism.
FT SIGNAL 1 17
FT CHAIN 18 247
FT DOMAIN 45 110
FT DOMAIN 111 247
FT DISULFID 39 39
FT MOD_RES 47 47
FT MOD_RES 50 50
FT MOD_RES 56 56
FT MOD_RES 65 65
FT MOD_RES 79 79
FT MOD_RES 98 98
FT MOD_RES 107 107
FT MOD_RES 113 113
FT VARIANT 50 50
FT CONFLICT 74 74
FT CONFLICT 117 117
FT CONFLICT 148 148
FT CONFLICT 243 243
FT CONFLICT 247 AA; 26841 MW; 137B667DB7398C4 CRC64;
FT SEQUENCE

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Alignment Scores:	
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Best Local Similarity:	40.64%
Query Match:	17.07%
DB:	1
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Mismatches:	92
Indels:	25
Gaps:	8

US-09-944-944-41 (1-1377) x APM1_MOUSE (1-247)

qy 227 ATGAGGCCACTCCTCGTCCGTGCTGCCTGG--GGCCTGGCGGCCCGGCTGCCCCCACTG 283

Db	4	LeuGlnAlaLeuLeuPheLeuLeuLeuLeuLeuLeuProSerHisAlaLysAspValAlaThrThr	23
QY	234	GACGACACACAAATCCCAAGCTCTCCGCGGGGACCCCGGCG-----CTT	328
Db	24	ThrgLgLuLeuAlaPheAlaProAlaLeuValAProProProLysGluYhrCysAlaGluYhrMet	43
QY	329	CCAGCAGCGCGCGGCGACCATGGACCGACCGAGGGCTCCGGGCGCGCGATGGCGCGAGCG	388
Db	44	AlaGluYhrLeuProGluYhrHisProGluYhrHisAsnGluYhrProGluYhrAspGluYhrAsp	62
QY	389	CGCGACGCGCGCGCGCGGCTCCGGAGAGAAAGCGAGCGCGAGCGCGAGACTCCG	448
Db	63	-----GluYhrProGluYhrGluYhrGluYhrLysAlaGluYhrLeu	77
QY	449	GGACCTCGAGGCGGAC-----CGCGGCGCGAGAGAG	483
Db	78	GluProLysGluYhrGluYhrGluYhrValGluYhrMetThrGluYhrAlaGluYhrProAlaGluYhr	97
QY	482	CGCGGAGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGAGTGGCTCCGCGCGCGCGCGCGCG	544
Db	98	ProGluYhrProGluYhrGluYhrGluYhrGluYhrProGluYhrAlaAlaLeuYhrMetYhrAspGlu	117
QY	542	TTGACGCGGACCGCGCTCCGACAGCGCGGGCTCCCGCGCGCTGACGCGCGCGCTCCGCTTC	601
Db	118	PheSerVal--GluYhrGluYhrAspValAlaThrValPro--AspValProAlaThrPhe	1351
QY	602	GACCGCGCTGCTGGTGAACGACGAGGACGACATTCACGACGCGCGTACCGCGGACATTCACGCTG	661
Db	136	ThruYhrPheYhrGluYhrAsnGluYhrHisAsnGluYhrAspGluYhrSerThrGluYhrPheYhrGlu	1555
QY	652	CAGTGGCTGGGCTGTACTACTCTCCGCGCGTGCATGCGACGCGTACGCGCGCGCGCGCGCG	721
Db	156	AsnThrProGluYhrLeuYhrGluYhrPheSerYhrHisThrValYhrMetYhrAspValYhr	777
QY	722	TTTGATCTGGTGAAGAGATGGCGAATTCGCTCTGCTCCAGATTTTCGGGGGCTGG	781
Db	176	ValSerLeuPheYhrLysYhrAspValAlaValLeuPheThrYhrGluYhrGluYhrGluYhr	1944
QY	782	CCGACGCGCGCGCTCCGCTCCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	841
Db	195	LysAlaValAlaPheGluYhrAlaSerGluYhrSerValLeuYhrHisLeuYhrGluYhrAlaGluYhr	2144
QY	842	TGGGTCGACGCTG--GCTGGGCTGACTGATTCGATGCGATGATGCGCGCGCGCGCGCGCG	898
Db	215	TrpLeuGluYhrGluYhrAspGluYhrAspGluYhrHisAsnGluYhrLeuYhrAlaAspValAsp	2344
QY	899	AGCAGCTTCGCGGATTCCTGCTGCTGCTCCGAG	931
Db	235	SerThrPheThrGluYhrPheLeuLeuYhrHisAsp	245
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AC	PI4282;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	01-NOV-1995 (Rel. 32, Last annotation update)		
DE	Collagen alpha 1(VIII) chain precursor (Endothelial collagen).		
GN	COL8A1.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=89380199; PubMed=2476437;		
RA	Yamaquuchi N., Benya P.D., van der Rest M., Nimniya Y.;		
RT	"The cloning and sequencing of alpha 1(VIII) collagen cDNAs		
RT	demonstrate that type VIII collagen is a short chain collagen and		
RT	contains triple-helical and carboxyl-terminal non-triple-helical		
RT	domains similar to those of type X collagen."		
RL	J. Biol. Chem. 264:16022-16029(1989).		

CC -1 FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC
CC -1 SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC
CC -1 PWM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC
CC -1 MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
CC AT THE C-TERMINUS OF THE TRIPE-HELICAL REGION. THESE MAY PROVIDE
CC HIGH THERMAL STABILITY OF THIS REGION OF THIS REGION.
CC
CC -1 SIMILARITY: STRONG. TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC
CC -1 SIMILARITY: CONTAINS 1 C10 DOMAIN.
CC
CC -----
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CC or send an email to license@isb-sib.ch).

DR	EMBL: J05042; AAA31204.1; -. .	
DR	PIR: A34246; A34246.	
DR	InterPro: IPR001073; C1q.	
DR	InterPro: IPR000087; Collagen.	
DR	Pfam: PF00386; C1q; 1.	
DR	Pfam: PF01391; Collagen; 8.	
DR	PRINTS: PRO0007; COMPLEMNC1Q.	
DR	SMART: SMO0110; C1Q; 1.	
DR	PROSITE: PS01113; C1Q; 1.	
KW	Extracellular matrix; Connective tissue; Repeat; Hydroxylation;	
KW	Glycoprotein; Cell adhesion; Collagen; Signal..	
FT	SIGNAL	1 20
FT	CHAIN	21 744
FT	DOMAIN	29 117
FT	DOMAIN	118 571
FT	DOMAIN	572 744
FT	DOMAIN	609 744
FO	SEQUENCE	744 AA; 73358 MW; 288CEP1EF8274E99 CRC64; C1Q.

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Mismatches:	130
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US-09-944-944-41 (1-1377) x CA18_RABIT (1-744)

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82 GCGGC-----TGGCCGGGGAGAAAGCGCGGGGGCTGGAGACCA 120

Db 369 G1yAlaIaLeuGlyProArgGlyGluLysGlyProValGlyAlaProGlyMetCylGlyPro 388

QY 121 CCA-----ACTTGAGGGTCCGAGTAGCGAGC-----GCCCGAAGAGGCCATCGGG 168
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Db 389 ProGlyGluProGlyLeuProGlyTleProGlyPrometGlyProProGlyAlaIleGly 408

169 GAGCCGGGA-----GGGGGACTGCAGAGGACCCGGCGTCCGGGCTCCGG 216

db 409 PheProGlyProLysGlyGlyGlyLeuVal---GlyProGlnGlyProProGlyPro 427

217 TGCAGCGCTGAGGCGACTCTCTGCTCTGCTCTCTGAGGCGCTGAGGCGCGGCGCTGCCC 276

Db 428 LysGlyGluProGlyLeuGlnGlyPheProGlyLysProGlyPheLeuGlyGluValGly 447

277 CCCACTGGACGACACAGATCCCCAGCT----- 306

Db 448 ProProGlyIleargGlyLeuProGlyProIleGlyProGlyGlyGlnaGlyHisLys 467

QY 307 -----CTGCGGCGGCGAGCCGCGGCGCTTCCAGGCGAGCGCGGCGGCGAGCGAGCGCTT 363
 DB 468 G1YLeuProG1YLeu -ProG1YAla1ProG1YLeuG1YProG1YAla1ProG1YAla1 487
 QY 364 GCGGCGGCGGCGAGCGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423
 DB 487 eProG1YAla1ProG1YLeuG1YProG1YAla1ProG1YLeuG1YProG1YAla1ProG1Y 507
 QY 424 CGAGGCGGCGGCGAGCGGCGGCGAGCGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
 DB 507 YProG1YLeuG1YProG1YLeuG1YProG1YLeuG1YProG1YLeuG1YProG1YLeuG1Y 527
 QY 466 ----- 466
 DB 527 oG1YrheProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1Y 547
 QY 467 -----GCGGCGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 507
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 DB 567 oProG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1Y 587
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 DB 587 pMeG1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1Y 607
 QY 562 GAGCGG 576
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 QY 577 GCGGCGTTCAGCGG 636
 DB 627 oProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1Y 647
 QY 637 CCGCGG 696
 DB 647 nProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1YProG1YAla1YLeuG1Y 667
 QY 697 CAGCGG 754
 DB 667 lH1ScYsYsG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1Y 687
 QY 755 -TCCTTCCTTCAGCTTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
 DB 687 rThrTYrAspG1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1Y 705
 QY 814 GCGGAGCGG 873
 DB 705 lLeuLeuLeuAlaYProG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1Y 725
 QY 874 CATCTATGCGG 925
 DB 725 YLeuTYrAlaG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1YAla1YLeuG1Y 742

RC TISSUE-Adipose tissue;
 RX MEDLINE-96224171; PubMed-8619847;
 RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,
 RA Matsubara K.;
 RT "cDNA cloning and expression of a novel adipose specific collagen-like
 factor, apM1 (Adipose Most abundant Gene transcript 1).";
 RL Biochem. Biophys. Res. Commun. 221:286-289(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99196984; PubMed-10095105;
 RA Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,
 RA Nakano Y., Shimizu N., Tomita M.;
 RT "Organization of the gene for gelatin-binding protein (GBP28).";
 RL Gene 229:67-73(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99333693; PubMed-10403784;
 RA Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,
 RA Fuerst A., Scholmerich J., Schmitz G.;
 RT "The human apM-1, an adipocyte-specific gene linked to the family of
 TNF's and to genes expressed in activated T cells, is mapped to
 RT chromosome 1q21.3-q23, a susceptibility locus identified for familial
 RT combined hyperlipidemia (FCH).";
 RL Biochem. Biophys. Res. Commun. 260:416-425(1999).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE-20417747; PubMed-10961870;
 RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,
 RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,
 RA Matsuzawa Y.;
 RT "Adiponectin, a new member of the family of soluble defense collagens,
 RT negatively regulates the growth of myelomonocytic progenitors and the
 RT functions of macrophages.";
 RL Blood 96:1723-1732(2000).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE-20440368; PubMed-10982546;
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,
 RA Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y.,
 RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Adiponectin, an adipocyte-derived plasma protein, inhibits
 RT endothelial NF-kappaB signaling through a C1q-dependent pathway.";
 RL Circulation 102:1296-1301(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-21372498; PubMed-11479627;
 RA Yamauchi T., Kamon J., Maki H., Teranishi Y., Kubota N., Hara K.,
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
 RA Akanuma Y., Gavrilova O., Vinson C., Reisman M.L., Kagechika H.,
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
 RA Froguel P., Kadowaki T.;
 RT "The fat-derived hormone adiponectin reverses insulin resistance
 RT associated with both lipodystrophy and obesity.";
 RL Nat. Med. 7:941-946(2001).
 RN [7]
 RP VARIANT ADIPONECTIN DEFICIENCY CYS-112.
 RX MEDLINE-20378830; PubMed-10918532;
 RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.,
 RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,
 RA Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Genomic structure and mutations in adipose-specific gene,
 RT adiponectin.";
 RL Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).
 RN [8]
 RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.
 RX MEDLINE-21671103; PubMed-11812756;
 RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,
 RA Otake S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y.,
 RA Yazaki S., Nagai R., Tanigawa M., Matsubara K., Yoda M., Nakano Y.,
 RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;
 RT "Genetic variation in the gene encoding adiponectin is associated with
 RT an increased risk of type 2 diabetes in the Japanese population.";
 RL Diabetes 51:536-540(2002).

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 21, 2003, 15:31:46 ; Search time 92.5 Seconds
(without alignments) 6134.635 Million.cell updates/sec

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Perfect score: 2540
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 20604715 residues
Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=SPTRMBL_21 -OPMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09944944_QCN_1.1.79 -runat_13062003_145846_22773 -NCPU=6 -ICPU=3
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-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: SPTRMBL_21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhce.*
9: sp_organelle.*
10: sp_phage.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*
16: sp_bacteriopl.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	457	18.0	675	6	09N178	09n178 sus scrofa
3	429	16.9	295	11	09Z1K4	09z1k4 rattus norv
4	425.5	16.8	240	6	095M04	095m04 bos taurus
5	423	16.7	243	6	095UD7	095ud7 macaca mula
6	418	16.5	744	11	09D2V4	09d2v4 mus musculu
7	418	16.5	744	11	0921S8	0921s8 mus musculu
8	415.5	16.4	744	4	096D07	096d07 homo sapien
9	414	16.3	705	4	08REJ5	08rej5 homo sapien
10	398	15.7	294	11	09D8U4	09d8u4 mus musculu
11	373.5	14.7	194	6	095J95	095j95 canis famill
12	325	12.8	1458	13	0910B9	0910b9 oncorhynch
13	322	12.7	1461	4	076045	076045 homo sapien
14	321.5	12.7	1450	13	09YIB4	09yib4 cynops pyrr
15	320	12.6	1419	11	0631Z3	0631z3 rattus norv
16	319.5	12.6	1445	13	0932S1	0932s1 rana catesb
17	317	12.5	678	13	0934B6	0934b6 oncorhynch
18	314	12.4	245	11	09DCK6	09dck6 mus musculu
19	313.5	12.3	1442	11	0620J1	0620j1 mus musculu
20	313.5	12.3	1442	11	0620J3	0620j3 mus musculu
21	310.5	12.3	889	16	09F2N5	09f2n5 streptomyc
22	310.5	12.2	1459	11	0620J2	0620j2 mus musculu
23	308	12.1	902	5	016161	016161 mytilus edu
24	308	12.1	1418	6	028396	028396 equus cabal
25	308	12.1	1487	6	077753	077753 canis famill
26	307.5	12.1	1160	4	014046	014046 homo sapien
27	307.5	12.1	1487	4	014047	014047 homo sapien
28	307	12.1	1420	13	090W37	090w37 gallus gall
29	306.5	12.1	1447	13	091B81	091b81 xenopus lae
30	305	12.0	1453	11	063079	063079 rattus norv
31	300.5	11.8	1486	13	091717	091717 xenopus lae
32	299	11.8	1840	11	09J103	09j103 rattus norv
33	298.5	11.8	809	13	093485	093485 oncorhynch
34	298.5	11.8	888	13	090796	090796 gallus gall
35	298.5	11.8	1449	13	0910C0	0910c0 oncorhynch
36	298	11.7	1745	4	09WZQ6	09wzq6 homo sapien
37	297	11.7	1549	11	060444	060444 cricetus
38	296	11.7	684	5	P90679	P90679 arenicola m
39	295.5	11.6	589	11	099LJ6	099lj6 mus musculu
40	295.5	11.6	730	5	026052	026052 paracentrot
41	295.5	11.6	922	5	044367	044367 mytilus edu
42	295	11.6	2944	11	063870	063870 mus musculu
43	294	11.6	1352	13	090YJ0	090yj0 brachydanio
44	294	11.6	1840	11	060467	060467 cricetus
45	293	11.5	1418	13	09W7R9	09w7r9 cynops pyrr

ALIGNMENTS

RESULT 1
08R002 PRELIMINARY; PRT: 243 AA.

AC 08R002, 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC023068; AAH23068.1; -
DR EMBL; BC025174; AAH25174.1; -
KW Hypothetical protein.
SQ SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;


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Db 455 eglYpProglYleProglYpHeProglYseYsGLyAspProglYAsnProglYpr 475
OY 449 -----GGACCTCGAGGGGA 462
Db 475 oProglYpRoAlaGlYleAlaThrLYsGLYLeuAsnGLYProThrGLYleYpProglYpr 495
OY 463 CCGCGGGCCGCGAGAGAGCGG-----GGACCCCGGGGGCCCGACCG 504
Db 495 oProglYpRoLYsGLYhSLaGLYGLuProglYLeuProglYpRoProglYpRoProgl 515
OY 505 GCGTCGCGGGAGAGTCGTCGTCGCG-----CGATCCGC 540
Db 515 yProProglYGLn---AlaValProProglYGLYpHeValLYsGLYGLnArgAlaPh 534
OY 541 CTTGAGCGCCAAAGCGCTCCGAGACCGGGTCCCT----- 574
Db 534 eValSerAlaAsnGLYnGLYValThrGLYMeProValSerAlaPheThrValILeLeuSe 554
OY 575 -----CGCCCGTCTGACGACACCTTCGCTCCGACCGCGTGTGTGAACGACA 624
Db 554 rLYsAlaThrProAlaILeGLYAlaProILeProPheAspLYsILeULeYrAsnGLYGL 574
OY 625 GGAACATTACGACCGCGCTACCGGCAAGTTGACCTGCCAGTGGCTGGGTCTACTACT 684
Db 574 nGLhISlyrAspProLYsThrGLYILePheThrCysArgILeProGLYILeYrYrPh 594
OY 685 CGCCGTCACATCCACCGCTCTACCGGCGACGCTGACGTTGATCTGGTGAAGAATGGCGA 744
Db 594 eSerYrThrILeSLeValLYsGLYThrILeSLaITrValILeULeYrLYsAsnGLYTh 614
OY 745 ATTCATTGCC---TCCTTCCTCAGTTTTCGGGGGGGCGCCAAAGCCAGCTCGCTCTC 801
Db 614 rProValMeYrThrYrAspGLYrValLYsGLYrLeuAspGLnAla-----Se 632
OY 802 GGGGGGGGCGCATGTGAGCGCTGAGACCTGAGACCAAGTGTGGTGCAGTGGGTGGG 861
Db 632 rGLYSerAlaILeLeuAspLeuThrAspAsnAspGLnValTrpLeuGLnLeuProAsnAl 652
OY 862 TGACTACTTGGCANTCTATGCGAGCANTCAAGACAGACACGACCTTCGCGATTCCTGT 921
Db 652 aGLYSerAsnGLYLeuYrSerSerGLYrValILeHisSerPheSerGLYpHeLeuVa 672
OY 922 G 922
Db 672 1 672

```

RESULT 3

0921K4 PRELIMINARY: PRT: 295 AA.

AC 0921K4: STRAIN-SPRAGUE-DAMLEY;

DT 01-MAY-1999 (Tremblrel. 10. Created)

DT 01-MAY-1999 (Tremblrel. 10. Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21. Last annotation update)

DE COLLAGEN alpha 1 type X (Fragment).

GN COL10A1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAMLEY;

RX MEDLINE-20310874; PubMed-10853827;

RA Marks S.A., Lundmark C., Christensen C., Wurtz T., Odgren P.R.,

RA Seifert M.F., Mackay C.A., Mason-Savas A., Popoff S.E.;

RT "Endochondral bone formation in toothless (osteopetrotic) rats:

RT failures of chondrocyte patterning and type x collagen expression.";

RL Int. J. Dev. Biol. 44:309-316(2000).

DR EMBL; AJ131848; CAA10518.1;

DR InterPro; IPR001073; Clg.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; Clg; 1.

```

DR Pfam; PF01391; Collagen. 3.
DR PRINTS; PRO0007; COMPLETEC10.
DR SMART; SM00110; Clg; 1.
DR PROSITE; PS01113; Clg; 1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 30012 MW; FFA3BI548028B13E CRC64;

Alignment Scores:
Pred. No.: 1,58e-18 Length: 295
Score: 429.00 Matches: 110
Percent Similarity: 46.93% Conservative: 35
Best Local Similarity: 35.60% Mismatches: 91
Query Match: 16.89% Indels: 73
DB: 11 Gaps: 11

US-09-944-944-41 (1-1377) x 0921K4 (1-295)
OY 166 GGGGAGCCGGAGGGGGAGCTGCGAGAGACCCCGG---CGTCCGGCTCCCGGTGCCAG 222
Db 1 GLYrYrProGLYAspProGLYLeuAsnGLYProLYsGLYAsnProGLY----- 16
OY 223 CGCTATGAGGCCACTCTCTGCTCT-----GCTGCTCTGGGCT 261
Db 17 -----LeuProGLYpRoLYsGLYAspProGLYValGLYGLYAlaPProGLYLeu 32
OY 262 GGGCGCGGCTCGCCCGCCAGTGGAGACACAGATCCAGCGCTCTGCGGGGCGAC-- 319
Db 33 ArgGLYLeuValGLYrProThrGLY-----ProLYsGLYVal-ProGLYhSLAs 48
OY 320 -----CGCGGCTTCACAGCACCGCCGCGCCACCATGCGAG 354
Db 48 nGLYGLnAlaGLYProArgGLYGLuProGLYILeProGLYhSLaArgGLYProILeGLYr 68
OY 355 CGAGGCTTCCCGCGCGCGCGATGCGCGAGCGCCGCGACGGCGCGCGGCTCCGGG 414
Db 68 oProGLYILeProGLYpHeProGLYSerLYsGLYAspProGLYLYsProGLYAlaProGL 88
OY 415 AGAG-----AAGGCGAGGGCGGAGGCGGGGACTGCGCGG 450
Db 88 yProAlaGLYILeValILeThrLYsGLYLeuAsnGLYProAlaGLYpRoProGLYArgProGL 108
OY 451 ACCTCGA-----GGGACCCCGGGCGCGAGAGAGCGGAGCCCGCGGGCGCCAC 501
Db 108 yProArgGLYhSLThrGLYGLuProGLYLeuProGLYpRoProGLYpRoProGLYProPr 128
OY 502 CGGGCTCTCCGGGAGTCTCGGTCCCT----- 529
Db 128 oGLYpRoProSerGLnAlaValILeProAspGLYpHeThrLYsSerGLYGLnArgProAr 148
OY 530 -----CCGCGATCCGC 540
Db 148 GLeULSerGLYMeTrProLeuValSerAlaAsnGLnGLYValILeThrGLYMeTrProValSerAl 168
OY 541 CTTGAGCGCCAAAGCGCTCCGAGAGCGGGTCTCCGCGCTGACGACCGCTTGGCTT 600
Db 168 aPheThrValILeLeuSerLYsAlaTYr-----ProAlaValGLYAlaPProILeProPh 186
OY 601 CGAGCGCTGCTGTGAACAGACAGGACATTTAGACGCGCTCACCGGCAAGTTACACT 660
Db 186 eAspGLYILeULeULeULeULeULeULeULeULeULeULeULeULeULeULeULeULeULe 206
OY 661 CCAGGCTCTGGGCTCTACTCTCTGCGCTCCAGTCCAGCGCACGCTTCACGCGGCGCGCA 720
Db 206 sLYsILeProGLYILeYrYrYrPheSerTYrILeSLaValLYsGLYhSLaValTYr 226
OY 721 GTTTCATCTGTGAAGAATGCG---GAATCATTCGCTCTTCTTCAGATTTTTCGGGGG 777
Db 226 pValGLYLeuYrLYsAsnGLYhSLThrProThMeTYrThLYrAspGLYrYrSerLYsGL 246
OY 778 GTGCGCCAAAGCCACCTCGCTCTGCGGGGGGCGATGCTGAGCTGAGCCTGAGACCA 837
Db 246 yTYrLeuAspGLnAla-----SerGLYSerAlaILeMeTGLuULeULeULeULeULeULeULeULe 264

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Oy	888	AGTGGGATGCAGGGGTGGTGCTACCATTCATTCGCAATCGCCAGCATTCAAGACAGA	897
		::: :::	::: ::
Dd	264	nvalrrpleuglnhleuprhnalaglucubersnnglyleutyserSerglutyralhl	284
Oy	898	CAGCACCTTCTCCGGATTTCGTGTG	922
		:	
Dd	284	sSerSerPheSerGlyPheLeuVal	292
 RESULT 4 ID O95MQ4 PRELIMINARY; PRT; 240 AA. O95MQ4			
AC	O95MQ4:		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)		
DE	Adipose tissue-specific protein adipo Q.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCB1_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21369933; PubMed=11382781;		
RA	Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K. ;		
RT	"Identification and Adipocyte Differentiation-dependent Expression of		
RT	the Unique Distal Acid Residue in an Adipose Tissue-specific		
RT	Glycoprotein, Adipo Q."		
RL	J. Biol. Chem. 276:28849-28856(2001).		
DR	EMBL; AF269230; AAK58902.1; -		
DR	InterPro; IPR001073; Clq.		
DR	InterPro; IPR000087; Collagen.		
DR	Pfam; PF00386; Clq; 1.		
DR	Pfam; PF01391; Collagen; 1.		
DR	ProDom; PD000007; Collagen; 1.		
DR	PROSITE; PS01113; Clq; UNKNOWN_1.		
QO	SEQUENCE 240 AA: 26091 MW; G6Z53BA803B9A668 CRC64;		

[illegible]

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Db      117  ArgValIthValPro--AsnValProIleAhrPhrThIlystIlePherYAsnGInGln 135
QY      626  GGACATTCAGACGCGCGTCACGCGGACAAATTACCTGACCGAGTGGCTGGGCTACTACTC 685
Db      136  AsnHsIstYAspGlySerThrcIglysPherYtCYsAsnIleProDilyLeuYtYrPhe 155
QY      686  GCGGCGATCCAGCCGCTACGCGGCGCCACGCGACGTTGATGGTGAAGATGGCGAA 745
Db      156  SerYtHsIstIleThrValIlytMetYlsAspValYlsValSerIleuPhelysAspYls 175
QY      746  TCCATTCGCGCTTTCTCTCCAGATTTTTCGGGGGGTGCGCCAAAGCCACCTCGCTCGGG 805
Db      176  AlaValIleuPherThrYtYrAspGlnYtYrGInGln--LysAsnValAspGlnIleAsp 194
QY      806  GGGGCGCATGCTAGGCTGGAGCGCTGAGAGCAAGTGGTGGGTGCAGGTGGGTGGTGCAC 865
Db      195  SerValIleuHsIstIleValGlyAspGlnValYtYrPheuIlnValYtGInGlyGln 214
QY      866  --TACATTCGCGCTATTCGCCAGCATCAAGACAGACAGACACTTCGCGATTTTCGGTG 922
Db      215  AsnHsAsnGlnYValYtYrAlaAspAsnValAsnAspSerThrPherThrcIglyPheLeu 234
QY      923  TAC 925
Db      235  Tyr 235

RESULT 5
Q95JD7 PRELIMINARY; PRT; 243 AA.
ID 095JD7
OS 095JD7;
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DF Adiponectin.
GN APM1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RX MEDLINE-21232234; PubMed-11334417;
RA Hotta K., Funahashi T., Bodkin N.L., Ortmeyer H.K., Arita Y.,
RA Hansen B.C., Matsuzawa Y.;
RT "Circulating concentrations of the adipocyte protein adiponectin are
RT decreased in parallel with reduced insulin sensitivity during the
RT progression to type 2 diabetes in rhesus monkeys.";
RL Diabetes 50:1126-1133(2001).
DR EMBL, AF404407; AAK92202.1; -.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF001391; Collagen; 1.
DR ProDom: PD000007; Collagen; 1.
DR PROSITE, PS01113; C10; UNKNOWN.1.
SQ SEQUENCE 243 AA; 26264 MW; 49A45DAF24613FD CRC64;

Alignment Scores:
Pred. No.: 3,65e-18 Length: 243
Score: 423.00 Matches: 104
Percent Similarity: 52.33% Conservative: 31
Best Local Similarity: 40.31% Mismatches: 79
Query Match: 16.65% Indels: 44
DB: 6 Gaps: 10

US-09-944-944-41 (1-1377) x Q95JD7 (1-243)
QY 191 GAGAGACCCCGGCGGCTCCCGGCTCCCGGCTATGAGGCGCACTCCTGTCGTCG 250
DB 17 GlnAspIrrThrThrGlnGlnYrPro-----Val 26

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ID	095JUD7	PRELIMINARY;	PRT;	243 AA.
AC	095JUD7;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Adiponectin.			
GN	APXL.			
OS	Macca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=ADIPOSE TISSUE;			
RA	MEDLINE=21232234; PubMed=11334417;			
RA	Hotta K., Funahashi T., Bodkin N.L., Ortmeier H.K., Arlt Y.,			
RA	Hansen B.C., Matsuzawa Y.;			
RT	"Circulating concentrations of the adipocyte protein adiponectin are			
RT	decreased in parallel with reduced insulin sensitivity during the			
RT	progression to type 2 diabetes in rhesus monkeys.";			
RL	Diabetes 50:1126-1133(2001).			
DR	EMBL: AF404407; AAK92202.1; "			
DR	InterPro: IPR001073; Clq.			
DR	InterPro: IPR000087; Collagen.			
DR	Pfam: PF00386; Clq; 1.			
DR	Pfam: PF01391; Collagen; 1.			
DR	ProDom: PD000007; Collagen; 1.			
DR	PROSITE: PS01113; Clq; UNKNOWN_1.			
SO	SEQUENCE 243 AA; 26264 MW; 49A45DAF2B4613FD CRC64;			

Alignment Scores:			
Pred. No.:	3.65e-18	Length:	243
Score:	423.00	Matches:	104
Percent Similarity:	52.33%	Conservative:	31
Best Local Similarity:	40.31%	Mismatches:	79
Query Match:	16.65%	Indels:	44
DB:	6	Gaps:	10

US-944-944-41 (1-1377) x 095JUD7 (1-243)			
07	191	GAGAGCCCCGGCGTCGGCGTCGCCAGCGCATGAGGCGCACTCCTGTCGTCGCG	250
DB	17	Ginsprhrtrhrthnglnclyprrdy-----Val 26	

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QY 251 CTCTGGGCGTGGCGGGCTCGGCCCTGACGACGACACAGATCCCGAGCTCTGC 310
    ||||| ||| |||||
Db 27 LeuLeuProLeuProLySGlyAla-----Cys 35
QY 311 CCGGGGCAACCCCGGCTTCACGACGCGCGGCCACATGGCAGCCAGGCGTCCGGGC 370
    ||| ||| ||||| |||||
Db 36 ThrGly-----TrpMetAlaGlyLeuProGlyHisProGlyHisAlaGlyValProGly 53
QY 371 CGCGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
    ||||| ||||| ||||| |||||
Db 54 ArgAspGlyArgAsp-----GlyThrProGlyLeuLysGlyLys 67
QY 431 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
    ||| ||||| ||||| |||||
Db 68 GlyAspProGlyLeuLeuIleGlyProLySGlyAspThrGlyLysThrGlyValThrGlyAla 87
QY 464 CCGCGGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 523
    ||||| ||||| ||||| |||||
Db 88 GluGlyProArgGlyPheProGlyIleGlnGlyArgGlyGluProGlyGluGlyAla 107
QY 524 GTGCTCCGCGCATCCGCTTCAGCGCCAGCGCTCCGAGCGCGCGCGCGCGCGCTCT 583
    ||||| ||||| ||||| |||||
Db 108 TyrValTyrArgSerAlaPheSerVal---GlyLeuGluThrTyrValThrValPro--- 125
QY 584 GACGACCGCTGCGCTTCGACCGCGCTGCGTGAACAGAGACGACGACATTCAGCGCG 643
    ||||| ||||| ||||| |||||
Db 126 AsnMetProIleArgPheThrIlePheThrArgGlnGlnGlnHisThrAspLys 145
QY 644 ACCGCGAAGTTCACCTCGCAGGTGCGTGGGTCTACTACTCTCGCGCGCGCGCGCTC 703
    ||||| ||||| ||||| |||||
Db 146 ThrGlyLysPheHisCysAsnIleProGlyLeuTyrTyrPheAlaTyrHisIleThrVal 165
QY 704 TACCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
    ||||| ||||| ||||| |||||
Db 166 TyrMetLysAspValLysValSerLeuPheLysAspLysAlaMetLeuPheThrTyr 185
QY 761 TTCGATTTTTCGCGGGGTGGGCCCAAGCGCGCTCTCGCGGGGGCGCGCTGAGG 820
    ||||| ||||| ||||| |||||
Db 186 AspGlnTyrGlnGlnAsnAsnValAspGlnAla-----SerGlySerValLeuLeuHis 203
QY 821 CTGACGCTGAGAGACCAAGTGTGGTGCAGGTG---GGTGGCGTGCCTACTTGGCATC 877
    ||||| ||||| ||||| |||||
Db 204 LeuGluValGlyAspGlnValThrLeuGlnValTyrGlyGluGlyLysGlyLysGly 223
QY 878 TATGCGACGATCAGACAGACGACGCTTCCTCCGATTTCTGCTACTCCGAC 931
    ||||| ||||| ||||| |||||
Db 224 TyrAlaAspAsnAspAsnAspSerThrPheThrGlyPheLeuLeuTyrHisAsp 241

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RESULT 6

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Q9D2V4 PRELIMINARY: PRT: 744 AA.
ID 09D2V4.
AC 09D2V4.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shintawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Koehliwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Mikalido I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.O., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Rung B., Schoenbach M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK018742; BAB31383.1; -.
DR MGD: MGI:88463; Col8a1.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Alignment Scores:
Pred. No.: 7,566-18 Length: 744
Score: 418.00 Matches: 124
Percent Similarity: 41.31% Conservative: 40
Best Local Similarity: 31.23% Mismatches: 134
Query Match: 16,46% Indels: 99
DB: 11 Gaps: 12

US-09-944-944-41 (1-1377) x Q9D2V4 (1-744)
QY 22 GGAGGAGGAAGCGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGG 81
    ||| ||||| ||||| |||||
Db 350 GlyValGlyLysProGlyPheProGlyProLysGlyAspArgGlyIleGlyValPro 369
QY 82 GCGCGCG-----TGGCGGGGAGAGAGCGCGGGGCGTGGACACCA 120
    ||| ||||| ||||| |||||
Db 370 GlyValLeuGlyProArgGlyGlyLysGlyProIleGlyAlaProGlyMetGlyLys 389
QY 121 CCA-----ACTGAGGCTCGCGAGTACGAGAC-----GCCCGAGAGGCGCATCGG 168
    ||||| ||||| ||||| |||||
Db 390 ProGlyLysProGlyLeuProGlyLysProGlyLysProGlyLysProGlyLys 409
QY 169 GAGCGCGGA-----GGGCGACTGCGGAGAGACCGCGCGCGCGCGCGCGCGG 216
    ||||| ||||| ||||| |||||
Db 410 PheProGlyProLysGlyLysGlyValVal-----GlyProGlnGlyProProGlyPro 428
QY 217 TGGCAGCGCGTATGAGCGCACCTCGCTGCTGCTGCTGCTGCGCGCGCGCGCGCG 276
    ||||| ||||| ||||| |||||
Db 429 LysGlyLysProGlyLeuGlnGlnGlyPheProGlyLysProGlyPheLeuGlyValGly 448
QY 277 CCCACTGGACGACACAGATCCCGACCT----- 306
    ||||| ||||| ||||| |||||
Db 449 ProProGlyMetArgGlyLeuProGlyProIleGlyProLysGlyLysGlyLys 468
QY 307 ---CTGCCCGGGGCGACCCCGGCTTCAGAGACGCGCGCGCGCGCACCATGGCAGCGCT 363
    ||||| ||||| ||||| |||||
Db 469 GlyLeuProGlyLeu---ProGlyValProGlyLeuLeuLysProLysGlyLysProGlyI 488
QY 364 GCGCGCGCGCGATGGCGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGGAGGAAG 423
    ||||| ||||| ||||| |||||
Db 488 eProLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 508
QY 424 CGAGGCGGAGCGCGGAGCTGCGGAGCTCGAGGAGCGCGCGCGCGCGCGCGCGCGCG 466
    ||||| ||||| ||||| |||||
Db 508 yProIleGlyProProGlyLysProGlyProLysGlyLysGlyLysGlyLysProPro 528
QY 466 ----- 466
Db 528 -oGlyPheProGlyValGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLysPr 548

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QY 467 -----GGGCGGAGAGAGAGCGGAGCCCGGAGCCCGGAGCCCGGAGGGA 516
DB 548 ogyAlaLeuGlyProGlnGlyInProGlyLeuProGlyProProGlyProProGlyPr 568
QY 517 GTGCTCGTGCT----- 529
DB 568 oProGlyProProAlaValMetProThrProSerProGlnGlyLutryLeuProAspMe 588
QY 530 -----CGCGATCCGCTTCAGCGCCCAAGCGC----- 556
DB 588 tGlyLeuGlyLLeaSpelYVallysProProHnSalatYAlaGlyLysGlySh 608
QY 557 -----TCCGAGAGCGCGTGCT---CCGCC 579
DB 608 sGlyGlyProAlaLyrGluMetProAlaPheThAlaGluLeuThyValProPheProPr 628
QY 580 GTCTGAGCAGCCCTTGCCCTTCAGCCGCTGCTGTAAGAGAGGACATTACAGCGC 639
DB 628 oValGlyAlaProValLysPheAspLysLeuLeuTyAsnGlyYarGlnAsnTyAsnPr 648
QY 640 CGTCACCGGAGAGTTCACCTGCGAGTGGCGGCTGCTACTGCGCCGCTGCGCAC 699
DB 648 oGlnThGlyLLeaPheThrcysGlyValProGlyValTyTyTyGlnHisValH 668
QY 700 CGTCTACCGGAGCCAGCTGCACTGCTGTAAGAAATGCGAATCCATTGCGC---TC 756
DB 668 sCysLysGlyGlyAsnValTrpValAlaLeuPheLysAsnAsnGluProMetMetYrth 688
QY 757 TTTCTCCAGCTTTTTCGGGGGGTGGCCCAAGCCCTGCTGCGGGGGGCGCANGT 816
DB 688 rTyAspGlnTyTyLysLysGlyPheLeuAspGlnAla---SerGlySerAlaValle 706
QY 817 GAGGCTGAGACCTGAGCAAGTGGGTGCGAGTGGGTGCTGCTGCTGCTGCTGCTGCT 876
DB 706 uLeuLeuArgProLysAspGlnValPheLeuGlnMetProSerGlnGlnAlaGlyLe 726
QY 877 CTATGCGAGATCAAGACAGACAGACCTTCTCCGATTTCTGCTGCTAC 925
DB 726 uTyAlaGlyGlnTyTyValHisSerSerPheSerGlyTyLeuLeuTy 742

```

RESULT 7

```

QY 0921S8 PRELIMINARY; PRT; 744 AA.
AC 0921S8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011061; AHH1061.1;
DR MGD: MGI:88463; Col8a1.
DR InterPro: IPR001073; Clq.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 7.
DR PROSITE, PS01113; Clq; UNKNOWN_1.
KW Collagen.
SQ SEQUENCE 744 AA; 73621 MW; BF7A7FD79D8463AA CRC64;

```

Alignment Scores:

```

Pred. No.: 7, 56e-18 Length: 744
Score: 418.00 Matches: 124
Percent Similarity: 41.318 Conservative: 40
Best Local Similarity: 31.238 Mismatches: 134

```

```

Query Match: 16.46% Indels: 99
DB: 11 Gaps: 12
US-09-944-944-41 (1-1377) x 0921S8 (1-744)
QY 22 GAGAGGAGAAAGCGAGCCGCGAGAGCCAGCAAGCATGCGGTGACGAGGCGAGG 81
DB 350 GValAlaLysProGlyPheProGlyProLysGlyAspArgGlyGlyGlyValPro 369
QY 82 GGGCGC-----TGGCGGAGAGAGCGGCGGCGGCGGAGGAGGAGGAGGAGGAG 120
DB 370 GValLeuGlyProAlaGlyGlyGlyGlyGlyGlyProLLeValaProLLeValaPro 389
QY 121 CCA-----ACTGAGAGGTCGAGTACGAGCAGC-----GCCCGAAGAGGCGCATGGG 168
DB 390 ProGlyLysProGlyLeuProGlyLLeProGlyProMetGlyProProGlyAlaLeGly 409
QY 169 GAGCGGAGG-----GGGAGACTTCGAGAGAGACCCGCGGCGTCCGGGCTCCCGG 216
DB 410 PheProGlyProLysGlyGlyGlyGlyGlyValaVal---GlyProGlnGlyProProGlyPro 428
QY 217 TGGCAGGCGTATGAGGCGACCTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276
DB 429 LysGlyLysProGlyLeuGlnGlyPheProGlyLysProGlyPheLeuGlyGlyValGly 448
QY 277 CCCACTGAGAGCAACAAGATCCCGACCT----- 306
DB 449 ProProGlyMetArgGlyLeuProGlyProLLeGlyProLysGlyGlyGlyHisLys 468
QY 307 ---CTGCGCGGAGCAGCCCGGCTTCAGAGCAGCGCGGCGCCATGAGCAGCAGGCTT 363
DB 469 GValProGlyLeu---ProGlyValProGlyLeuGlyGlyProLysGlyGlyProGlyL 488
QY 364 GCGGCGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGG 423
DB 488 eProGlyAspGlnGlyLeuGlnGlyProProGlyLLeProGlyLLeValGlyProSerG 508
QY 424 CAGAGCGGAGAGGAGCGGAGCTGCGGAGCTCGAGGAGGAGCC----- 466
DB 508 YProLLeGlyProProGlyLLeProGlyProLysGlyGlyProGlyLeuProGlyProPr 528
QY 466 ----- 466
DB 528 oGlyPheProGlyValGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLysPr 548
QY 467 -----GGGCGGAGAGAGAGCGGAGCCCGGAGCCCGGAGGCGGCGGCGGAGGGA 516
DB 548 ogyAlaLeuGlyProGlnGlyInProGlyLeuProGlyProProGlyProProGlyPr 568
QY 517 GTGCTCGTGCT----- 529
DB 568 oProGlyProProAlaValMetProThrProSerProGlnGlyLutryLeuProAspMe 588
QY 530 -----CGCGATCCGCTTCAGCGCCCAAGCGC----- 556
DB 588 tGlyLeuGlyLLeaSpelYVallysProProHnSalatYAlaGlyLysGlySh 608
QY 557 -----TCCGAGAGCGCGTGCT---CCGCC 579
DB 608 sGlyGlyProAlaLyrGluMetProAlaPheThAlaGluLeuThyValProPheProPr 628
QY 580 GTCTGAGCAGCCCTTGCCCTTCAGCCGCTGCTGTAAGAGAGGACATTACAGCGC 639
DB 628 oValGlyAlaProValLysPheAspLysLeuLeuTyAsnGlyYarGlnAsnTyAsnPr 648
QY 640 CGTCACCGGAGAGTTCACCTGCGAGTGGGTGCGGCTGCTACTGCGCCGCTGATGCGCAC 699
DB 648 oGlnThGlyLLeaPheThrcysGlyValProGlyValTyTyTyGlnHisValH 668
QY 700 CGTCTACCGGAGCCAGCTGCACTGCTGTAAGAAATGCGAATCCATTGCGC---TC 756
DB 668 sCysLysGlyGlyAsnValTrpValAlaLeuPheLysAsnAsnGluProMetMetYrth 688

```

QY 757 TTTTCCAGTTTTCGGGGGTCGCCAGCCAGCCTTCGCTCTCGGGGGGCGCATGTGT 816
 Db 688 RTTASpSLuTyrLysGlyPheLeuAspGlnAla-----SerGlySerAlaValle 706
 QY 817 GAGCTGAGCCCTGAGACCAAGTGTGGTGCAGGTGGTGTGGTGCATCATTTGGCAT 876
 Db 706 uLeuLeuArpProGlyAspGlnValPheLeuGlnMetProSerGlnGlnAlaAlaGlyLe 726
 QY 877 CTATGCCAGCATCAAGACAGACAGCAGCCTTCCTCCGATTTCTGGGTAC 925
 Db 726 uTyrAlaGlyGlnTyrValHisSerSerPheSerGlyTyrLeuLeuTyr 742

RESULT 8

096D07 PRELIMINARY: PRT: 744 AA.

AC 096D07:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 73.4 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013581; AAH13581.1; -
 DR InterPro; IPR001073; C1q
 DR InterPro; IPR000087; Collagen.
 DR Pfam; PF00386; C1q; 1.
 DR ProDom; PD000007; Collagen; 7.
 DR ProSite; PS01113; C1Q; UNKNOWM_1.
 KW Collagen, Hypothetical protein.
 SQ SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;

Alignment Scores:

Score: 1.07e-17 Length: 744
 Percent Similarity: 41.50 Matches: 128
 Best Local Similarity: 41.46% Conservative: 37
 Query Match: 16.36% Mismatches: 133
 DB: 4 Indels: 100
 Gaps: 13

US-09-944-944-41 (1-1377) x 096D07 (1-744)

QY 22 GGAGGAGGAAAGCGGAGCGGAGCGAGCAACGACGTGGGTGACGGCAGGCG 81
 Db 349 GlyIleGlyLysProGlyPheProGlyProLysGlyAspArgGlyMetGlyGlyValPro 368
 QY 82 GCGCGC-----TGCGCGGGGAGCAAGCGCGGGGGGTGAGCACCA 120
 Db 369 GlyAlaLeuGlyProArgGlyGlyLysGlyProIleGlyAlaProGlyIleGlyGlyPro 388
 QY 121 CCA-----ACTGGAGGTCCGGAGTACGAGC-----GCCCGCAAGAGGCCCATCGGG 168
 Db 389 ProGlyLysProGlyLysProGlyLysProGlyLysProGlyLysProGlyLysProGlyLys 408
 QY 169 GAGCGGGA-----GGGCGACATCGAGAGGAGCCCGCGGTCCGGCGCGG 216
 Db 409 PheProGlyProLysGlyGlyGlyLeuVal-----GlyProGlnGlyProProGlyPro 427
 QY 217 TGCAGCGCTATGAGCGCATCTCTGCTCTGCTCTGCTCTGCGGCGCGGCGCTCGCC 276
 Db 428 LysGlyGlyProGlyLysGlyGlyGlyPheProGlyLysProGlyPheLeuGlyGlyValGly 447
 QY 277 CCCACTGAGCAGACCAAGATCCCGACCT----- 306
 Db 448 ProProGlyMetArgGlyLysProGlyProIleGlyProLysGlyGlyLysGlyLys 467

QY 307 -----CTGCCGGGGGACCCCGGCTT-----CCAGGCAC 336
 Db 468 GlyValProGlyLysProGlyVal-ProGlyLeuGlyProLysGlyGlyProGlyLys 487
 QY 337 GCCGGGCAACCATGCGACCGAG-----GGCTTGGCGGGCGCGATGCCGCGAGCG 387
 Db 487 eProLysAspGlnGlyLeuGlnGlyProProGlyLysProGlyLysGlyProSerGly 507
 QY 388 CCGCAGCGCGCGCGCGCGCGCGAGAGAAAGCGAGGCGGGGAGCGCGGACTGCC 447
 Db 507 yProIleGlyProProGlyLysProGlyProLysGlyGlyLysProGlyLysPro 527
 QY 448 G----- 448
 Db 527 oGlyPheProGlyLysGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLysPr 547
 QY 449 -----GGACCTGAGGGGAGCCCGCGCGGAGAGAGCGCGGAGCCCGCGGGCC 498
 Db 547 oGlyAlaLeuGlyProGlnGlyGlnProGlyLeuProGlyProProGlyProGlyPr 567
 QY 499 CACCGGGGCT----- 508
 Db 567 oProGlyProProAlaValMetProProThProProProGlnGlyGlyTyrLeuProAs 587
 QY 509 -----GCCGGGAGTGCCTCGCTCCCGCATCCGCTTCAGCGCCAGCGCTCGCA 561
 Db 587 pMetGlyLeuGlyLysAspGlyValLysProProHisAlaTyrGlyAlaLysGlyGly 607
 QY 562 GAGCGGGTGCT-----CC 576
 Db 607 sAsnGlyGlyProAlaTyrGlyLysMetProAlaPheThrAlaGlyLeuThrAlaProPhePr 627
 QY 577 GCCGTGACGACGACCTTCGCTTCGACCGCGGTGCTGTGAGAACGACGAGCATATGCA 636
 Db 627 oProValGlyAlaProValLysPheAsnLysLeuLeuTyrAsnGlyArgLysAsnTyrAs 647
 QY 637 CGCCGTACAGGCAAGTTCACCTGCAGGAGGCGGTGCTACTTCTGCGCGTCCATGC 696
 Db 647 nProGlnThrGlyIlePheThrCysGlyValProGlyAlaTyrTyrPheAlaTyrHisVa 667
 QY 697 CACCGTACCGGGGACCGCTGCAGTTGATCTGTGAAGAATGCGCAATCCATTGCC-- 754
 Db 667 HisCysLysGlyGlyAsnValTyrValAlaLeuPheLysAsnGlnProValMetTy 687
 QY 755 -TCTTCTTCCAGTTTTCGGGGGCGCGCCAGCGACCGCTGCTCGGGGGGCGCAT 813
 Db 687 ThrTyrAspGlyTyrLysGlyPheLeuAspGlnAla-----SerGlySerAlaVal 705
 QY 814 GGTGAGGCTGAGCCTGAGAGCAAGTGTGGTGCAGGTGGTGTGGTGCATCATTTGG 873
 Db 705 lLeuLeuLeuArpProGlyAspArgValPheLeuGlnMetProSerGlnGlnAlaAlaGly 725
 QY 874 CATCTATGCCAGCATCAAGACAGACAGCAGCCTTCCTCCGATTTCTGGGTAC 925
 Db 725 yLeuTyrAlaGlyGlnTyrValHisSerSerPheSerGlyTyrLeuLeuTyr 742

RESULT 9

08TEJ5 PRELIMINARY: PRT: 705 AA.

AC 08TEJ5:
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE FLJ00201 protein (Fragment).
 GN FLJ00201.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 12:24:30 ; Search time 2191 Seconds
(without alignments)
10178.542 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1 gactagctctcttgagctc.....aaaaaaaaaaaaaaaaaa 1377

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estfun:*
17: gb_gss:*
18: em_gss_hum:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	667	48.4	1093	BM924569
2	647	47.0	1154	BM547549
3	631	45.8	1623	BM926477
4	596	43.3	596	BM893587
5	584	42.4	724	BM171879
6	578	42.0	578	BM893691

7	570	41.4	574	13	BM021127	BM021127	1e76e01.x
8	560	40.7	596	13	BM544255	AGENCOCURT	BM544255
9	551	40.0	801	13	BM190880	BM190880	BM190880
10	549	38.9	553	12	BF882978	IL3-ET011	BF882978
11	532	38.6	521	14	BF724241	bx02e11.y	BF724241
12	521	37.8	521	14	BM966810	BM966810	BM966810
13	517	37.5	517	14	BM966954	BM966954	BM966954
14	508	36.9	630	12	BM706609	BM706609	BM706609
15	481	34.9	567	13	BM021381	BM021381	BM021381
16	480	34.9	846	13	BM458455	BM458455	BM458455
17	476	34.6	792	13	BM170921	BM170921	BM170921
18	446	32.4	454	9	AI805087	AI805087	AI805087
19	435	31.6	879	13	BM20945	BM20945	BM20945
20	392	28.5	392	10	BE138819	BE138819	BE138819
21	367	26.7	869	13	BM763193	BM763193	BM763193
22	361	26.2	887	13	BM190062	BM190062	BM190062
23	359	26.1	410	14	BM707291	BM707291	BM707291
24	359	26.1	413	9	AI083823	AI083823	AI083823
25	356	25.9	408	9	AI085548	AI085548	AI085548
26	353	25.6	405	9	AI083824	AI083824	AI083824
27	352	25.6	442	14	BM693336	BM693336	BM693336
28	345	25.1	1045	14	BM920874	BM920874	BM920874
29	343	24.9	445	14	BM673416	BM673416	BM673416
30	339	24.6	462	10	AM070344	AM070344	AM070344
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35	308	22.4	449	13	BM668611	BM668611	BM668611
36	302	21.9	361	10	AM172659	AM172659	AM172659
37	301	21.9	315	14	F33371	F33371	F33371
38	294	21.4	702	12	BF055285	BF055285	BF055285
39	285	20.7	317	10	AM137263	AM137263	AM137263
40	277	20.1	277	9	AI564511	AI564511	AI564511
41	269	19.5	370	9	AA775561	AA775561	AA775561
42	266	19.3	439	13	BM913487	BM913487	BM913487
43	263	18.4	253	9	AI924106	AI924106	AI924106
44	248	18.0	316	14	M91217	M91217	M91217
45	247	17.9	536	9	AI346326	AI346326	AI346326

ALIGNMENTS

RESULT 1	BM924569	1093 bp	mRNA	linear	EST 12-MAR-2002	
LOCUS	AGENCOCURT_6767665	NIH_MGC_116	Homo sapiens	CDNA clone	IMAGE:5760942	
DEFINITION	5', mRNA sequence.					
ACCESSION	BM924569					
VERSION	BM924569.1	GI:19374948				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	NIH-MGC	http://mgc.ncl.nih.gov/				
AUTHORS	1 (bases 1 to 1093)					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					
	Email: cgaphs@mail.nih.gov					
	Tissue Procurement: Life Technologies, Inc.					
	CDNA Library Preparation: Life Technologies, Inc.					
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Agencourt Bioscience Corporation					
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:					
	http://image.llnl.gov					
	Plate: L1AM12808	row: m	column: 07			
	High quality sequence stop: 590.					
FEATURES	Location/Qualifiers					
SOURCE	1..1093					

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5760942"
/clone_1lb="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."

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BASE COUNT      197 a      339 c      356 g      198 t      3 others
ORIGIN

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Query Match      48.4%; Score 667; DB 14; Length 1093;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 331 AGGACGCCGGGCGCCAGCATGCGACAGGCGTTCGCGCGCATGCGCGCGGACGCGCG 390
DB 1 AGGACGCCGGGCGCCAGCATGCGACAGGCGTTCGCGCGCATGCGCGCGGACGCGCG 60
QY 391 CGAGCGCGCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
DB 61 CGAGCGCGCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 451 ACCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
DB 121 ACCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 511 CGGGAAGTGCCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 570
DB 181 CGGGAAGTGCCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 240
QY 571 GCGTCCGCGCGTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 630
DB 241 GCGTCCGCGCGTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
QY 631 TTAGAGAGCGGTGACCGGCAAGTTCACCTGCGAGTGCCTGCGGTCTACTACTGCGCGT 690
DB 301 TTAGAGAGCGGTGACCGGCAAGTTCACCTGCGAGTGCCTGCGGTCTACTACTGCGCGT 360
QY 691 CCATGCCACGCTACCGGCGCAGCTGACAGTTGATGTGTAAGATGGCGAATCCAT 750
DB 361 CCATGCCACGCTACCGGCGCAGCTGACAGTTGATGTGTAAGATGGCGAATCCAT 420
QY 751 TGCCCTTTTCCAGTTTTCGCGGGGTGGCCCAAGCCAGCCTGCTCGGGGGGGGCG 810
DB 421 TGCCCTTTTCCAGTTTTCGCGGGGTGGCCCAAGCCAGCCTGCTCGGGGGGGGCG 480
QY 811 CATGCTAGAGCTGAGAGCTGAGAGCAAGTGTGGGTGAGGTGTGGTGTGACTCAT 870
DB 481 CATGCTAGAGCTGAGAGCTGAGAGCAAGTGTGGGTGAGGTGTGGTGTGACTCAT 540
QY 871 TGCGATATAGCGAGCATCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 930
DB 541 TGCGATATAGCGAGCATCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 600
QY 931 CTGGACAGCTCCCGAGCTTTTGTAGTGGCCCAAGTGAAGTGAAGTGAAGTGAAGT 990
DB 601 CTGGACAGCTCCCGAGCTTTTGTAGTGGCCCAAGTGAAGTGAAGTGAAGTGAAGT 660
QY 991 CCTAGAA 997
DB 661 CCTAGAA 667

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RESULT 2

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BM547549      1154 bp      mRNA      linear      EST 20-FEB-2002
LOCUS      AGENCOURT 6507694 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724522
DEFINITION      5', mRNA sequence.
ACCESSION      BM547549
VERSION      BM547549.1 GI:18781410
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1154)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgepds-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL12713. Row: O column: 19
High quality sequence stop: 591.
Location/Qualifiers
1. 1154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5724522"
/clone_1lb="NIH_MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

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BASE COUNT      178 a      382 c      401 g      193 t
ORIGIN

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Query Match      47.0%; Score 647; DB 13; Length 1154;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGGACGAGAGAGCGAAGCAAGAGTGGGTGACGCGCAGGCGAGGGGCGCTGGCGGGAGA 60
QY 100 AGCGCGGGGGGTGGAGACACCAAGTGAAGAGGTCGCGAGTAGAGAGAGAGAGAGAG 159
DB 61 AGCGCGGGGGGTGGAGACACCAAGTGAAGAGGTCGCGAGTAGAGAGAGAGAGAGAG 120
QY 160 GCCATCGGGGAGCGCGGAGAGGGGAGCTGCGAGAGAGACCCGCGCTCCGGGTGCG 219
DB 121 GCCATCGGGGAGCGCGGAGAGGGGAGCTGCGAGAGAGACCCGCGCTCCGGGTGCG 180
QY 220 CAGCGCTATAGAGGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 279
DB 181 CAGCGCTATAGAGGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 280 ACGGAGAGACAAGATGCCCAAGCTCTGCGCGCGGCGGCGGCGGCGGCTTCAAGCAGAG 339
DB 241 ACTGAGAGACAAGATGCCCAAGCTCTGCGCGGCGGCGGCGGCGGCTTCAAGCAGAG 300
QY 340 GGGCAGCAGTGGAGCGGAGGCTGCGGGGCGGAGTGGCGAGCGAGCGGCGAGCGGCG 399
DB 301 GGGCAGCAGTGGAGCGGAGGCTGCGGGGCGGAGTGGCGAGCGGCGAGCGGCGGCGG 360

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QY 400 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGCCGGGACTGCCGGGACCTCGAGG 459
 Db 361 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGCCGGGACTGCCGGGACCTCGAGG 420
 QY 460 GGACCCCGGGCGCGAGGAGAGGGCGGACCCCGGGGGCCACCGGGCTGCCGGGAGTG 519
 Db 421 GGACCCCGGGCGCGAGGAGAGGGCGGACCCCGGGGGCCACCGGGCTGCCGGGAGTG 480
 QY 520 CTCGGTGCCTCCGGGAGATCCGGCTTCAGAGCCGACCGCTCCGAGACCGGGGTGCTCCGCC 579
 Db 481 CTCGGTGCCTCCGGGAGATCCGGCTTCAGAGCCGACCGCTCCGAGACCGGGGTGCTCCGCC 540
 QY 580 GTCTGAGCAGCACCCTTGCCTTCGACCGCGCTGCTGGTGAAGCAGAGGAGACATTACGAGC 639
 Db 541 GTCTGAGCAGCACCCTTGCCTTCGACCGCGCTGCTGGTGAAGCAGAGGAGACATTACGAGC 600
 QY 640 CGTCACCGGCAAGTTACCTGCCAGAGTGCCTGGGGGTCTACTACTTCG 686
 Db 601 CGTCACCGGCAAGTTACCTGCCAGAGTGCCTGGGGGTCTACTACTTCG 647

RESULT 3
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 LOCUS AGENCOURT_6644538 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5766864
 DEFINITION 5', mRNA sequence.
 ACCESSION BM926477
 VERSION BM926477.1 GI:19376856
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS 1 (bases 1 to 1623)
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strussberg, Ph.D.
 Email: cgaapb-rt@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.lnl.gov

Plate: LLM12824 row: d column: 01
 High quality sequence stop: 558.

FEATURES

Location/Qualifiers

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 /note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."
 BASE COUNT 263 a 505 c 550 g 299 t 6 others
 ORIGIN

Query Match 45.8%; Score 631; DB 14; Length 1623;
 Best Local Similarity 100.0%; Pred. No. 5.6e-143;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 71 GCAGGGCAGGGGGCGCTGGCGGGGAGAGAGCGGGGGCTGAGCACCACCAACTGAG 130

Db 1 GCAGGGCAGGGGGCGCTGGCGGGGAGAGAGCGGGGGCTGAGCACCACCAACTGAG 60
 QY 131 GGTCCGAGATGACGAGCGCCCGGAAAGAGCCATTCGGGAGCCGGAGGGGAGACTGCGA 190
 Db 61 GGTCCGAGATGACGAGCGCCCGGAAAGAGCCATTCGGGAGCCGGAGGGGAGACTGCGA 120
 QY 191 GAGGACCCCGGGGCTCCGGGGCTCCGGGTTCAGAGCCGCTATGAGGCCATCTCTGCTGCTG 250
 Db 121 GAGGACCCCGGGGCTCCGGGGCTCCGGGTTCAGAGCCGCTATGAGGCCATCTCTGCTGCTG 180
 QY 251 CTCCTGGGCTTGGGGCGCGGCTCGCCCTCAGTGCAGCAGCAAGATCCCAAGCTCTGCG 310
 Db 181 CTCCTGGGCTTGGGGCGCGGCTCGCCCTCAGTGCAGCAGCAAGATCCCAAGCTCTGCG 240
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 Db 241 CGGGGGCACCCTGGCTTCCAGGACGCGCGGACACATGAGCAGGAGCTTGGCGGGC 300
 QY 371 CGCGATGGCGCGAGCGCGCGGAGAGCGCGCGCGGCTCGGGGAGAGAAAGCGAGGAGC 430
 Db 301 CGCGATGGCGCGAGCGCGCGGAGAGCGCGCGCGGCTCGGGGAGAGAAAGCGAGGAGC 360
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 QY 491 GCGGGGCCACCGGGGCTCGCGGGAGAGTGTCTGCTCCGCCATCCGCTTCAGGCC 550
 Db 421 GCGGGGCCACCGGGGCTCGCGGGAGAGTGTCTGCTCCGCCATCCGCTTCAGGCC 480
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 Db 481 AAGCGCTCCGAGAGCGGGGCTCGCGGCTTCGAGCAGCACCCTTCGAGCGCGCTG 540
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RESULT 4

BM893587 596 bp mRNA linear EST 29-APR-2002
 LOCUS 1126910.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 DEFINITION cDNA clone IMAGE:6136122 3' similar to TR:Q9UFY4 Q9UFY4

HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.
 ACCESSION BM893587
 VERSION BM893587.1 GI:19349055
 KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 596)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blaisdell, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,
 Jackson, Y., and Bowers, Y.

AUTHORS

Endocrine Pancreas Consortium
 Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557

OY	940	CTCCCAAGTCCTTTCCTAGTGTCCCACTGCAGCAAGAGAGTCATATGGCTCCTACCTCTAAGAG	999
Db	242	CTCCCAAGTCCTTTCCTAGTGTCCCACTGCAGCAAGAGAGTCATATGGCTCCTACCTCTAAGAG	301
OY	1000	AGGCTGTAGAGCTACAAACAGATCATCCAGAGAGGGGTGGGCCCTTGGAATATTGTGAA	1059
Db	302	AGGCTGTAGAGCTACAAACAGATCATCCAGAGAGGGGTGGGCCCTTGGAATATTGTGAA	361
OY	1060	TGACTAAGGAGAGTGGGGTAGAGCACTCTCCGTCCTGTGCTGAGGCAAGGAATGGGAAACGT	1119
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OY	1120	GCGTGTCTGGCATAGCTGTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAG	1179
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OY	1180	AGGAGTGTGCGTGTCTGGCAAGTCATAGTATCCCAAGTTGCTCTGTGTCCAGGAGGCCAAGG	1239
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OY	1240	TGGAGTGTCTCTTCTGTGATCCTGTGATCTGTGATTCCTGATTCCTGCC	1283
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RESULT 6					
LOCUS	BM893691	578 bp	mRNA	linear	EST 29-APR-2002
DEFINITION	J128e08.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens				
	cDNA IMAGE:6136046 3' similar to TR-09UXA Q9UXX4				
HYPOTHETICAL	22.8 KD PROTEIN ; , mRNA sequence.				
Accession:					

ACCESSION	BM893691	GI:19349159
VERSION	BM893691.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	REFERENCE
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.	
1 (bases 1 to 578)	
Melton, D., Brown, J., Keny, G., Pernutt, A., Lee, C., Kaestner, K.,	

TITLE
JOURNAL
COMMENT

Liemiška, I., Scearcă, M., Brestelli, J., Grawohn, G., Clifton, S., Halliker, L., Marra, M., Pape, D., Wille, T., Martin, J., Bistahk, A., Schmitt, A., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsigarelakis, R., Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel.: 617-495-1812
Fax: 617-495-8557
Email: dmeltone@iobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for Information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Seq primer: -40UP from G1bco
High quality sequence stop: 408.

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FEATURES
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Location/Qualifiers
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/clone_image="6136046"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
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/notes="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using

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SuperScript plasmid library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 micrograms single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

Query Match	42.0%	Score 578;	DB 14;	Length 578;
Best Local Similarity	100.0%	Pred. No. 7.6e-130;		
Matches 578; Conservative	0;	Mismatches	0;	Gaps 0;

Q7 770 TTTCGGGGGGTGGCCCAAGCCAGCCTCGCCTCGGGGGGGGCGCATGGTGAAGGCTGAGACCT 829
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Db 578 TTTCGGGGGGTGGCCCAAGCCAGCCTCGCCTCGGGGGGGGCGCATGGTGAAGGCTGAGACCT 519
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Qy	830	GAGGACCAAGTGTGGGTGCAGGTGGGTGGGTGAC TM ACATTTGGCATCTATGCCAGATC	889
Db	518	GAGGACCAAGTGTGGGTGCAGGTGGGTGGGTGAC TM ACATTTGGCATCTATGCCAGATC	459

Qy 890 AAGACAGACACACTTCTCCGATTTCTGGTGACTCCGACTGGACAGCTCCCAgTC 949
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 Db 458 AAGACAGACACACTTCTCCGAGATTTCTGGTGACTCCGACTGGACAGCTCCCAgTC 399
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950 TTTTGCTTAGTGCACATGCAAAAGTAGCTCATGTCTCACTCTAGAGAGAGGCTTGAG 1009
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D6 GGATGGGAGACACTCTCCGTCCGCGTGCAGGGAATGGGAAACAGTCGCTGTCTGC 215

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Db 158 TGTCTCGGCAAGTAAAGTCCCCAGTTGGCTGTGTCCAGAGACCCACGGTGGGGTGTCT 99

Qy 1250 TCTTCTTGCTCCCTGTGCTCTCTGGATCTTCCACCCCTCCTTGCTCTGGGGCCGACC 1309

Db 98 TCTTCCGAGTCCCTGTGCTTCCTGAGATCTCCCAACCCCTCCGCTGCTGAGGCGCGGCG 39

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Db 38 CTTTCTCAGATCACTCATATAAAGCTAAGAACCTTC 1

LOCUS	574 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	BM021127	ie16e01.x1	Melton Normalised Human Islet 4 N4-HIS 1 Homo sapiens	

ACCESSION
VERSION
CDNA CLONE IMAGE:3072903 3
SIMILAR TO IR:Q90U44 Q90FA4
HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.
BM021127
BM021127.1 GI:16535483

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 574)
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarsdale,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blalstein,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCarroll,R., Cole,R., Tsagarisvill,I., Williams,T., Jackson,Y. and Bowers,Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohpc.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov
 High quality sequence stop: 413.

FEATURES
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 /note="Organ: Pancreas; Vector: pSPORT1; Site:1: Not 1; Site:2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806: 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 128 a 175 c 162 g 109 t
 ORIGIN

Query Match 41.4%; Score 570; DB 13; Length 574;
 Best Local Similarity 100.0%; Pred. No. 6.3e-128;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 779 TGGCCCAAGCCAGCTCTGCTGGGGGGGGCCATGTGAGCTGACCTGAGACCAA 838
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 DB 574 TGGCCCAAGCCAGCTCTGCTGGGGGGGGCCATGTGAGCTGAGACCAA 515
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 QY 839 GTGTGGGTGAGGTGGGTGGGTGACTACATTCATTCGACAGCATCAAGACAGAC 898
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 DB 514 GTGTGGGTGAGGTGGGTGGGTGACTACATTCATTCGACAGCATCAAGACAGAC 455
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 QY 899 AGCAGCTTCTCCGATTTCTGCTACTCCGAGTGGACAGCTCCCGAGCTTTGGCTTA 958
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 DB 454 AGCAGCTTCTCCGATTTCTGCTACTCCGAGTGGACAGCTCCCGAGCTTTGGCTTA 395
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 QY 959 TGGCCACATGCAAGTGAAGTCACTGCTCTACTCTTGAAGAGAGGGGTGAGCTGACAC 1018
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 DB 394 TGGCCACATGCAAGTGAAGTCACTGCTCTACTCTTGAAGAGAGGGGTGAGCTGACAC 335
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 QY 1019 CAGGTATTCAGAGAGGGGTGGGGCCCTGGAATATATGTGAATACAGAGAGGTGGGGTA 1078
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 DB 334 CAGGTATTCAGAGAGGGGTGGGGCCCTGGAATATATGTGAATACAGAGAGGTGGGGTA 275
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QY 1079 GAGCAGCTCTCCGCTCTGCTGCTGCGCAAGATGGAGAACAGTGTCTGCGATCAGGTC 1138
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 DB 274 GAGCAGCTCTCCGCTCTGCTGCTGCGCAAGATGGAGAACAGTGTCTGCGATCAGGTC 215
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 QY 1139 TGGCAGCATGGGGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198
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 DB 214 TGGCAGCATGGGGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 155
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 QY 1199 AAGGTAAAGTCCCGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1258
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 DB 154 AAGGTAAAGTCCCGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 95
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 QY 1259 TCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1318
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 DB 94 TCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 35
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 QY 1319 GAGATCAGCTCAATTAACCTTAAGAACCTCA 1348
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 DB 34 GAGATCAGCTCAATTAACCTTAAGAACCTCA 5
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RESULT 8
 BM544255
 LOCUS 596 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6490655 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587759
 5', mRNA sequence.
 ACCESSION BM544255
 VERSION BM544255.1 GI:18775356
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 596)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@nsi-femail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 Plate: LHM12357 row: m column: 08
 High quality sequence stop: 595.

FEATURES
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 1..596
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5587759"
 /clone_lib="NIH_MGC_125"
 /lab_host="DH10B"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site:1: EcoRV (destroyed); Site:2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

BASE COUNT 138 a 158 c 172 g 127 t 1 others
 ORIGIN

Query Match 40.7%; Score 560; DB 13; Length 596;
 Best Local Similarity 100.0%; Pred. No. 1.5e-125;
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CAGCTCTGCTCTCGGGGGGGGGCCATGAGTGAAGCTGAGGCTGAGGACCAAGTGTGGTGC 848
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Db	1	CAGCCTGCCTCGGGGGGGGGCCATGTTGAGGCTGGAGCCTAGAGACCACAACTGTGGTGC	60
OY	849	AGGTGGGTGTGGGTGACTACTATTGGCATCTATTGCCAGCATATGACAGACAGACACTTCT	908
Db	61	AGGTGGGTGTGGGTGACTACTATTGGCATCTATTGCCAGCATATGACAGACAGACACTTCT	120
OY	909	CCGATTTTCTGGTGTACTCCGACTGGGACACCTCCCGTCTTTTGCTTAGTGGCCACTGC	968
Db	121	CCGATTTTCTGGTGTACTCCGACTGGGACACCTCCCGTCTTTTGCTTAGTGGCCACTGC	180
OY	969	AAATGTAGCTCATCTCTCACTCTAGAGAGAGGGGTGTGAGCTGTACAAACCAAGTCAATCC	1028
Db	181	AAATGTAGCTCATCTCTCACTCTAGAGAGAGGGGTGTGAGCTGTACAAACCAAGTCAATCC	240
OY	1029	AGGAGGGGTGGCCCCCTTGGAAATTTTGAAATGACTTAGGAGAGTGGGTATAGCACTCTC	1088
Db	241	AGGAGGGGTGGCCCCCTTGGAAATTTTGAAATGACTTAGGAGAGTGGGTATAGCACTCTC	300
OY	1089	CGTCCCTGCTGTGGCAAGGAATGGGAACAGTGGGTGTCTGCGATCAGTCTGGCAGCATG	1148
Db	301	CGTCCCTGCTGTGGCAAGGAATGGGAACAGTGGGTGTCTGCGATCAGTCTGGCAGCATG	360
OY	1149	GGGCAAGTGTGATTTCTGCTCCCAAGACAGAGATGTGCTGTGCTGGCAAGTGTAAAT	1208
Db	361	GGGCAAGTGTGATTTCTGCTCCCAAGACAGAGATGTGCTGTGCTGGCAAGTGTAAAT	420
OY	1209	CCCCCAGTGTCTGTGAGTCCAGAGAGCCAGGTGGGGTCTCTCTCCGTGGTCTGTGCT	1268
Db	421	CCCCCAGTGTCTGTGAGTCCAGAGAGCCAGGTGGGGTCTCTCTCCGTGGTCTGTGCT	480
OY	1269	CTGTGATCTCTCCCAACCCTCTCTGTCTGTGGGGCGGCCCTTTTCTCAGAGATCACTC	1328
Db	481	CTGTGATCTCTCCCAACCCTCTCTGTCTGTGGGGCGGCCCTTTTCTCAGAGATCACTC	540
OY	1329	AATAACCTAGAACCTCTCA 1348	
Db	541	AATAACCTAGAACCTCTCA 560	
RESULT 9			
BI490880/c			
LOCUS	603033867T1	NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172880 3',	
DEFINITION		mRNA sequence.	
ACCESSION	BI490880		
KEYWORDS	BI490880.1	GI:15330108	
SOURCE		EST.	
ORGANISM		human.	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL		1 (bases 1 to 801)	
COMMENT		NIH-MGC http://mgc.nci.nih.gov/ .	
		National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgabbs-remail.nih.gov	
		Tissue Procurement: Life Technologies, Inc.	
		cDNA Library Preparation: Life Technologies, Inc.	
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
		DNA sequencing by: Incyte Genomics, Inc.	
		Clone distribution: MGC clone distribution information can be	
		found through the I.M.A.G.E. Consortium/LLNL at:	
		http://image.llnl.gov	
		Plate: L14M1430 Row: f Column: 17	
		High quality sequence start: 8	
		High quality sequence stop: 738.	
		Location/Qualifiers	
		1. 801	
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		/db_xref="taxon:9606"	
		/clone="IMAGE:5172880"	

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730	GGTGAAGAAATGGCGAATCCATTGCTGCTTTTCCAGTTTTCGGGGGGTGGCCCAAGCC	789		
580	GGTGAAGAAATGGCGAATCCATTGCTGCTTTTCCAGTTTTCGGGGGGTGGCCCAAGCC	521		
790	AGCCTCGCTCGGGGGGGGGCCATGGTGGAGGCTGGAGCCCTGAGACCAAGTGGGTGCA	849		
520	AGCCTCGCTCGGGGGGGGGCCATGGTGGAGGCTGGAGCCCTGAGACCAAGTGGGTGCA	461		
850	GGTGGGTTGGGTGACTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	909		
460	GGTGGGTTGGGTGACTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	401		
910	CGGATTTCTGTTGTTACTCCGACTGGACAGCTCCCAAGTCTTTGCTTATGATCCCAATGCA	969		
400	CGGATTTCTGTTGTTACTCCGACTGGACAGCTCCCAAGTCTTTGCTTATGATCCCAATGCA	341		
970	AAGTGAAGTCAATGCTCTCATCTCCATGAAGAGGGGTGAGAGGCTGACCAACCAAGTATGCA	10239		
340	AAGTGAAGTCAATGCTCTCATCTCCATGAAGAGGGGTGAGAGGCTGACCAACCAAGTATGCA	281		
1030	GGAGGGGCTGGCCCCCTTGGATATTGTGAATGATAGGAGGTTGGGGTGAAGACACTGTC	10898		
280	GGAGGGGCTGGCCCCCTTGGATATTGTGAATGATAGGAGGTTGGGGTGAAGACACTGTC	221		
1090	GTCTCTGCTGTGGCAAGGATGGGAACAGTGGTGTCTGCGATCAAGGCTTGGCAAGCATGG	11494		
220	GTCTCTGCTGTGGCAAGGATGGGAACAGTGGTGTCTGCGATCAAGGCTTGGCAAGCATGG	161		
1150	GGCAGTGGCTGGATTTTCGCCCAAGACCAAGAGAGGTGGTGGTGGTGGTGGTGGTGGTGGT	1209		
160	GGCAGTGGCTGGATTTTCGCCCAAGACCAAGAGAGGTGGTGGTGGTGGTGGTGGTGGTGGT	101		
1210	CCCCAGTTGCTGTGGTCCAGAGAGCCAGAGGAGGAGGTGCTCTCTCTCTCTCTCTCTCTCT	1265		
100	CCCCAGTTGCTGTGGTCCAGAGAGCCAGAGGAGGAGGTGCTCTCTCTCTCTCTCTCTCTCT	41		
1270	TCTGTGATCCTC 1280			
40	TCTGTGATCCTC 30			

RESULT 10

BF882978/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

553 bp mRNA linear EST 17-JAN-2001

BF882978

BF882978

BF882978.1 GI:12273104

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

/clone.lib="NIH_MGC_115"

/lab_host="DHI0B"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-Sp0R6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

180 a 251 c 237 g 133 t

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&tl2=IL3-ET0113-
061200-374-C10&tl3=2000-12-06&tl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 553.

FEATURES
source
1. 553
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ET0113"
/dev_stage="Adult"
/note="Organ: Lung; tumor: Vector: puc18; site: 1: Sma1;
site: 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT
ORIGIN
Query Match 39.9%; Score 549; DB 12; Length 553;
Best Local Similarity 100.0%; Pred. No. 7.1e-123;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

749 ATGGCCCTTCTTCCGATTTTGGGGGGGCCCAAGCAGCTCTGCTGGGGGG 808
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553 ATGGCCCTTCTTCCGATTTTGGGGGGGCCCAAGCAGCTCTGCTGGGGGG 494
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809 GCATGGTGGAGCGGAGCTGAGGACCAAGTGTGGTGGAGTGGTGGTGGTAC 868
|||||
493 GCATGGTGGAGCGGAGCTGAGGACCAAGTGTGGTGGAGTGGTGGTGGTAC 434
|||||
869 ATGGCATCTATGGCAGCATCAAGACAGACAGCCTTCCGATTTCTGTTACTCC 928
|||||
433 ATGGCATCTATGGCAGCATCAAGACAGACAGCCTTCCGATTTCTGTTACTCC 374
|||||
929 GACTGGACAGCTCCCGAGCTTCTTCTAGTCCCAAGTGCAGAGTGCATGCTCA 988
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373 GACTGGACAGCTCCCGAGCTTCTTCTAGTCCCAAGTGCAGAGTGCATGCTCA 314
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989 CTCTAGAGAGGAGTGGAGCTGACACAGAGTCAATCCAGAGAGGCTGGCCCCCTGG 1048
|||||
313 CTCTAGAGAGGAGTGGAGCTGACACAGAGTCAATCCAGAGAGGCTGGCCCCCTGG 254
|||||
1049 AATATTGTGATGACTAGAGAGTGGAGTGGAGACACTCTCCGTCTCTGTGCAAGA 1108
|||||
253 AATATTGTGATGACTAGAGAGTGGAGTGGAGACACTCTCCGTCTCTGTGCAAGA 194
|||||
1109 ATGGGAACAGTGGCTGTCTCGATCAGTCTGGCAGCAGTGGGAGTGGATTTCTG 1168
|||||
193 ATGGGAACAGTGGCTGTCTCGATCAGTCTGGCAGCAGTGGGAGTGGATTTCTG 134
|||||
1169 CCCAAGCCAGAGAGTGTCTGTCTGCGCAAGTGAAGTCCCGCAATTCTCTGTGCA 1228
|||||

Db 133 CCCAAGCCAGAGAGTGTCTGTCTGCGCAAGTGAAGTCCCGCAATTCTGTGCA 74
Oy 1229 GGAGCCACAGGTGGGGTGTCTCTCTGCGCCTCTGCTGTGATCCGCCACCC 1288
|||||
Db 73 GGAGCCACAGGTGGGGTGTCTCTCTGCGCCTCTGCTGTGATCCGCCACCC 14
Oy 1289 CTCTGCTC 1297
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Db 13 CTCTGCTC 5

RESULT 11
BF724241 532 bp mRNA linear EST 05-JAN-2001
LOCUS BF724241
DEFINITION bx02ell.y1 Human Iris cDNA (un-normalized, unamplified): BX Homo
sapiens cDNA clone bx02ell 5', mRNA sequence.
ACCESSION BF724241
VERSION BF724241.1 GI:12040150
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 532)
Wistow G.J., Bernstein S., Behal A. and Smith D.
NEIBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gdraemel@nei.nih.gov
Plate: 02 row: e column: 11
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1. 532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bx02ell"
/clone_id="Human Iris cDNA (un-normalized, unamplified):
BX"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMD10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem Iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the Superscript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-pGACTAGTCTAGATCGGAGCGGCCGCC(TT)15-3'
]. Not I blunt end inserts were cloned into the Not I/EcoR
V sites in the vector. EST analysis was performed on the
unamplified library at the NIH Intramural Sequencing
Center (NISC)."

BASE COUNT
ORIGIN
Query Match 38.6%; Score 532; DB 12; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.8e-119;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

39 CCGGCAAGGAGCAACAGAGTGGGTGACGCGAGGAGGGGGCCCTGGCGGGAG 98
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Db 1 CCGGCAAGGAGCAACAGAGTGGGTGACGCGAGGAGGGGGCCCTGGCGGGAG 60
Oy 99 AACGGGGGGGCTGAGACACCAACATGAGAGGTCCGAGTAGCAGAGGCCCGCAAGA 158
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[illegible]

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RESULT 12
LOCUS      BM966810
DEFINITION
            BM966810.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            cDNA clone IMAGE:6136122 5' similar to TR:090FX4 090FX4
            HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.
ACCESSION
            BM966810
VERSION
            EST.
KEYWORDS
            human.
SOURCE
            ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
            1 (bases 1 to 521)
AUTHORS
            Melton,D., Brown,J., Keny,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,W., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,D., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
            Jackson,Y. and Bowers,Y.
            Endocrine Pancreas Consortium
            Unpublished (2000)
            Other-ESTs: 1j26g10.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Douglas Melton DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Juliana Brown
            (brown@fas.harvard.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 447.
FEATURES
            Location/Qualifiers
                1..521
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            /db_xref="taxon:9606"

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			/dev_stage="Adult"	
			/lab_host="DH10B"	
			/note="Organ: Pancreas; Vector: pSPORN1; Site.1: Not 1; Site.2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life technologies). cDNA fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."	
BASE COUNT	95 a	140 c	167 g	119 t
ORIGIN				
Query Match	37.8%	Score 521;	DB 14;	Length 521;
Best Local Similarity	100.0%;	Pred. No.	3.9e-116;	
Matches 521;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
OY	657	CCTGCCAGGTCCTCGGGGTACTACATCTCCGCATCAAGCCACGCTACCGGGCACC	716	
Dd	1	CCCTGCCAGTGCTCTGGGGTCTACTACTTTCCGCTCATGCCCACGCTACCGGGCACC	60	
OY	717	TGCAGTTTGATCTGGTGAAGAATGGCGAATCATTTGCTCTTCCAGTTTTTCGGGG	776	
Dd	61	TGCAGTTTGATCTGGTGAAGAATGGCGAATCATTTGCTCTTCCAGTTTTTCGGGG	120	
OY	777	GGTGGCCCCAACCGACGCTCGCTCTCCGGGGGGGGCCATGCTGAGGCTGAGGCTGAGAC	836	
Dd	121	GGTGGCCCCAACCGACGCTCGCTCTCCGGGGGGGGCCATGCTGAGGCTGAGAC	180	
OY	837	AAGTGTGGGTCAGATGGGTGGTGGTGACTACATTGGGATCTATGCCAGATCAAGACAG	896	
Dd	181	AAGTGTGGGTCAGATGGGTGGTGGTGACTACATTGGGATCTATGCCAGATCAAGACAG	240	
OY	897	ACACAGACCTTCTCCGGATTCTTGGTGTACTCCGACTGGCAACAGCTCCCAATCTTGGTT	956	
Dd	241	ACACAGACCTTCTCCGGATTCTTGGTGTACTCCGACTGGCAACAGCTCCCAATCTTGGTT	300	
OY	957	AGTCCCACTCAAAAGTAGCTCANTGCTCTACATCTCTAGAAAGGAGGTGAGGCTGCACA	1018	
Dd	301	AGTCCCACTCAAAAGTAGCTCANTGCTCTACATCTCTAGAAAGGAGGTGAGGCTGCACA	360	
OY	1017	ACCAAGTTCATCCAGAGAGGCTGGCCCCCTCGAATATTGTGAATGACTAGGAGGTGGGG	1078	
Dd	361	ACCAAGTTCATCCAGAGAGGCTGGCCCCCTCGAATATTGTGAATGACTAGGAGGTGGGG	420	
OY	1077	TAGAGCACTCTCCGCTCGTGGTGGCAAGGAATGGGAACAGTGGCTTCGCGATACGG	1136	
Dd	421	TAGAGCACTCTCCGCTCGTGGTGGCAAGGAATGGGAACAGTGGCTTCGCGATACGG	480	
OY	1137	TCTTGAGCAGCATGGGCGAGTGGCTGGATTTCGCCCAAGACC	1177	
Dd	481	TCTTGAGCAGCATGGGCGAGTGGCTGGATTTCGCCCAAGACC	521	
RESULT 13				
BM966954				
LOCUS	517 bp	mRNA	linear	EST 29-Apr-2002
DEFINITION	cDNA clone IMAGE:6136046 5' similar to TR:Q9URX4 Q9URX4			
ACCESSION	BM966954 GI:19560490			
VERSION	BM966954.1			
KEYWORDS	EST.			

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Melton, D., Brown, J., Kenly, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bilstain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other_ESTS: 1j28e08.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@lhp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
(Brown@fas.harvard.edu)
Seq primer: -40bp from Glibco
High quality sequence stop: 456.
Location/Qualifiers
1. 517
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/dev_stage="Adult"
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/note="Organ: Pancreas; Vector: pSPORT1, site_1: Not 1; Site_2: Sal 1; Starting library constructed using Superscript Plasmid Library Kit (Life Technologies). cDNA made by oligo-dt priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 94 a 138 c 166 g 119 t
ORIGIN
Query Match 37.5%; Score 517; DB 14; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.6e-115;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 657 CCGTCCAGTGCCTGGGCTACTACTCCGCTCCATGCACGCTACGGGCGCC 716
Db 1 CCGGCCAGTGCCTGGGCTACTACTCCGCTCCATGCACGCTACGGGCGCC 60
QY 717 TCGAGTTGATCTGTGAAGATGGCAATGCATTCCTCTTCCAGTTTTCGGG 776
Db 61 TCGAGTTGATCTGTGAAGATGGCAATGCATTCCTCTTCCAGTTTTCGGG 120
QY 777 GGTGGCCCAAGCAGCTGCTCGGGGGGGGCCATGTGAGCTGAGACCTGAGACC 836
Db 121 GGTGGCCCAAGCAGCTGCTCGGGGGGGGCCATGTGAGCTGAGACCTGAGACC 180
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ACCESSION Bg706609
VERSION Bg706609.1 GI:13982121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: c9apbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshiyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
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DEFINITION
ACCESSION      AL110261
VERSION        AL110261.1 GI:5817222
KEYWORDS
SOURCE
ORGANISM       Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1068)
AUTHORS        Ottenwaelder, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and
                Wiemann, S.
TITLE           Direct Submission
JOURNAL         Submitted (15-AUG-1999) MIPS, Am Klopfersplitz 18a, D-82152
                Martinsried, GERMANY
COMMENT         Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
                sequenced by Medigenomix (Martinsried/Germany) within the cDNA
                sequencing consortium of the German Genome Project. This clone
                (DKF2p586B0621) is available at the RZPD in Berlin. Please contact
                the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                information about the clone and the sequencing project is available
                at http://www.mips.biochem.mpg.de/proj/cDNA/.

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sequences.
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VERSION AP003396.1 GI:20302607
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published only in Database (2002)
REFERENCE 2 (bases 1 to 191362)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@psc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
This work was done in collaboration with Aral, Y., Kubo, T. and
Ohki, M.
COMMENT National Cancer Center Research Institute
Cancer Genomic Division
5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN
zip: 104-0045
phone: 81-3-3542-2511 ex 4752, fax: 81-3-3542-0688 e-mail:
yara@ncc.go.jp.
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REFERENCE 1
AUTHORS    Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Homo sapiens 219,574 genomic DNA of 11q
JOURNAL    Published Only in Database (2002)
REFERENCE 2 (bases 1 to 219574)
AUTHORS    Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@isc.riken.go.jp, URL:http://hnp.igsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Overlapping Clones: pd71A4, PQ3868
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Contamination: none detected
non-AGCT bases: none
Additional author information
Arai,Y., Kubo,T., Ohki,M.
National Cancer Center Research Institute
Cancer Genomic Division
5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN
zip: 104-0045
phone: +81-3-3542-2511 ext4752, fax: +81-3-3542-0688 e-mail:
yara@ncic.go.jp.
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Db 208522 GGGCCCCCTGGAATATTTGTAATGACTAGGAGGTGGGTAGACACTCTCCCTCTCTCT 208463
QY 1098 GCTGGCAAGAAATGGGAACAGTGTCTGTCTGATGAGTGTGACAGATGGGAGTGGG 1157
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BASE COUNT 45724 a 42083 c 43875 g 48747 t 2000 others
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Best Local Similarity 99.6%; Pred. No. 5.8e-145;
Matches 909; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 858 TGGGTGACTACATTTGGCATCTATGCGCAGCATCAAGACAGACACCTTCTCCGATTTC 917
DB 108430 TGGGTGACTACATTTGGCATCTATGCGCAGCATCAAGACAGACACCTTCTCCGATTTC 108489
QY 918 TGGTGTACTCGACGTGGACAGCTCCCGACCTTGTCTAGTCCCACTGCAAGTGGC 977
DB 108490 TGGTGTACTCGACGTGGACAGCTCCCGACCTTGTCTAGTCCCACTGCAAGTGGC 108549
QY 978 TCATGCTCTCACTCTCTAGAGAGAGGTGTGAGGTGACACACAGTCTATCCAGAGGGCT 1037
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DB 108730 CTGATTTCTGCCCAAGACAGAGAGGTGTCTGCTGGCAAGTGAATGCCCACTT 108789
QY 1218 GCTGTGTGTCAGAGACCCAGAGGTGGGTGTCTCTCTGCTGCTCTCTCTCTCTGATC 1277
DB 108790 GCTGTGTGTCAGAGACCCAGAGGTGGGTGTCTCTCTGCTGCTCTCTCTCTCTGATC 108849
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DB 108850 CTCGCCACCCCTCTGCTCTGCTGGGCGGCGCCCTTTTCTGAGATCTCAATTAACCT 108909
QY 1338 AAGAACCTCATTA 1350
DB 108910 AAGAACCTCTCTA 108922

RESULT 9
AF469650
LOCUS
DEFINITION Mus musculus membrane-type frizzled-related protein (Mfrp) and complement-C1q tumor necrosis factor-related protein (Clqtnf5)
ACCESSION AF469650
VERSION AF469650.1 GI:22023766
KEYWORDS
SOURCE
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 4220)
Kameya,S., Hawes,N.L., Chang,B., Heckenlively,J.R., Nagert,J.K.
and Nishina,P.M.
Mfrp, a gene encoding a frizzled related protein, is mutated in the
mouse retinal degeneration 6
Hum. Mol. Genet. 11 (16), 1879-1886 (2002)
JOURNAL 12140190
PUBMED 2 (bases 1 to 4220)
Kameya,S., Nagert,J.K. and Nishina,P.M.
Direct Submission
Submitted (17-JAN-2002) The Jackson Laboratory, 600 Main Street,
Bar Harbor, ME 04609, USA
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Best Local Similarity	78.0%; Pred. No. 2.3e-110;	
Matches 921; Conservative 0; Mismatches 238; Indels 22; Gaps 6;		
QY	189	GAGAGGACCCGGGGTCCGGGGCTCCGGGTGCACGCGTATGAGGCCATCTCTGCTGCG 248
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QY	249	TGCTCTTGAGGCTTGAGGCGCGGCTCGCCCGACCTGAGACAAAGATCCCGACCTCT 308
DB	3119	TGCTTCTGAGGCTTGAGGCTCTCTCTCTGAGACAAAGATCCCGACCTCTG 3178
QY	309	GCCCGGGGACCCCGGCTTCAGGACACCGCGGCGCACCATGAGCGACGCGCTTGCGG 368
DB	3179	GTCCCGGACACCCCGGCTTCAGGACACCATGAGCGCACCATGAGCGCGCTTGCGG 3238
QY	369	GCCCGGATGAGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
DB	3239	GCCCTGACGCGCGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3298
QY	429	GCGGAGAGCGGAGCTGCGGAGCTCGAGGAGACCCCGGCGCGCGGAGAGGCGGAGC 488
DB	3239	GCGGAGACCGGAGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3358
QY	489	CCGCGGGGCGCACCGGGCTTGCAGGAGTGTCTGCTGCTCTCCGCGATTCGCTTCAGCG 548
DB	3359	CCATGGGGGCGTATGGGGCTGCGGGGGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTG 3418
QY	549	CCAAGCGCTCCGAGACCGGGTGCCTCGCGCTTGAACGACCTTGCGCTTGACCGCG 608
DB	3419	CCAAGCGCTCCGAGACCGGGTGCCTCGCGCTTGAACGACCTTGCGCTTGACCGCG 3478
QY	609	TGCTGGTGAACAGACAGGACATTAACAGACCGCGTCAACCGCAATTCACCTGCCAGGTGC 668
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 Best Local Similarity 98.8%; Pred. No. 4e-110;
 Matches 741; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

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QY 664 GGTGCGTGGGTCTACTACTTCCGCGCCATGCCACCGTGTACCGGGCCAGCTGCAGTT 723
DB 166817 GGTGCGTGGGTCTACTACTTCCGCGCCATGCCACCGTGTACCGGGCCAGCTGCAGTT 166876
QY 724 TGAATCTGTGAAGATGCGAATCCATTCCTCTTTTTC- GGGGGGGTGGC 782
DB 166877 TGAATCTGTGAAGATGCGAATCCATTCCTCTTTTTC- GGGGGGGTGGC 166936
QY 783 CCAAGCCAGCCTCGCTCTCGGGGGGGGCGCATGTGAGGCTGAGACCTGAGACCAACTGT 842
DB 166937 CCAAGCCAGCCTCGCTCTCGGGGGGGGCGCATGTGAGGCTGAGACCTGAGACCAACTGT 166996
QY 843 GGGTGAAGGTGGGTGGGTGACTACTTGGCATCTATGCGACGATTAAGACAGACAGCA 902
DB 166997 GGGTGAAGGTGGGTGGGTGACTACTTGGCATCTATGCGACGATTAAGACAGACAGCA 167056
QY 903 CTTTCCGGAATTTCTGTACTTCGACATGCGACAGCTCCCAAGTCTTTGCTTAGTGGC 962
DB 167057 CTTTCCGGAATTTCTGTACTTCGACATGCGACAGCTCCCAAGTCTTTGCTTAGTGGC 167116
QY 963 CACTGCAAGTGAAGTCACTCTCACTCTTAGAAGAGAGGTGTGAGGCTGACAAACAGG 1022
DB 167117 CACTGCAAGTGAAGTCACTCTCACTCTTAGAAGAGAGGTGTGAGGCTGACAAACAGG 167176
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DB 167177 TCATCCAGAGAGGCTGGCCCC- TGGAAATATTGATGATGACTAGGAGAGTGGGTAGA 167236
QY 1081 GCACTCCGCTCTGCTGCTGCGGAGAGAAATGGGAAACAGTGGCTGCGGATCAGGCTG 1140
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QY 1261 CTCGTCTTCTGTGATCTCCCAACCCCTCTGCTGCTGGGGCCGCTTTTTCAGCA 1320
DB 167417 CTCGTCTTCTGTGATCTCCCAACCCCTCTGCTGCTGGGGCCGCTTTTTCAGCA 167476
QY 1321 GATCAGTCATTAACCTAAGACCCCTGATA 1350
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RESULT 11
BC025174 1234 bp mRNA linear ROD 07-AUG-2002
LOCUS BC025174 Mus musculus, clone MGC:36714 IMAGE:3978387, mRNA, complete cds.
DEFINITION BC025174
ACCESSION BC025174
VERSION BC025174.1 GI:19263583
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1234)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-MGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: angbcm.tmc.edu
Gunnarone, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRK Plate: 61 Row: f Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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location/Qualifiers
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RASLPDLYKNGOSIASFPOYEGGMPKRSALSSGAMRLBEEEDQVWVGVGDYIGIT
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Best Local Similarity 77.9%; Pred. No. 7e-110;
Matches 919; Conservative 0; Mismatches 239; Indels 22; Gaps 6;
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Db 973 GGTCCACATGCTGGCAATGAATGAGACA--GGCTGTCTGAGGTCA---AGACAGCGTG 1026
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RESULT 12
BC023068
LOCUS
DEFINITION Mus musculus, Similar to Dkfpz586B0621 protein, clone MGC:38635
IMAGE:5355789, mRNA, complete cds.
ACCESSION BC023068
VERSION BC023068.1 GI:18605993
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1271)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Guanaraine, P.H., Garcia, A.M., Lu, X., HuYK, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNLI at: http://image.llnl.gov
Series: IRK Plate: 54 Row: b Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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CDS

are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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66905 73970 contig of 7066 bp in length
74071 81007 contig of 6937 bp in length
81108 87320 contig of 6213 bp in length
87421 93250 contig of 5830 bp in length
93351 97965 contig of 4615 bp in length
98066 102941 contig of 4876 bp in length
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109118 113391 contig of 4274 bp in length
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197808 198902 contig of 1095 bp in length

Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 191270 192527: contig of 1258 bp in length
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* 192628 194288: contig of 1661 bp in length
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FEATURES

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DEFINITION 72 unordered pieces.
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VERSION AC112557.2 GI:21735369
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
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REFERENCE 1 (bases 1 to 173657)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
        Alshrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T.,
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JOURNAL
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COMMENT

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Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
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Worley,K.C.
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173657)
Worley,K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
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On Jul 12, 2002 this sequence version replaced gi:18860143.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GKAB
Center clone name: CH230-904
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Assembly program: Phrap; version 0.990329
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Consensus quality: 111210 bases at least Q30
Consensus quality: 115587 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
8426.635 Million cell updates/sec

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Searched: 2185239 seqs, 112599159 residues

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Listing first 45 summaries

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8	1322.2	96.0	1347	20	AAK24684
9	1296.6	94.2	1338	22	AAK44970

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18	717	52.1	728	22	AAK44997	Human secreted pro
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22	692.8	50.3	1263	22	AAK49972	Murine TANGO 253 O
23	691.2	50.2	1263	22	AAK45006	Murine secreted pr
24	691.2	50.2	1263	22	AAK45007	Murine secreted pr
25	691.2	50.2	1263	22	AAK45008	Murine secreted pr
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34	564.2	41.0	729	22	AAK44973	Murine TANGO 253 c
35	562.6	40.9	729	22	AAK45038	Murine secreted pr
36	562.6	40.9	729	22	AAK45039	Murine secreted pr
37	562.6	40.9	729	22	AAK45040	Murine secreted pr
38	562.6	40.9	729	22	AAK45041	Murine secreted pr
39	504	36.6	729	20	AAK24685	Degenerate DNA enc
40	347	25.2	502	21	AAK98154	Human signal pepti
41	257.8	18.7	601	22	AAK44991	Rat TANGO 253 codi
42	247.4	18.0	536	23	AAK76910	DNA encoding novel
43	149.6	10.9	393	21	AAK61631	CDNA encoding rat
44	149.6	10.9	393	22	AAK99564	SKN cell CDNA, SE
45	149.6	10.9	393	24	ABL34716	Rat CDNA isolated

ALIGNMENTS

RESULT 1		AAK87258		standard; CDNA: 1377 BP.	
ID	AAK87258				
AC	AAK87258				
XX	27-SEP-1999	(first entry)			
XX	CDNA clone encoding human PRO344, amplified in tumour cells.				
XX	PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human; ss				
OS	Homo sapiens.				
XX					
PH	Key	Location/Qualifiers			
FT	CDS	227..958			
FT	sig_peptide	/*tag= a			
FT		227..271			
FT	mat_peptide	/*tag= b			
FT		272..955			
XX		/*tag= c			
XX					
PN	W09935170-A2.				
XX					
PD	15-JUL-1999.				
XX					
PP	05-JAN-1999;	99WO-US00106.			
XX					
PR	20-NOV-1998;	98US-0109304.			
PR	05-JAN-1998;	98US-0070440.			
PR	29-APR-1998;	98US-0083500.			
PR	22-MAY-1998;	98US-0086414.			

PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WJ;
 XX WPI; 1999-430385/36.
 DR P-PSDB; AAY06481.
 XX
 PT Antibody against proteins expressed in neoplastic cells, useful for
 PT tumor diagnosis and treatment
 PS
 PS Example 1; Fig 9; 162pp; English.
 XX
 XX This is the nucleotide sequence of cDNA clone DNA40592 (ATCC 209492)
 CC coding for human PRO344 (UNQ303) (see AAY06481). The clone was
 CC isolated from a foetal kidney library. Amplification of DNA40592
 CC was observed in primary lung tumours and in primary colon tumours,
 CC suggesting an association with tumour formation or growth.
 CC Antagonists (e.g. antibodies) directed against PRO344 may have
 CC utility in cancer therapy. The invention identifies 14 genes (see
 CC AAX87254-67) that are amplified in the genome of tumour cells. Such
 CC amplification is expected to be associated with overexpression of
 CC the gene product and to contribute to tumorigenesis. The encoded
 CC proteins (see AAY06477-90) may be useful targets for the diagnosis
 CC and/or treatment (including prevention) of certain cancers, and may
 CC act as predictors of the prognosis of tumour treatment.
 XX
 SO Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;
 Query Match 100.0%; Score 1377; DB 20; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 1,7e-244;
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAAAGGCGCGGAGGAGCGGACCAACCGAC 60
 DB 1 GACTAGTCTCTTGGAGTCTGGAGAGAAAGGCGCGGAGGAGCGGACCAACCGAC 60
 QY 61 TGGGGTACAGGCGAGGAGGCGCGCTGCGCGGAGAAAGCGGGGGCTGGAGACCA 120
 DB 61 TGGGGTACAGGCGAGGAGGCGCGCTGCGCGGAGAAAGCGGGGGCTGGAGACCA 120
 QY 121 CCAACTGAGAGGCTCCGAGTAGAGGAGCGCCCGGAGAGGAGCGGAGGAGG 180
 DB 121 CCAACTGAGAGGCTCCGAGTAGAGGAGCGCCCGGAGAGGAGCGGAGGAGG 180
 QY 181 GGGAGTGGAGAGAGCGCGGCGTCCGGGCGCGGAGGAGCGGAGGAGGAGG 240
 DB 181 GGGAGTGGAGAGAGCGCGGCGTCCGGGCGCGGAGGAGCGGAGGAGGAGG 240
 QY 241 CGTCTCTCTCTCTGGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 DB 241 CGTCTCTCTCTCTGGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 301 CAGCCTCTGCTCTCTGGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 DB 301 CAGCCTCTGCTCTCTGGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 QY 361 CTTTCCGGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 DB 361 CTTTCCGGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 421 AGCGGAGGCGGAGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 DB 421 AGCGGAGGCGGAGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 QY 481 GGGGGAGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 DB 481 GGGGGAGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 QY 541 CTTTACGGCGCAAGGCGTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

DB 541 CTTTACGGCGCAAGGCGTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 QY 601 CGACCGGCTGCTGGTGAACGAGAGGAGCATTTAGAGCGGCGGCGGCGGCGGCGG 660
 DB 601 CGACCGGCTGCTGGTGAACGAGAGGAGCATTTAGAGCGGCGGCGGCGGCGGCGG 660
 QY 661 CCAGGTGCTGGGCTTACTACTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
 DB 661 CCAGGTGCTGGGCTTACTACTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
 QY 721 GTTGTACTGTGAAGATGGCGAATCCATTCGCTCTTCTTCCAGTTTTCGGGGGG 780
 DB 721 GTTGTACTGTGAAGATGGCGAATCCATTCGCTCTTCTTCCAGTTTTCGGGGGG 780
 QY 781 GCCCAGCAGCCTCTGCTCTGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 DB 781 GCCCAGCAGCCTCTGCTCTGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 QY 841 GTGGGTGAGGTGGGTGGGTGAGTACATATTGCGATTCAGCAGCATCAAGACAG 900
 DB 841 GTGGGTGAGGTGGGTGGGTGAGTACATATTGCGATTCAGCAGCATCAAGACAG 900
 QY 901 CACCTTCCGCGATTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 DB 901 CACCTTCCGCGATTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 CCCACTGCAAGTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 DB 961 CCCACTGCAAGTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 QY 1021 GGTATTCAGAGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 DB 1021 GGTATTCAGAGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 QY 1081 GCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 GCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1141 GCACATGAGGCGAGTGGCTGATTTCTGCGCAAGACCAAGAGAGTGTGCTGCG 1200
 DB 1141 GCACATGAGGCGAGTGGCTGATTTCTGCGCAAGACCAAGAGAGTGTGCTGCG 1200
 QY 1201 GTTAAATGCCCCAGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 DB 1201 GTTAAATGCCCCAGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 QY 1261 CTCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1261 CTCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1321 GATCAGTCAATTAACCTTAAGAACCTTCAATAAAAAAAAAAAAAAAAAAAAA 1377
 DB 1321 GATCAGTCAATTAACCTTAAGAACCTTCAATAAAAAAAAAAAAAAAAAAAAA 1377
 RESULT 2
 ID AAX80052 standard; cDNA; 1377 BP.
 XX AAX80052;
 XX
 DT 12-AUG-1999 (first entry)
 XX
 DE Human PRO344 nucleotide sequence.
 XX
 KW Human: PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder; ss.
 OS Homo sapiens.
 XX
 PN W09928462-A2.
 XX

DT	08-NOV-2000	(first entry)
XX	Human PRO344 protein encoding cDNA clone, DNA40592-1242.	
DE		
XX	PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative;	
KW	neoplastic cell growth inhibitor; cytosolic; treatment; cancer; tumour;	
KW	breast; prostate; colon; lung; renal; ovarian; central nervous system;	
KW	CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;	
KW	extracellular domain; ECD; ss.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	CDS	227..958
FT		/tag= a
FT		/product= "Human PRO344 protein"
FT		/note= "Derived from clone DNA40592-1242"
FT	sig_peptide	227..271
FT		/tag= b
FT	mat_peptide	272..955
FT		/tag= c
FT		/product= "Mature human PRO344 protein"
XX		
PM	WO200032778-A2.	
PD	08-JUN-2000.	
XX		
PF	30-NOV-1999;	99WO-US28409.
XX		
PR	01-DEC-1998;	98WO-US25108.
PR	16-DEC-1998;	98US-0112850.
PR	22-DEC-1998;	98US-0113296.
PR	20-JUL-1999;	99US-0144758.
PR	26-JUL-1999;	99US-0145698.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;	
XX		
DR	WPI: 2000-412325/35.	
DR	P-PSDB; AAV71468.	
XX		
PT	New composition useful for inhibiting neoplastic cell growth and for	
PT	treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or	
PT	their antagonists -	
XX		
PS	Claim 20; Fig 5; 108pp; English.	
XX		
CC	The present sequence is the cDNA clone, designated as DNA40592-1242,	
CC	encoding the human PRO344 polypeptide. It is isolated from human foetal	
CC	lung tissue cDNA library, identified using probes based on a consensus	
CC	sequence DNA34398, derived from secreted protein extracellular domain	
CC	(ECD) expressed Sequence Tag (EST). This clone is assigned ATCC deposit	
CC	No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and	
CC	is used for treating tumours, using an effective amount of PRO655, PRO364	
CC	and PRO344. This composition is especially useful for treatment of human	
CC	cancers such as breast, prostate, colon, lung, renal, ovarian and CNS,	
CC	leukemia and melanoma.	
XX		
Seq	Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other:	
Query Match	100.0%; Score 1377; DB 21; Length 1377;	
Best Local Similarity	100.0%; Pred. No. 1.7e-244;	
Matches 1377;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GACTAGTCTCTTGAGAGCTGTGGAGAGAAAGCGAGCCGGACAGGAGCAACGAGAC 60	
DB	1 GACTAGTCTCTTGAGAGCTGTGGAGAGAAAGCGAGCCGGACAGGAGCAACGAGAC 60	
OY	61 TGGGGTGACGCGACAGGCGAGGGGGCCCTGGCGCGGGGAGAAACCGCGGGCTGGACACCA 120	
DB	61 TGGGGTGACGCGACAGGCGAGGGGGCCCTGGCGCGGGGAGAAAGCGCGGGGCTGGACACCA 120	

QY	121	CCAACTGGAGGGTCCGGAGTGAACGAGCCGCCGAGAGAGAGCCATCGGGGAGCCGGGAGGG	180
Db	121	CCAACTGGAGGGTCCGGAGTGAACGAGCCGCCGAGAGAGAGCCATCGGGGAGCCGGGAGGG	180
QY	181	GGAGCTGGAGAGAGACCCCGGGCTCCGAGGCTCCCGGTGCACAGCCTATGAGGCCACTCT	240
Db	181	GGAGCTGGAGAGAGACCCCGGGCTCCGAGGCTCCCGGTGCACAGCCTATGAGGCCACTCT	240
QY	241	CGTCCTGGTGGTCCCTGGGGCTGGGGCGGGCGGCGGCCACTGTGAGCGAACAAATATCC	300
Db	241	CGTCCTGGTGGTCCCTGGGGCTGGGGCGGGCGGCGGCCACTGTGAGCGAACAAATATCC	300
QY	301	CAGCCTTGCCCGGGGCAACCCCGGGCTTCCAGGCAAGCCGGGCCACATGCGAGCCAGG	360
Db	301	CAGCCTTGCCCGGGGCAACCCCGGGCTTCCAGGCAAGCCGGGCCACATGCGAGCCAGG	360
QY	361	CTTGCCGGGGCCCGATGCGCCGAGAGCGCCGCGAGCGCGCCCGGGGGCTCCGGAGAGAA	420
Db	361	CTTGCCGGGGCCCGATGCGCCGAGAGCGCCGCGAGAGCGCGCCCGGGGGCTCCGGAGAGAA	420
QY	421	AGGCGAGGGCGGAGAGCCGGGACTCCGGAGCTTGAGAGGGAGCCCGGGCGCGAGAGAG	480
Db	421	AGGCGAGGGCGGAGAGCCGGGACTCCGGAGCTTGAGAGGGAGCCCGGGCGCGAGAGAG	480
QY	481	GGCGGGACCCGCGGGGCCACACCGGGCTGCCGGGGAGTCTCGGTGCCCGATCCGC	540
Db	481	GGCGGGACCCGCGGGGCCACACCGGGCTGCCGGGGAGTCTCGGTGCCCGATCCGC	540
QY	541	CTTCAAGCGCCCAAGGCTCCGAGAGCGGGGTACCTCCGGCGTCTGACAGACCTTGCCCTT	600
Db	541	CTTCAAGCGCCCAAGGCTCCGAGAGCGGGGTACCTCCGGCGTCTGACAGACCTTGCCCTT	600
QY	601	CGACCGCGCTGTGGTGAACGAGAGAGGAGATTACAGCCCGCTACACCGGCAAGTTCACTG	660
Db	601	CGACCGCGCTGTGGTGAACGAGAGAGGAGATTACAGCCCGCTACAGCCCGGCAAGTTCACTG	660
QY	661	CCAGGTGCTTGGGGTCTACTACTTCGCCGTCCATGACACCGTCTTACCGGGCCAGCTTCA	720
Db	661	CCAGGTGCTTGGGGTCTACTACTTCGCCGTCCATGACACCGTCTTACCGGGCCAGCTTCA	720
QY	721	GTTTGATCTGTGAAGATGCGATGCATTCATTCGCTCTTCTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTGAAGATGCGATGCATTCATTCGCTCTTCTCCAGTTTTCGGGGGGTG	780
QY	781	GCCCAAGCAGACCTCTCTCTCGGGGGGGCCATGTGAGGCTGGAAGCTGAGAGACCAAGT	840
Db	781	GCCCAAGCAGACCTCTCTCTCGGGGGGGCCATGTGAGGCTGGAAGCTGAGAGACCAAGT	840
QY	841	GTTGGGTGAGGTGGGTGTGGGTGACTATTCATTCGGCATCTATCCAGATCAAGACAGACAG	900
Db	841	GTTGGGTGAGGTGGGTGTGGGTGACTATTCATTCGGCATCTATCCAGATCAAGACAGACAG	900
QY	901	CACCTTCTCGGATTTTGTGTACTCCGACTGGCAGAGCTCCCAAGCTTTTGCTTAAGT	960
Db	901	CACCTTCTCGGATTTTGTGTACTCCGACTGGCAGAGCTCCCAAGCTTTTGCTTAAGT	960
QY	961	CCCACTGCAAGTGAAGTCATGCTCTACTCTTGAAGAGAGAGGTGTAGGCTGACAAACA	1020
Db	961	CCCACTGCAAGTGAAGTCATGCTCTACTCTTGAAGAGAGAGGTGTAGGCTGACAAACA	1020
QY	1021	GGTATATCAGAGAGGGTGGCCCTCGGAATATTGTGAATACTAAGAGAGGTGGGGTGA	1080
Db	1021	GGTATATCAGAGAGGGTGGCCCTCGGAATATTGTGAATACTAAGAGAGGTGGGGTGA	1080
QY	1081	GCACCTTCOCGCTCTGCTGTGGCAAGAGATGGGAACAGTGGCTGTCCGATCAGGCTCG	1140
Db	1081	GCACCTTCOCGCTCTGCTGTGGCAAGAGATGGGAACAGTGGCTGTCCGATCAGGCTCG	1140
QY	1141	GCACCATGGGGCAATGGCTGATTTCTGGCCCAAGACCAAGAGAGAGTGTGGTGGGCAA	1200
Db	1141	GCACCATGGGGCAATGGCTGATTTCTGGCCCAAGACCAAGAGAGAGTGTGGTGGGCAA	1200
QY	1201	GTTGAATGCCCCAGTTGCTCTGTGGTCCAGAGCCACAGTGGGGTGTCTTCTTGCTGTC	1260

Db 1201 GTGTAAATCCCAATGCTCTGCTCAGAGACCAGGTGGGTCTCTCTCTGCTC 1260
QY 1261 CTGTGCTCTCTGATGCTCCCAACCCCTCTCTCTCTGCTGCTGCTCTTCTCAGA 1320
Db 1261 CTGTGCTCTCTGATGCTCCCAACCCCTCTCTCTCTGCTGCTGCTCTTCTCAGA 1320
QY 1321 GATCAGTCATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCAGTCATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377
RESULT 4
AAAA6907
ID AAAA6907 standard; cDNA: 1377 BP.
AC AAAA6907;
XX
XX 03-OCT-2000 (first entry)
DE CDNA encoding novel polypeptide PRO344.
XX
XX PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357,
KW PRO1715, PRO1017, PRO1112, PRO509, PRO853, PRO882, tumour cell;
KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 227..958
FT /tag= a
PN MO20037640-A2.
XX
XX 29-JUN-2000.
PD
XX
XX 16-DEC-1999; 99WO-US30095.
PF
XX
XX 22-DEC-1998; 98US-0113296.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28365.
XX
XX (GETH) GENENTECH INC.
PA
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
PI Wood WT;
XX
XX WPI: 2000-452188/39.
DR P-PSDB: AAY93688.
XX
XX New anti-polypeptide antibody useful in the treatment and diagnosis of
PI neoplastic cell growth and proliferation -
XX
XX Claim 50; Fig 9; 220pp; English.
XX
XX The present sequence encodes a novel human polypeptide. The
CC specification describes novel polypeptides designated PRO201, PRO292,
CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1715, PRO1017,
CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
CC the genome of tumour cells. The polypeptides are believed to contribute
CC to tumorigenesis. The polypeptides are useful target for the
CC identification of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies against these polypeptides
CC are useful in the treatment and diagnosis of neoplastic cell growth
CC and proliferation in mammals.
XX
XX Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

Query Match 100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 1,7e-244;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTAGTCTCTTGTAGTCTGTGAGAGAGAAAGCGAGCCCGCAGAGAGCGAAGCAGAGC 60
Db 1 GACTAGTCTCTTGTAGTCTGTGAGAGAGAGAAAGCGAGCCCGCAGAGAGCGAAGCAGAGC 60
QY 61 TGGGTGACGAGGAGGCGAGGGGGCGCTTGGCCGGGAGAGAGCGGGGGCTTGGAGCACCA 120
Db 61 TGGGTGACGAGGAGGCGAGGGGGCGCTTGGCCGGGAGAGAGCGGGGGCTTGGAGCACCA 120
QY 121 CCAACTGAGAGGGTCCGAGGTAGCGAGCGCCCGAAGAGAGGCGATCGGGGAGCGGGAGG 180
Db 121 CCAACTGAGAGGGTCCGAGGTAGCGAGCGCCCGAAGAGAGGCGATCGGGGAGCGGGAGG 180
QY 181 GGGAGTGGAGAGAGACCCCGGCTCCGGGCTCCGGTCCAGCGCTATGAGGCCACTCT 240
Db 181 GGGAGTGGAGAGAGACCCCGGCTCCGGGCTCCGGTCCAGCGCTATGAGGCCACTCT 240
QY 241 GGTCTGTGCTCTCTGGGCTTGGGCGCGGCTCGCCCTGACGACGACACAGATCCC 300
Db 241 GGTCTGTGCTCTCTGGGCTTGGGCGCGGCTCGCCCTGACGACGACACAGATCCC 300
QY 301 CAGCCTTGGCCGGGAGACCCCGGCTTCCAGGAGCGCGGGGGACCAATGAGCAGG 360
Db 301 CAGCCTTGGCCGGGAGACCCCGGCTTCCAGGAGCGCGGGGGACCAATGAGCAGG 360
QY 361 CTGTGCGGCGCGATGAGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAA 420
Db 361 CTGTGCGGCGCGATGAGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAA 420
QY 421 AGCGAGGCGGAGAGCGCGGAGCTGCGGAGCTTGAAGGAGACCCGGGCGGAGAGA 480
Db 421 AGCGAGGCGGAGAGCGCGGAGCTGCGGAGCTTGAAGGAGACCCGGGCGGAGAGA 480
QY 481 GGGGGAGCGCGGGGGCCACCGGGCGGCGGGGAGTGTGCTTCCGCGATCCGC 540
Db 481 GGGGGAGCGCGGGGGCCACCGGGCGGCGGGGAGTGTGCTTCCGCGATCCGC 540
QY 541 CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGCTCCGCGCTGAGAGCAGCCCTTCCCT 600
Db 541 CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGCTCCGCGCTGAGAGCAGCCCTTCCCT 600
QY 601 CGACCGGCTGCTGTGTAAGAGAGCAGGACATTTAGAGCGCCGTACCGGCAAGTTCACTG 660
Db 601 CGACCGGCTGCTGTGTAAGAGAGCAGGACATTTAGAGCGCCGTACCGGCAAGTTCACTG 660
QY 661 CCAAGTGTGGGGGTCTACTTGTGCGGCTCATGCGCCAGCGGTCATGCGGGGCGAGCTGCA 720
Db 661 CCAAGTGTGGGGGTCTACTTGTGCGGCTCATGCGCCAGCGGTCATGCGGGGCGAGCTGCA 720
QY 721 GTTGTATCTGTGTAAGATGCGAATCCATTGCTCTTCTTCCAGTTTTCGGGGGTG 780
Db 721 GTTGTATCTGTGTAAGATGCGAATCCATTGCTCTTCTTCCAGTTTTCGGGGGTG 780
QY 781 GCCCAAGCCAGCTCTGCTCGGGGGGGCCATGATGAGCTGAGGCTGAGAGCAAGT 840
Db 781 GCCCAAGCCAGCTCTGCTCGGGGGGGCCATGATGAGCTGAGGCTGAGAGCAAGT 840
QY 841 GTGGGTGAGGTTGGGTGGTGGTGAATTAATGGCATTAATGCGACATCAAGAGAGAG 900
Db 841 GTGGGTGAGGTTGGGTGGTGGTGAATTAATGGCATTAATGCGACATCAAGAGAGAG 900
QY 901 CACCTTCCCGGATTTCTGTACTCCGACTGGCAGCAGTCCCGAGCTTGTGTAGTG 960
Db 901 CACCTTCCCGGATTTCTGTACTCCGACTGGCAGCAGTCCCGAGCTTGTGTAGTG 960
QY 961 CCCACTGCAAGAGTCACTACTCTCACTCTAGAGAGAGGTTGAGGCTGACACCA 1020
Db 961 CCCACTGCAAGAGTCACTACTCTCACTCTAGAGAGAGGTTGAGGCTGACACCA 1020


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Db      841 GTGGGTGCAGGTGGGTGGGTGACTACATATGTCATATGCCAGCATCAAGACAGACAG 900
QY      901 CACCTTCCCGGATTTCTGGTGTACTCCGACGTGGACAGACCTCCAGTCTTGTGCTAGTG 960
Db      901 CACCTTCCCGGATTTCTGGTGTACTCCGACGTGGACAGACCTCCAGTCTTGTGCTAGTG 960
QY      961 CCCACTGCAGAACTGAGCTCATGCTCTCACTCTAGAGAGAGGAGTGTGAGAGTACACCA 1020
Db      961 CCCACTGCAGAACTGAGCTCATGCTCTCACTCTAGAGAGAGGAGTGTGAGAGTACACCA 1020
QY      1021 GGTCAATCCAGAGAGGCTGGCCCCCTCGAATATTTGAAATGACTAGAGAGTGGGGTAGA 1080
Db      1021 GGTCAATCCAGAGAGGCTGGCCCCCTCGAATATTTGAAATGACTAGAGAGTGGGGTAGA 1080
QY      1081 GCACATCCGCTCTGCTGTGGCAGAGATGGGAACAGTGTCTGTGGATCAGAGTCTG 1140
Db      1081 GCACATCCGCTCTGCTGTGGCAGAGATGGGAACAGTGTCTGTGGATCAGAGTCTG 1140
QY      1141 GCAGCATGGGGGAGTGGTGTGATTTCTGCCCCAAGACAGAGAGTGTGTGTGCA 1200
Db      1141 GCAGCATGGGGGAGTGGTGTGATTTCTGCCCCAAGACAGAGAGTGTGTGTGCA 1200
QY      1201 GTGTAAATCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db      1201 GTGTAAATCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY      1261 CTCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
Db      1261 CTCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY      1321 GATCACTCAATTAACCTAAGAACCCCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377
Db      1321 GATCACTCAATTAACCTAAGAACCCCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377
RESULT 6
AAS21424
ID      AAS21424 standard; cDNA; 1377 BP.
XX
AC      AAS21424;
XX
DT      24-OCT-2001 (first entry)
XX
DE      Human cDNA sequence encoding for PRO344 polypeptide.
XX
KW      Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW      breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW      cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW      adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS      Homo sapiens.
XX
PN      WO200140466-A2.
XX
PD      07-JUN-2001.
XX
PF      01-DEC-2000; 2000MO-US32678.
XX
PR      01-DEC-1999; 99WO-US28301.
PR      01-DEC-1999; 99WO-US28634.
PR      02-DEC-1999; 99WO-US28551.
PR      02-DEC-1999; 99WO-US28564.
PR      02-DEC-1999; 99WO-US28565.
PR      09-DEC-1999; 99US-0170262.
PR      16-DEC-1999; 99WO-US30095.
PR      20-DEC-1999; 99WO-US30911.
PR      20-DEC-1999; 99WO-US30999.
PR      30-DEC-1999; 99WO-US31243.
PR      06-JAN-2000; 2000MO-US00277.
PR      06-JAN-2000; 2000MO-US00376.
PR      11-FEB-2000; 2000MO-US03565.
PR      18-FEB-2000; 2000MO-US04341.
PR      18-FEB-2000; 2000MO-US04342.

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PR      22-FEB-2000; 2000MO-US04414.
PR      24-FEB-2000; 2000MO-US04914.
PR      01-MAR-2000; 2000MO-US05004.
PR      01-MAR-2000; 2000MO-US05601.
PR      20-MAR-2000; 2000MO-US07377.
PR      21-MAR-2000; 2000MO-US07532.
PR      30-MAR-2000; 2000MO-US08439.
PR      17-MAY-2000; 2000MO-US13705.
PR      22-MAY-2000; 2000MO-US14042.
PR      30-MAY-2000; 2000MO-US14941.
PR      02-JUN-2000; 2000MO-US15264.
PR      10-NOV-2000; 2000MO-US30873.
PR
PA      (GENENTECH INC.
PI      Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI      Gerritsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;
PI      Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
PR
XX      MPI: 2001-408281/43.
XX      P-PSDB; AAU12352.
XX
DR      Isolated, secretory and transmembrane PRO polypeptide used to detect
XX      other PRO polypeptides, link bioactive molecules to cells expressing
XX      PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX      lung, breast, prostate, cervical.
XX
PS      Claim 3; Fig 361; 813pp; English.
XX
XX      AAS21244-AAS21518 encode for novel human secretory and transmembrane
XX      PRO polypeptides. The PRO polypeptides are useful to detect other
XX      PRO polypeptides, to link bioactive molecules to cells expressing
XX      PRO polypeptides, to modulate biological activities of cells expressing
XX      PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX      breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX      polypeptide expression in a cell sample to that in a control sample.
XX      Some of the 275 sequences are also useful to stimulate the release of
XX      tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX      proliferation or differentiation of chondrocytes, the proliferation or
XX      gene expression in pericyte cells, the release of proteoglycans from
XX      cartilage, the proliferation of inner ear utricular supporting cells or
XX      of T-lymphocytes, the release of a cytokine from peripheral blood
XX      CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX      the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX      skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX      to factor VIIA. The PRO polypeptides can be used in assays to identify
XX      CC molecules involved in binding interactions. The polynucleotides encoding
XX      CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX      transgenic or knock out animals and can be used in gene therapy.
XX
SQ      Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;
Query Match      100.0%; Score 1377; DB 22; Length 1377;
Best Local Similarity 100.0%; Pred. No. 1.7e-244;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GACTAGTCTCTTGGAGTGTGGAGAGAGAAAGCGGAGCGGAGGAGCGAAGCAGAC 60
Db      1 GACTAGTCTCTTGGAGTGTGGAGAGAGAAAGCGGAGCGGAGGAGCGAAGCAGAC 60
QY      61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db      61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY      121 CCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db      121 CCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY      181 GGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db      181 GGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      241 GGTCTGTGCTCTGTGGGCTGGGCGGCTGGCCGCCCACTGAGAGAGAGAGAGAGATCCC 300

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|||||
Db 241 CGTCTGCTCTCTGGGCTTGCGGCGGCTCGCCCTCGACGCAACAAGATCCC 300
OY 301 CAGCCTTGCCCGGGGACCCCGGCTTCCAGGACGCGGGGCAACATGGCAGCGAGG 360
Db 301 CAGCCTTGCCCGGGGACCCCGGCTTCCAGGACGCGGGGCAACATGGCAGCGAGG 360
OY 361 CTTCGCGGGCGCGCATGGCCGCGACGGCCGCGAGCGCGCCCGGGGCTCCGGGAGAGAA 420
Db 361 CTTCGCGGGCGCGCATGGCCGCGACGGCCGCGAGCGCGCCCGGGGCTCCGGGAGAGAA 420
OY 421 AGGCGAGGCGCGGAGCGCGGACTGCGGGGACCTTCGAGGGAGACCCCGGGCGCGAGAGA 480
Db 421 AGGCGAGGCGCGGAGCGCGGACTGCGGGGACCTTCGAGGGAGACCCCGGGCGCGAGAGA 480
OY 481 GGGCGGAGCCGCGGGGGCCACCGGGGCTGCGGGGAGTGCCTGGGCTCCGCGATCCG 540
Db 481 GGGCGGAGCCGCGGGGGCCACCGGGGCTGCGGGGAGTGCCTGGGCTCCGCGATCCG 540
OY 541 CTTCAGGCGCAAGCGCTCCGAGAGCCCGGGTGCCTCCGCGCTTCAGCGACCCCTTGCCCTT 600
Db 541 CTTCAGGCGCAAGCGCTCCGAGAGCCCGGGTGCCTCCGCGCTTCAGCGACCCCTTGCCCTT 600
OY 601 CGACCGCGTGTGTGAACGACGAGGACATTCAGAGCGCGTCAACCGGCAAGTTACCTG 660
Db 601 CGACCGCGTGTGTGAACGAGGACATTCAGAGCGCGTCAACCGGCAAGTTACCTG 660
OY 661 CCAGTGTGCTGGGTCTACTACTTCCGCGTCATGCCACGCTACCGGGGCGACCTGCA 720
Db 661 CCAGTGTGCTGGGTCTACTACTTCCGCGTCATGCCACGCTACCGGGGCGACCTGCA 720
OY 721 GTTTGATCTGTGTGAAGATGGCGAATCCATTCCTTTCTCCAGTTTTCGGGGGGTG 780
Db 721 GTTTGATCTGTGTGAAGATGGCGAATCCATTCCTTTCTCCAGTTTTCGGGGGGTG 780
OY 781 GCGCAAGCGACCGCTCGCTCGGGGGGGGGGCGCATGTGAGGCTTGAGGACCAAGT 840
Db 781 GCGCAAGCGACCGCTCGCTCGGGGGGGGGGCGCATGTGAGGCTTGAGGACCAAGT 840
OY 841 GTGGTGCAGGTGGGTGGGTGACTACATTCGATCGCATCCAGCATCAAGACAGAG 900
Db 841 GTGGTGCAGGTGGGTGGGTGACTACATTCGATCGCATCCAGCATCAAGACAGAG 900
OY 901 CACCTTCCGGATTTCTGTGTACTCGACTGGCAGAGCTCCCAAGTCTTTGCTAGTG 960
Db 901 CACCTTCCGGATTTCTGTGTACTCGACTGGCAGAGCTCCCAAGTCTTTGCTAGTG 960
OY 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTTGAAGAGAGGCTGAGGCTGACAACA 1020
Db 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTTGAAGAGAGGCTGAGGCTGACAACA 1020
OY 1021 GGTCTATCCAGAGGGGTGGCCCGCTCGAATATTGTGAATAGTACAGGAGGTGGGTAGA 1080
Db 1021 GGTCTATCCAGAGGGGTGGCCCGCTCGAATATTGTGAATAGTACAGGAGGTGGGTAGA 1080
OY 1081 GCACCTTCCTCTCTGCTGCTGCTGGAAGAAATGGAAAGTAGTGCTCTGCGATCAGGCTG 1140
Db 1081 GCACCTTCCTCTCTGCTGCTGCTGGAAGAAATGGAAAGTAGTGCTCTGCGATCAGGCTG 1140
OY 1141 GCACGATGGGCAATGGCTGGATTTCTGCCCCAACAACAGAGAGATGCTGTGGCGAA 1200
Db 1141 GCACGATGGGCAATGGCTGGATTTCTGCCCCAACAACAGAGAGATGCTGTGGCGAA 1200
OY 1201 GTGTAACTGCCCGAGTTGCTGTGTCAGAGAGCCACAGGTTGGGTCTCTTCTCTGCTC 1260
Db 1201 GTGTAACTGCCCGAGTTGCTGTGTCAGAGAGCCACAGGTTGGGTCTCTTCTCTGCTC 1260
OY 1261 CTCTGCTTCTCTGATCTCTCCACCCCTCTCTGCTCTGCGGCGCGCCCTTTCTCAGA 1320
Db 1261 CTCTGCTTCTCTGATCTCTCCACCCCTCTCTGCTCTGCGGCGCGCCCTTTCTCAGA 1320
OY 1321 GATCAGTCATTAACCTTAAGAACCTCTATATAAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCAGTCATTAACCTTAAGAACCTCTATATAAAAAAAAAAAAAAAAAAAAAA 1377

Db 1321 GATCAGTCATTAACCTTAAGAACCTCTATATAAAAAAAAAAAAAAAAAAAAAA 1377
RESULT 7
ID AACS8626 standard; cDNA: 1377 BP.
XX AACS8626;
AC AACS8626;
DT 29-JAN-2001 (first entry)
XX
DE Human PR0344 protein UMO303 encoding cDNA SEQ ID NO:240.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antihypertic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antiporiatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO20053758-A2.
XX
PD 14-SEP-2000.
XX
PE 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99WO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0142287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 20-SEP-1999; 99US-014758.
PR 26-SEP-1999; 99US-014758.
PR 01-SEP-1999; 99WO-US21547.
PR 05-SEP-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30995.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.

QY	1300	GGGGGGGGCCCTTTTCTCAGAGATCAGATCAATTAACCTTAAGAACCCCTATATAAAAAAAA	1337		
Db	1271	GGGGGGGGCCCTTTTCTCAGAGATCAGATCAATTAACCTTAAGAACCCCTATATAAAAAAAA	1330		
QY	1360	AAAAAAA 1366			
Db	1331	AAAAAAA 1337			
RESULT 9					
AAAF44970					
ID	AAAF44970	standard; cDNA; 1338 BP.			
XX	AAAF44970;				
XX	AC				
XX	DT				
XX	28-MAR-2001	(first entry)			
DE	Human TANGO 253 coding sequence SEQ ID NO: 1.				
XX					
KW	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;				
KW	INTERCEPT 258; coronary disorder; olfactory disorder;				
KW	neurological disorder; pulmonary disorder; immunological disorder;				
KW	developmental disorder; kidney disorder; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200078808-A1.				
XX					
PD	28-DEC-2000.				
XX					
PF	19-JUN-2000; 2000WO-US16883.				
XX					
PR	18-JUN-1999; 99US-0336536.				
XX					
PA	(MILL-) MILLENNIUM PHARM INC.				
XX					
PI	Leidy KR, McKay C, Bossone S;				
XX					
DR	WPI; 2001-050109/06.				
XX					
PT	New nucleic acids for treating diseases and disorders, e.g.				
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear				
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple				
PT	sclerosis and asthma				
XX					
PS	Claim 1; Page 210; 332pp; English.				
CC					
CC	The present invention provides the protein and coding sequences of the				
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,				
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of				
CC	coronary, pulmonary, olfactory, immunological, neurological,				
CC	developmental and kidney disorders.				
XX					
SO	Sequence 1338 BP; 229 A; 423 C; 460 G; 226 T; 0 other;				
Query Match					
Best Local Similarity 94.2%; Score 1296.6; DB 22; Length 1338;					
Matches 1310; Conservative 0; Mismatches 4; Indels 1; Gaps 1;					
QY	54	CCAGAGCTGGGGTGCAGCGCAGGAGGAGGGGGCGCTGGCCGGGAGAAAGCGGGGGCTGG	113		
Db	15	CCGGAGCTGGGGTGCAGCGCAGGAGGAGGGGGCGCTGGCCGGGAGAAAGCGGGGGCTGG	74		
QY	114	AGCACACCAACTGGAGGGTCCGAGATAGCGAGCGCCGCCGAAGAGGCGCATCGGGAGCC	173		
Db	75	AGCACACCAACTGGAGGGTCCGAGATAGCGAGCGCCGCCGAAGAGGCGCATCGGGAGCC	134		
QY	174	GGGAGGGGGGACTGGAGAGGAGACCCCGGCGTCCGGGGTCCGGGAGGCGCATCGGGAGCC	233		
Db	135	GGGAGGGGGGACTGGAGAGGAGACCCCGGCGTCCGGGGTCCGGGAGGCGCATCGGGAGCC	194		
QY	234	CATCTCTGCTGCTGCTGCTGCGGCGTGGCGGCGGCGCTGCCCGCCCACTGGAGCAACA	293		

[illegible]

Db	1274	TCTCAGAGATCAGCTCAATAAAGCTAAGAACCCCTCCAAAAA	1328
RESULT 10			
ID	AAAF44998	standard; cDNA; 1338 BP.	
AC	AAAF44998;		
XX			
DT	28-MAR-2001	(first entry)	
XX			
DE		Human secreted protein related coding sequence SEQ ID NO: 103.	
XX			
KW	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;		
KW	INTERCEPT 258; coronary disorder; olfactory disorder;		
KW	neurological disorder; pulmonary disorder; immunological disorder;		
KW	developmental disorder; kidney disorder; ss.		
OS	Homo sapiens.		
XX			
PN	WO200078808-A1.		
XX			
PD	28-DEC-2000.		
XX			
PF	19-JUN-2000; 2000WO-US16883.		
XX			
PR	18-JUN-1999; 99US-0336536.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Leidy KR, McKay C, Bossone S;		
XX			
DR	WPI; 2001-050109/06.		
XX			
PT	New nucleic acids for treating diseases and disorders, e.g.		
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear		
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple		
PT	sclerosis and asthma -		
PS			
CC	Disclosure; Page 271, 332pp: English.		
XX			
CC	The present invention provides the protein and coding sequences of the		
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,		
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of		
CC	coronary, pulmonary, olfactory, immunological, neurological,		
CC	developmental and kidney disorders.		
XX			
SEQ	Sequence 1338 BP; 229 A; 422 C; 460 G; 227 T; 0 other;		
Query Match	94.0%; Score 1295; DB 22; Length 1338;		
Best Local Similarity	99.5%; Pred. No. 2e-229;		
Matches 1309; Conservative	.0; Mismatches 5; Indels 1; Gaps 1		
0Y	54 CCAGAGCTGGGGTGTGACGGCAGGCGCGGGGCGCGCGGGGAGAAAGCGCGGGGCTGG	113	
DB	15 CCGGAGCTGGGGTGTGACGGCAGGCGCGGGGCGCGCGGGGAGAAAGCGCGGGGCTGG	74	
0Y	114 AGCACACCAACTGAGAGGCTCGGAGTAGCGAGCCGCCCGAAGAGAGCCATCGGGAGCC	173	
DB	75 AGACACCACTGAGAGGCTCGGAGTAGCGAGCCGCCCGAAGAGAGCCATCGGGAGCC	134	
0Y	174 GGGAGGGGGAGCTGCGAAGAGAGACCCCGCGCTCCGGGCTCCGGTGCACGCTTATGAGGC	233	
DB	135 GGGAGGGGGAGCTGCGAAGAGAGACCCCGCGCTCCGGGCTCCGGTGCACGCTTATGAGGC	194	
0Y	234 CACTCGTCTGCTGTGCTGCTCCGCGGCTCGGGGCGGGGCGCGCCGACATGAGAGCAACA	293	
DB	195 CACTCGTCTGCTGTGCTGCTCCGCGGCTCGGGGCGGGGCGCGCCGACATGAGAGCAACA	254	
0Y	294 AGATCCAGAGCTTGGCCCGGGGAGACCCCGCGCTTCAAGAGACCGCGGGGACCAATGAGA	353	
DB	255 AGATCCAGAGCTTGGCCCGGGGAGACCCCGCGCTTCAAGAGACCGCGGGGACCAATGAGA	314	

QY	354	GGCAGAGGCTTGGCCGGGGCCCGATATGGCCGGGAGCGCCGACAGCGCCGCGCCGGGGCTCCGG	413
Db	315	GGCAGAGGCTTGGCCGGGGCCCGATATGGCCGGGAGCGCCGACAGCGCTGGCGGGGGCTCCGG	374
QY	414	GAGAGAAAGGCGAGGCGGAGAGCGCGGAGCTGCCGGAGCTCGAGGAGAACCCCGGGCCCG	473
Db	375	GAGAGAAAGGCGAGGCGGAGAG - GCGAGCTGCCGGAGACTCGAGGAGAACCCCGGGCCCG	433
QY	474	GAGAGAGGCGGGAGACCCCGGGGGCCACCGGGCTTCGCGGGAGTCTCGGTCTTCGCC	533
Db	434	GAGGAGAGGCGGGAGACCCCGGGGGCCACCGGGGGCTTCGCGGGAGTCTCGGTCTTCGCC	493
QY	534	GATCGGCTTCAGCGCCGACAGCGCTCCGAGAGCGGGGTGCCCGCGCTCGAGACACCTT	593
Db	494	GATCGGCTTCAGCGCCGACAGCGCTCCGAGAGCGGGGTGCCCGCGCTCGAGAGACACCTT	553
QY	594	TGCCCTTGACAGCGCGTGTGTGTGAAGAGAGACAGGAGATTACGAGCGCGCTACCGGCAAGT	653
Db	554	TGCCCTTGACAGCGCGGTGTGTGTGAAGAGAGGAGATTACGAGCGCGCTACCGGCAAGT	613
QY	654	TCACCTGCCAGGTGCCCTGGGGTCTACTACTTGCCTCATGCGCACCGTCTACCGGGCCA	713
Db	614	TCACCTGCCAGGTGCCCTGGGGTCTACTACTTGCCTCATGCGCACCGTCTACCGGGCCA	673
QY	714	GCCTCAGTTTATCTGGTGAAGAAATGGGAAATCCATTCCTTTCTTCACGTTTTCG	773
Db	674	GCCTCAGTTTATCTGGTGAAGAAATGGGAAATCCATTCCTTTCTTCACGTTTTCG	733
QY	774	GGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGTGAGGCTGAGACCTGAGG	833
Db	734	GGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGTGAGGCTGAGACCTGAGG	793
QY	834	ACCAAGTGTGGTGGCAGGTGGTGTGGTGTACTACTATTGGCATCTATGCCAGATCAAGA	893
Db	794	ACCAAGTGTGGTGGCAGGTGGTGTGGTGTACTACTATTGGCATCTATGCCAGATCAAGA	853
QY	894	CAGAGAGACCTTTCGCCGATTTCTGGGTACTCCGACATGGGACACCTCCCAAGCTTTTG	953
Db	854	CAGAGAGACCTTTCGCCGATTTCTGGGTACTCCGACATGGGACACCTCCCAAGCTTTTG	913
QY	954	CTTACTGCCCATGTGCAAGTGAAGTGAAGTCACTCACTCTAGAGAGAGGGTGTGAGGCTG	1011
Db	914	CTTACTGCCCATGTGCAAGTGAAGTGAAGTCACTCACTCTAGAGAGAGGGTGTGAGGCTG	973
QY	1014	ACAACAGGTCAATCCAGAGAGGAGGCTGGCCGCCCTGGAATATTGTGAATGACTAGGAGGTG	1071
Db	974	ACAACAGGTCAATCCAGAGAGGAGGCTGGCCGCCCTGGAATATTGTGAATGACTAGGAGGTG	1031
QY	1074	GGGTGAGACACTCTCCGTCCTCTGTCGCAAGAAATGGGAACAGTGGTCTGTGGATC	1131
Db	1034	GGGTGAGACACTCTCCGTCCTCTGTCGCAAGAAATGGGAACAGTGGTCTGTGGATC	1091
QY	1134	AGGTGTGGCAGCAGTGGGGCAGTGGCTGATTTTCTGCGCAAGACACAGAGAGTGTGCTGTG	1191
Db	1094	AGGTGTGGCAGCAGTGGGGCAGTGGCTGATTTTCTGCGCAAGACACAGAGAGTGTGCTGTG	1151
QY	1194	CTGGCAAGTGTAAATGCCCAAGTGTCTGTGTGTGTCAGAGAGCCACAGTGGGGTGTCTTT	1251
Db	1154	CTGGCAAGTGTAAATGCCCAAGTGTGTGTGTGTCAGAGAGCCACAGTGGGGTGTCTTT	1211
QY	1254	CCTGTGCTCTCTCTCTCTGATATCCGCCACACCCCTCTGTGCTCTGGGGCGGGCCCTTT	1311
Db	1214	CCTGTGCTCTCTCTCTCTGATATCCGCCACACCCCTCTGTGCTCTGGGGCGGGCCCTTT	1271
QY	1314	TCTCAGAGATCACTCAATTAACCTTAAGAACCTTCATATAAAAAAAAAAAAAAAAAAAAA	1368
Db	1274	TCTCAGAGATCACTCAATTAACCTTAAGAACCTTCATATAAAAAAAAAAAAAAAAAAAAA	1328

[illegible]

OY	474	GAGAGAGAGGGGAGACCCGGCGGGGGGCCACCGGGGGCCGGCCGGGGAGAGTCTGGTGGCTCCGC	533
Dd	434	GAGGAGAGGGCGGAGCCGGCGGGGGCCACCGGGGCTCTGGGGAGAGTCTGGTGGCTCCGC	493
OY	534	GATCGCGCTTGAAGCGCCCAAGCGCTTCCAGAGACCGGGGTCTCTCGCGCTCTGACGCAACCT	593
Dd	494	GATCGCGCTTGAAGCGCCCAAGCGCTTCCAGAGACCGGGGTCTCTCGCGCTCTGACGCAACCT	553
OY	554	TGCCCCCTTGACCCGGCTGCTGGTGAACGAGACAGGACATTTACAGCGCGCTCACCGGCAAGT	653
Dd	554	TGCCCCCTTGACCCGGCTGCTGGTGAACGAGAGGACATTTACAGAGCCCTGCACCGGCAAGT	613
OY	654	TCACCTGCGAGGTGGCTGGGGTCTACTACTTGGCGGTCCATGGCCACGCTACCGGGGCA	713
Dd	614	TCACCTGCGAGGTGGCTGGGGTCTACTACTTGGCGGTCCATGGCCACGCTACCGGGGCA	673
OY	714	GCTTCGACATTTGATCTGGTGAAGAATGAGCATCATTCATCCCTCTTCTTCACAGTTTTTCG	773
Dd	674	GCTTCGACATTTGATCTGGTGAAGAATGAGCATCATTCATCCCTCTTCTTCACAGTTTTTCG	733
OY	774	GGGGGTGGCCCAAGCCAGCCTTCGCTCTTCGGGGGGGGGCCATGATGAGCTGAGCCTGAGG	833
Dd	734	GGGGGTGGCCCAAGCCAGCCTTCGCTCTTCGGGGGGGGGCCATGATGAGCTGAGCCTGAGG	793
OY	834	ACCAAGTGTGGGTGCAGGTGGGTGGGGTGGACTCATTTGGATCATATGCCAGCATCAAGA	893
Dd	794	ACCAAGTGTGGGTGCAGGTGGGTGGGGTGGACTCATTTGGATCATATGCCAGCATCAAGA	853
OY	894	CAGACAGCACCTTCTCCCGATTTTGTGTACTCCGACTGGCAGACGCTCCCGAGTCTTTG	953
Dd	854	CAGACAGCACCTTCTCCCGATTTTGTGTACTCCGACTGGCAGACGCTCCCGAGTCTTTG	913
OY	954	CTTAGTGGCCCACTGCAAAAGTGACTCATGTCTCTCACTCTTGAAAGGAGGTGTAGAGCTG	1013
Dd	914	CTTAGTGGCCCACTGCAAAAGTGACTCATGTCTCTCACTCTTGAAAGGAGGTGTAGAGCTG	973
OY	1014	ACAACACAGGTATTCAGAGAGGGGCTGGCCGCCCTGGAAATATGTGAATGACTAGGAGAGTG	1073
Dd	974	ACAACCTGTGTATCCAGAGAGGGGCTGGCCGCCCTGGAAATATGTGAATGACTAGGAGAGTG	1033
OY	1074	GGGTAGAGACACTCCGCTCTGCTGTGGCAAGGAATGGGAACAGTGGCTCTTCGCATC	1133
Dd	1034	GGGTAGAGACACTCCGCTCTGCTGTGGCAAGGAATGGGAACAGTGGCTCTTCGCATC	1093
OY	1134	AGGTCTGGCACATGGGGCAATGGGTGGATTTCTTGCCCAACACAGAGAGATGTGTCTG	1193
Dd	1094	AGGTCTGGCACATGGGGCAATGGGTGGATTTCTTGCCCAACACAGAGAGATGTGTCTG	1153
OY	1194	CTGGCAAGTGAAGTCCCGCCAGTTGCTCTGTGTCAGAGAGCCACGAGTGGGGTGTCTCTT	1253
Dd	1154	CTGGCAAGTGAAGTCCCGCCAGTTGCTCTGTGTCAGAGAGCCACGAGTGGGGTGTCTCTT	1213
OY	1254	CTGTGGTCTGCTTCTCTGTGATCCTCCACCCGCCCTCTCTCTCTGGGGCGGGCCCTTT	1313
Dd	1214	CTGTGGTCTGCTTCTCTGTGATCCTCCACCCGCCCTCTCTCTCTGGGGCGGGCCCTTT	1273
OY	1314	TCTCAGAGATCACTCAATTAACCTTAAGAACCCTCATATAAAAAAAAAAAAAAAAAAAAA	1368
Dd	1274	TCTCAGAGATCACTCAATTAACCTTAAGAACCCTCCAAAAAAAAAAAAAAAAAAAAA	1328
RESULT 12			
AAAF45000			
ID	AAAF45000 standard; cDNA: 1338 BP.		
XX	AAF45000;		
XX	28-MAR-2001 (first entry)		
XX	Human secreted protein related coding sequence SEQ ID NO: 107.		
XX	Human; mouse;secreted protein: TANGO253; TANGO 257; TANGO 281;		

XX	28-DEC-2000.
-PD	
XX	19-JUN-2000; 2000WO-US16883.
PF	
XX	18-JUN-1999; 99US-0336536.
PR	
XX	(MILL-) MILLENNIUM PHARM INC.
PA	
XX	Leiby KR, McKay C, Bossone S;
PI	
XX	WPI; 2001-050109/06.
DR	
XX	
XX	New nucleic acids for treating diseases and disorders, e.g.
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT	sclerosis and asthma -
XX	
PS	Disclosure; Page 274-275; 332pp; English.
XX	
XX	The present invention provides the protein and coding sequences of the
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC	coronary, pulmonary, olfactory, immunological, neurological,
XX	developmental and kidney disorders.
XX	
XX	Sequence 1338 BP; 228 A; 424 C; 460 G; 226 T; 0 other;

Query Match	94.0%;	Score 1295;	DB 22;	Length 1338;
Best Local Similarity	99.5%;	Pred. No. 2e-229;		
Matches 1309; Conservative	0;	Mismatches 5;	Indels 1;	Gaps 1

OY	54	CCAGGACTGGGGTGCAGGCGCAGGGGGGGCGCTTGCGCGGGGAGAAACGCGGGGGCTGG	113
Db	15	CCGGGACTGGGGGTGACGGCGCAGGGGAGCGGGGGGGCGCTTGCGCGGGGAGAAACGCGGGGGCTGG	74
OY	114	AGCACACCAACTGGAGGGTCCGGAGTAGCGGAGCGCCCCGAAAGAGGCCATTGGGGAGCC	173
Db	75	AGCACACCAACTGGAGGGTCCGGAGTAGCGGAGCGCCCCGAAAGAGGCCATTGGGGAGCC	134
OY	174	GGGAGGGGGGACTCGAGAGGAGACCCGGCGTCGCGGGCTCCAGCGCTATGAGGC	233
Db	135	GGGAGGGGGGACTCGAGAGGAGACCCGGCGTCGCGGGCTCCAGCGCTATGAGGC	194
OY	234	CACTCCTGCTCCTGCTCTCTGGGCGCTGCGCGCGCGCTCGCCCCACTGACGACAA	293
Db	195	CACTCCTGCTCCTGCTCTCTGGGCGCTGCGCGCGCGCTCGCCCCACTGACGACAA	254
OY	294	AGATCCCCAGCTGCCCCCGGGGACCCCGGCGTTCAGAGGACGCGCGGGGCCACATGGCA	353
Db	255	AGATCCCCAGCTGCCCCCGGGGACCCCGGCGTTCAGAGGACGCGCGGGGCCACATGGCA	314
OY	354	GCCAGGGCTTCCGGGCGCGCATGGCGCGACGGCGGACGGCGCGCGGGGCTCCGG	413
Db	315	GCCAGGGCTTCCGGGCGCGCATGGCGCGCGACGGCGGCGCGCGGGGCTCCGG	374
OY	414	GAGGAAAGGGGAGGGGGGGGAGCGCGGGGACATGCGGGGACCTGGAAGGACCCCGGGCGC	473
Db	375	GAGGAAAGGGGAGGGGGGGGAGCGCGGGGACATGCGGGGACCTGGAAGGACCCCGGGCGC	433
OY	474	GAGGAGAGGCGGAGCCCGCGGGGCGCCACCGGGCGTCCCGGGAGTGTCTGATGCTCCGC	533
Db	434	GAGGAGAGGCGGAGCCCGCGGGGCGCCACCGGGCGTCCCGGGAGTGTCTGATGCTCCGC	493
OY	534	GATCGCGCTTACAGGCGCCAAGCGCTCCGAGAGCGCGGGTGCCTCCCGCTTGACGCACTT	593
Db	494	GATCGCGCTTACAGGCGCCAAGCGCTCCGAGAGCGCGGGTGCCTCCCGCTTGACGCACTT	553
OY	594	TGCCCTTGACCGCGCTGCTGGTGAACGAGCAGAGGACATTACGACCCCGTACCGGCAAGT	653
Db	554	TGCCCTTGACCGCGCTGCTGGTGAACGAGCAGAGGACATTACGACCCCGTACCGGCAAGT	613
OY	654	TGACCTGCAGGTGCTGGGGTCTTACTACTTGGCGGCTGCATGACCAAGCTTACGGGGCCA	713

D	b	614	TCACCTCCGACGGTGGCTGGGGGTCTACTACTTCCGCGCCATCGCACCGCTTACCGGGCCG	673
Q	y	714	GCCTGCAGTTTGAATCTGGTGAAGAATGGCGAATCCATTGCGCTCTTTCTCCAGTTTTCG	773
D	b	674	GCCCTCAGTTTGAATCTGGTGAAGAATGGCGAATCCCGCTTCTTTCTCCAGTTTTCG	733
Q	y	774	GGGGGTGGCCCCAAGCCAGCGCTCCGCTCTCGGGGGGGGGCGCAATGGTGGAGGCTGGACCTGAGG	833
D	b	734	GGGGGTGGCCCCAAGCCAGCGCTCCGCTCTCGGGGGGGGGCGCAATGGTGGAGGCTGGACCTGAGG	793
Q	y	834	ACCAAGTGTGGGTGACAGTGGGTGGGTGGGTACACTAATTTGGCATCTATATGCCAGCATCAAGA	893
D	b	794	ACCAAGTGTGGGTGACAGTGGGTGGGTGGGTACACTAATTTGGCATCTATATGCCAGCATCAAGA	853
Q	y	894	CAGACACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCGAGTCTTGG	953
D	b	854	CAGACACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCGAGTCTTGG	913
Q	y	954	CTTAGTGTCCCACTGCAAAAGTGAAGTCAATGCTCTCACTCTCAGAAAGAGAGGTGTGAGGCTG	1013
D	b	914	CTTAGTGTCCCACTGCAAAAGTGAAGTCAATGCTCTCACTCTCAGAAAGAGAGGTGTGAGGCTG	973
Q	y	1014	ACAACACAGTATCCACAGAGAGGGCGCCGCCCTGGATATTTGTCATATGACATAGAGGAGGTG	1073
D	b	974	ACAACCTGTGTATCCACAGAGAGGGCGCCGCCCTGGATATTTGTCATATGACATAGAGGAGGTG	1033
Q	y	1074	GGGTAGAGACACTCTCCGTCCTGCTGCTGCGGCAAGGAATGGAGACAGTGGCTGTGCGATC	1133
D	b	1034	GGGTAGAGACACTCTCCGTCCTGCTGCTGCGGCAAGGAATGGAGACAGTGGCTGTGCGATC	1093
Q	y	1134	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAAGCAGAGAGAGTGTGCTGTG	1193
D	b	1094	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAAGCAGAGAGAGTGTGCTGTG	1153
Q	y	1194	CTGGCAGTGTAAAGTCCCGCAGTTGCTGTGGTCCAGGAGCCACAGGGGGGTGCTCTT	1253
D	b	1154	CTGGCAGTGTAAAGTCCCGCAGTTGCTGTGGTCCAGGAGCCACAGGGGGGTGCTCTT	1213
Q	y	1254	CTGTGGTCTGTGCTTCTCTGGATCCCTCCACACCCCTCTGCTCTTGGGGCGGGCCCTTT	1313
D	b	1214	CTGTGGTCTGTGCTTCTCTGGATCCCTCCACACCCCTCTGCTCTTGGGGCGGGCCCTTT	1273
Q	y	1314	TCCTCAGATCACTCAATAAACCCTAAGACCCCTCATATAAAAAAAAAAAAAAAAAAAAAA	1368
D	b	1274	TCCTCAGATCACTCAATAAACCCTAAGACCCCTCATATAAAAAAAAAAAAAAAAAAAAAA	1328
RESULT 14				
AAL39624				
ID ID AAL39624 standard; DNA; 3248 BP.				
XX AAL39624:				
XX AC				
XX DT 05-SEP-2002 (first entry)				
XX DE				
XX XX Human secreted protein DNA SEQ ID NO 68.				
KW Antihistaminic; cardiatic; vasotropic; neuroprotective; anti-inflammatory;				
KW anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory;				
KW immunosuppressive; human secreted protein; cell proliferative disorder;				
KW arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS;				
KW allergy; anaemia; asthma; cardiovascular disease; developmental disorder;				
KW ischaemic heart disease; congestive heart failure; neurological disorder;				
KW renal tubular acidosis; hypochloridism; Alzheimer's disease; dementia;				
KW Parkinson's disease; epilepsy; stroke; knockin humanised animal;				
KW transgenic animal; gene therapy; gene; ds.				
OS Homo sapiens.				
XX				
XX WN W0200238602-A2.				
XX TX				

QY		1134	AGGCTGTGGCAGCAATGGGGGACAGTGGCTTGATTTCCTGCCAAGACCAGAGAGAGTGTGCTGTG	1193
Dd		1094	AGGCTGTGGCAGCATGGGGGACAGTGGCTTGATTTCCTGCCAAGACCAGAGAGAGTGTGCTGTG	1153
QY		1194	CTGGCAAGTTAAATGTCCTCCCGAATGGTCGTCGTGCAGGAAGCCACGAGGGGGTGTCTCTT	1253
Dd		1154	CTGGCAAGTTAAATGTCCTCCCGAATGGTCGTCGTGCAGGAAGCCACGAGGGGGTGTCTCTT	1213
QY		1254	CCTGGTCCCTGTGCTTCTCTGTGGATCCTCCCAACCCCTCTCTGTCTCTGGGGCCGGCCCTTT	1313
Dd		1214	CGTGGTCCCTGTGCTTCTCTGTGGATCCTCCCAACCCCTCTCTGTCTCTGGGGCCGGCCCTTT	1273
QY		1314	TCTCAGAGATCACATCAATAAACCTAAGAACCCTCATTAATAAAAAAAAAAAAAAA	1368
Dd		1274	TCTCAGAGATCACATCAATAAACCTAAGAACCCTCTCAAAAAAAAAAAAAAAA	1328

RESULT_14
 AAL39624
 ID AAL39624 standard; DNA; 3248 BP.
 XX AAL39624;
 AC
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE Human secreted protein DNA SEQ ID No 68.

XX	KW	Antiartherosclerotic; cytostatic; HIV; antiallergic; antihaemic;
XX	KW	antiaesthetic; cardiac; vasotropic; neuroprotective; nootropic; SECP;
XX	KW	anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory;
XX	KW	immunosuppressive; human secreted protein; cell proliferative disorder;
XX	KW	arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS;
XX	KW	allergy; anaemia; asthma; cardiovascular disease; developmental disorder;
XX	KW	ischemic heart disease; congestive heart failure; neurological disorder;
XX	KW	renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia;
XX	KW	Parkinson's disease; epilepsy; stroke; knockin humanised animal;
XX	KW	transgenic animal; gene therapy; gene; ds.
OS		Homo sapiens.
XX		
NN		WO200238602-A2.
XX		

ID	AAST76911 standard; cDNA; 1082 BP.
XX	AAST76911;
XX	AAST76911;
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #12715.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
RW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
PD	
PD	11-OCT-2001.
PF	30-MAR-2001; 2001WO-US08631.
PR	31-MAR-2000; 2000US-0540217.
DR	23-AUG-2000; 2000US-0649167.
XX	
PA	(HYSE-) HYSEQ INC.
PI	
PI	Drmnac RT, Liu C, Tang YT;
XX	
DR	WPI: 2001-639362/73.
PT	P-PSDB: ABG12724.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PS	
XX	Claim 1; SEQ ID NO 12715; 103bp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 1082 BP; 193 A; 334 C; 353 G; 202 T; 0 other;
	Query Match 67.1%; Score 923.6; DB 23; Length 1082;
	Best Local Similarity 96.5%; Pred. No. 4.4e-161;
	Matches 1042; Conservative 0; Mismatches 24; Indels 14; Gaps 9
OY	299 CCCAGCCTCTGCCCGGGACCCCGGCCTTCCAGGACGCGGGCCACCATTGACGCCAG 358
Db	1 CCCAGCCTCTGCCCGGGACCCCGGCCTTCCAGGACGCGGGCCACCATTGACGCCAG 60
OY	359 GGCTTGCCGGGCGGGATGGCGCGAGAGGCGCGAGCGCGCGCCCGGGGCTTCGGGAGAG 418
Db	61 GGCTTGCCGGGCGGGATGGCGCGAGAGGCGCGAGCGCGCGCCCGGGGCTTCGGGAGAG 120

[illegible]

Search completed: June 21, 2003, 09:46:23
Job time : 376 secs

XX	AAST76911	ID	AAST76911 standard; cDNA; 1082 BP.
XX	AAST76911;	AC	
XX	AAST76911;	AS	
DT	13-FEB-2002	(first entry)	
XX	DNA encoding novel human diagnostic protein #12715.		
DE			
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;	KW	
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss.	RW	
OS	Homo sapiens.		
XX			
PN	WO200175067-A2.		
PD	11-OCT-2001.		
PF	30-MAR-2001; 2001WO-US08631.		
PR	31-MAR-2000; 2000US-0540217.		
XX	23-AUG-2000; 2000US-0649167.		
PA	(HYSE-) HYSEQ INC.		
PI	Drmnac RT, Liu C, Tang YT;		
DR	WPI: 2001-639362/73.		
XX	P-PSDB: ABG12724.		
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
PS	Claim 1; SEQ ID NO 12715; 103bp; English.		
XX			
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. AAS64197-AAS94564 represent novel human		
CC	diagnostic coding sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
XX	at ftp.wipo.int/pub/published_pct_sequences.		
SQ	Sequence 1082 BP; 193 A; 334 C; 353 G; 202 T; 0 other;		
	Query Match	67.1%; Score 923.6; DB 23; Length 1082;	
	Best Local Similarity	96.5%; Pred. No. 4.4e-161;	
	Matches 1042; Conservative	0; Mismatches 24; Indels 14; Gaps 9	
OY	299 CCCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGCACGGCGACCACCATGGACGCG	358	
Db	1 CCCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGCACGGCGACCACCATGGACGCG	60	
OY	359 GGCTTGCCGGGCGGGATGGCGCGAGAGCGCGGACGGCGCGCCGGGGCTTCGGGAGAG	418	
Db	61 GGCTTGCCGGGCGGGATGGCGCGAGAGCGCGGACGGCGCGCCGGGGCTTCGGGAGAG	120	

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Db 311 GGGCCACCATGGCAGCAGGGCTTCCGGGGCCGCGATGGCCGACGCGCCGACGCGCC 370
QY 400 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGAGCCGGAGCTGGCCGGGACCTCGAG 459
Db 371 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGAGCCGGAGCTGGCCGGGACCTCGAG 430
QY 460 GGACCCCGGGCGCGAGAGAGGCGGAGACCCGGGGCCACCGGGCCCTGCGGGAGATG 519
Db 431 GGACCCCGGGCGCGAGAGAGGCGGAGACCCGGGGCCACCGGGCCCTGCGGGAGATG 490
QY 520 CTCGGTGCCTCCGGGATCCGGCTTCAGCGGCCAAGCGCTCCAGAGCCGGGGTGCCTCCGCC 579
Db 491 CTCGGTGCCTCCGGGATCCGGCTTCAGCGGCCAAGCGCTCCAGAGCCGGGGTGCCTCCGCC 550
QY 580 GTCGACGACACCTTGGCTTCGACCGCGTGTGTGAGACGAGGAGGACATTACGACGC 639
Db 551 GTCGACGACACCTTGGCTTCGACCGCGTGTGTGAGACGAGGAGGACATTACGACGC 610
QY 640 CGTCACCGGCAAGTTTACCTGCGCAGGTGCTGGGGTCTACTACTTCCCGCTCCATGCCAC 699
Db 611 CGTCACCGGCAAGTTTACCTGCGCAGGTGCTGGGGTCTACTACTTCCCGCTCCATGCCAC 670
QY 700 CGTCACCGGCGCCAGCTGCGAGTTTGTATGTGTGAGAAATGGCGAATCCATTTGCTCTTT 759
Db 671 CGTCACCGGCGCCAGCTGCGAGTTTGTATGTGTGAGAAATGGCGAATCCATTTGCTCTTT 730
QY 760 CTTCACATTTTTCGGGGGGGTGGCCCAAGCCGCTGCTCTCGGGGGGGGCCATGTGAG 819
Db 731 CTTCACATTTTTCGGGGGGGTGGCCCAAGCCGCTGCTCTCGGGGGGGGCCATGTGAG 790
QY 820 GCTGGACCTGAGAACCAATGTGTGTGAGGTGGGTGTGGGTACTACATTTGGCACTA 879
Db 791 GCTGGACCTGAGAACCAATGTGTGTGAGGTGGGTGTGGGTACTACATTTGGCACTA 850
QY 880 TGGCAGCATCAAGACAGACAGCACTTCTCCGATTTCTGTGTACTTCCGATGGCAGAG 939
Db 851 TGGCAGCATCAAGACAGACAGCACTTCTCCGATTTCTGTGTACTTCCGATGGCAGAG 910
QY 940 CTCGCCAGTCTTTGCTTATGTGCCACTGTCAAGATGACCTCATGCTCTACTCTAGAGG 999
Db 911 CTCGCCAGTCTTTGCTTATGTGCCACTGTCAAGATGACCTCATGCTCTACTCTAGAGG 970
QY 1000 AGGGTGTGAGGCTGACCAACCAAGGTCATCCAGAGAGGGGTGGGCCCTGGAAATATTGAA 1059
Db 971 AGGGTGTGAGGCTGACCAACCAAGGTCATCCAGAGAGGGGTGGGCCCTGGAAATATTGAA 1030
QY 1060 TGACTAGGAGGTGGGGTAGAGCACTTCCGCTCTGCTGTGCAAGAAATGGGACAGT 1119
Db 1031 TGACTAGGAGGTGGGGTAGAGCACTTCCGCTCTGCTGTGCAAGAAATGGGACAGT 1090
QY 1120 GGCCTGTGCGATCAGCTGTGGCAGCATGGGGCAGTGGGTGATTTCTGCCAAGACAG 1179
Db 1091 GGCCTGTGCGATCAGCTGTGGCAGCATGGGGCAGTGGGTGATTTCTGCCAAGACAG 1150
QY 1180 AGGAGTGTGCTGTGCTGGCAAGTGTAGTCCCGAGTTGCTGTGTGTCAGAGAGCCACAG 1239
Db 1151 AGGAGTGTGCTGTGCTGGCAAGTGTAGTCCCGAGTTGCTGTGTGTCAGAGAGCCACAG 1210
QY 1240 TGGGGTGTCTCTTCTGCTGTCTGTCTGTCTGTGATCTCCACCCCTGCTGCTCT 1299
Db 1211 TGGGGTGTCTCTTCTGCTGTCTGTCTGTCTGTGATCTCCACCCCTGCTGCTCT 1270
QY 1300 GGGGGCGGGCTTTTCTCAGAGATCACTCAATAAAGCTTAAGAACCTCATTAAGAAAAA 1359
Db 1271 GGGGGCGGGCTTTTCTCAGAGATCACTCAATAAAGCTTAAGAACCTCAAGAAAAA 1330
QY 1360 AAAAAA 1366
Db 1331 AAAAAA 1337

Sequence 1, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Lelby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1338
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536-1
Query Match 94.2%; Score 1296.6; DB 4; Length 1338;
Best Local Similarity 99.6%; Pred. No. 7.7e-252;
Matches 1310; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 54 CCAGGACTGGGGTGGAGGCGAGAGGGGGGCTGGCCGGGGAGAAAGCGGGGGTGG 113
Db 15 CCGGAGCTGGGGTGGAGGCGAGAGGGGGGCTGGCCGGGGAGAAAGCGGGGGTGG 74
QY 114 AGCACACCAACTGGAGGGTCCGAGTAGCAGAGCGCCCGAAGAGAGGCCATCGGGAGCC 173
Db 75 AGCACACCAACTGGAGGGTCCGAGTAGCAGAGCGCCCGAAGAGAGGCCATCGGGAGCC 134
QY 174 GGGAGGGGGACTCCGAGAGAGACCCCGGCTCCGGGCTCCGGGTGCGAGGGCTTTAGGC 233
Db 135 GGGAGGGGGACTCCGAGAGAGACCCCGGCTCCGGGCTCCGGGTGCGAGGGCTTTAGGC 194
QY 234 CACTCTCTGTCCTCTGCTCTGCTGCTGGGCTGGGGGCTGCGCCCGCACTGGAGACAA 293
Db 195 CACTCTCTGTCCTCTGCTCTGCTGCTGGGCTGGGGGCTGCGCCCGCACTGGAGACAA 254
QY 294 AGATCCCAAGCTTGTGCTCCGGGGACCCCGGCTTCCAGGACGCGGGGCCACCATGGA 353
Db 255 AGATCCCAAGCTTGTGCTCCGGGGACCCCGGCTTCCAGGACGCGGGGCCACCATGGA 314
QY 354 GCCAGGGCTTGGCGGGCGCGATGGCCGAGAGGGCCCGAGAGGGCCCGGGGGCTCCGG 413
Db 315 GCCAGGGCTTGGCGGGCGCGATGGCCGAGAGGGCCCGAGAGGGCCCGGGGGCTCCGG 374
QY 414 GAGAGAAAGGCGAGGGCGGGAGCGCGGAGCTCCGGGACCTCGAGGGAGACCCCGGGCGC 473
Db 375 GAGAGAAAGGCGAGGGCGGGAGG-CGGGACTGCGGGGACCTCGAGGGAGACCCCGGGCGC 433
QY 474 GAGAGAGGGCGGGACCCCGGGGGCCACCGGGGCTGCTGGGGAGTGTGCTGCTCCG 533
Db 434 GAGAGAGGGCGGGACCCCGGGGGCCACCGGGGCTGCTGGGGAGTGTGCTGCTCCG 493
QY 534 GATCCGCTTTCAGAGGCCAAGCGCTCCAGAGCCGGGTGCTCCCGCTGTGAGCCACCT 593
Db 494 GATCCGCTTTCAGAGGCCAAGCGCTCCAGAGCCGGGTGCTCCCGCTGTGAGCCACCT 553
QY 594 TGCCTTTCAGAGCGGCTGCTGGTGAAGCAGAGGACATTAGAGAGCCGCTGACCGGCAAGT 653
Db 554 TGCCTTTCAGAGCGGCTGCTGGTGAAGCAGAGGACATTAGAGAGCCGCTGACCGGCAAGT 613
QY 654 TCACCTTCAGAGTGCCTGGGGGTACTACTTGGCGCTCATGCAACCGCTTACCGGGCA 713
Db 614 TCACCTTCAGAGTGCCTGGGGGTACTACTTGGCGCTCATGCAACCGCTTACCGGGCA 673
QY 714 GCTGCAAGTTTGTATCTGTGAAGATGGCGAATCATTTGCTTTTCTCAAGTTTTCG 773
Db 674 GCTGCAAGTTTGTATCTGTGAAGATGGCGAATCATTTGCTTTTCTCAAGTTTTCG 733
QY 774 GGGGGTGGCCCAAGCCAGCTCGCTCGGGGGGGGGCCATGTGAGGCTGGAGGCTGAGG 833
Db 734 GGGGGTGGCCCAAGCCAGCTCGCTCGGGGGGGGGCCATGTGAGGCTGGAGGCTGAGG 793

QY	834	ACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTTGGCATCTATGCCAGATCAAGA	893
Db	794	ACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTTGGCATCTATGCCAGATCAAGA	853
QY	894	CAGACAGACCTTCTCCGGATTTTCGTTGGGTGTACTCCGACTGGCACAGCTCCCAAGCTTTG	953
Db	854	CAGACAGACCTTCTCCGGATTTTCGTTGGGTGTACTCCGACTGGCACAGCTCCCAAGCTTTG	913
QY	954	CTTAGTGCCCACTGCAAAGTAGCTCATAGCTCTCACTCTAGAAAGAGGTGTGAGCGTG	1013
Db	914	CTTAGTGCCCACTGCAAAGTAGCTCATAGCTCTCACTCTAGAAAGAGGTGTGAGCGTG	973
QY	1014	ACAACAGAGTCATCCAGGAGGGCTGGCCCCCTTGGAAATATTTGTGAATGACTAGGAGAGTG	1073
Db	974	ACAACCTGTGTCATCCAGGAGGGCTGGCCCCCTTGGAAATATTTGTGAATGACTAGGAGAGTG	1033
QY	1074	GGGTAGAGCACTCTCCCTGTGCTGTGTGTGGCAAGAAATGGGAACAATGGCTGTCTCCATC	1133
Db	1034	GGGTAGAGCACTCTCCCTGTGCTGTGTGTGGCAAGAAATGGGAACAATGGCTGTCTCCATC	1093
QY	1134	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTTCGCCCAAGCAGCAGAGAGTGTCTGTG	1193
Db	1094	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTTCGCCCAAGCAGCAGAGAGTGTCTGTG	1153
QY	1194	CTGGCAAGTGTAAGTCCCCAGTTTGCTTGTGTCCAGAGAGCCACAGTGGGGTGTCTCTTT	1253
Db	1154	CTGGCAAGTGTAAGTCCCCAGTTTGCTTGTGTCCAGAGAGCCACAGTGGGGTGTCTCTTT	1213
QY	1254	CTGTGTCCTGTCTTCTCTGTGATCCTCCCAACCCCTCTGTCTCTCTGTGGGCGGCGCTTTT	1313
Db	1214	CTGTGTCCTGTCTTCTCTGTGATCCTCCCAACCCCTCTGTCTCTCTGTGGGCGGCGCTTTT	1273
QY	1314	TCTTAGAGTACTCAATTAACCTTAAGAACCTCATMAAAAAAAAAAAAAAAAAAAAAA	1368
Db	1274	TCTTAGAGTACTCAATTAACCTTAAGAACCTCATMAAAAAAAAAAAAAAAAAAAAAA	1328

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RESULT 3
US-09-336-536--2
Sequence 2, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, S.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 728
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536--2

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Query Match	52.1%	Score 717;	DB 4;	Length 728;
Best Local Similarity	99.98%	Pred. No. 1.4e-135;		
Matches 728; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1.

QY	227	ATGAGGGCCACCTCCCTGCTCTCTGCTCTCGGGGCTGGGGGCGCGGCTCGCCCCCACTGGAC	286
Db	1	ATGAGGGCCACCTCCCTGCTCTCTGCTCTCGGGGCTGGGGGCGCGGCTCGCCCCCACTGGAC	60
QY	287	GACAAACAAGATCCCCAGCTCTGCGCCGGGGGCAACCCCGGCTTCCAGGAGCAAGCGCGGGCCAC	346
Db	61	GACAAACAAGATCCCCAGCTCTGCGCCGGGGGCAACCCCGGCTTCCAGGAGCAAGCGCGGGCCAC	120
QY	347	CATGGCAGCCAGGGGCTTGGCGGGCGGGCATGGCGCGGACGGCCGGAGAGGGCGCGCCGGG	406
Db	121	CATGGCAGCCAGGGGCTTGGCGGGCGGGCATGGCGCGGACGGCGGGAGAGGGCGCGCCGGG	180

QY	407	GCTCCGGAGAGAAAGCCAGGGCGGGAGGCTGGGACTGTCCGGGACTCTCAGGGAGACCC	466
Db	181	GCTCCGGGAGAGAAAGCGCAGGGCGGGAGAG - GGGAGCTCCGGGACCTCTCGAGGGAGACCC	239
QY	467	GGGCGCGAGAGAGAGCGGGAGACCGCGGGGGCCACCGGGCCCTGGCGGGGAGATGTCGGTG	526
Db	240	GGGCGCGAGAGAGAGCGGGAGACCGGGGGGCCACCGGGCCCTGCGGGGAGATGTCGGTG	299
QY	527	CTCTCCGCGATCCGCTCTTCAGCGCCAAAGCGCTCCAGAGCCGGGTGCTCCGCGCGCTTGAC	588
Db	300	CTCTCCGCGATCCGCTCTTCAGCGCCAAAGCGCTCCAGAGCCGGGTGCTCCGCGCGCTTGAC	359
QY	587	GCACCCCTTGCCCTTCGACCGCGCTGCTGTGAACGACGAGGACATTCAGACGCGCTCAC	646
Db	360	GCACCCCTTGCCCTTCGACCGCGCTGCTGTGAACGAGCGAGCATTCAGACGCGCTCAC	419
QY	647	GGCAGCTTCACCTGGCCAGGTGCTGGGGGCTACTACTTCGGCGGTCAGTCCAGCCGCTTAC	706
Db	420	GGCAGCTTCACCTGGCCAGGTGCTGGGGGCTACTACTTCGGCGGTCAGTCCAGCCGCTTAC	479
QY	707	CGGGCCAGCCTGCGAGTTTGATCTGGTGAGAGATGGCGAATCCATTGGCTCTTTCTTCAG	766
Db	480	CGGGCCAGCCTGCGAGTTTGATCTGGTGAGAGATGGCGAATCCATTGGCTCTTTCTTCAG	539
QY	767	TTTTTGGGGGGGTGGCCCAAGCCAGCCTTGCTCTGGGGGGGCCCATGTGAGGCTGGAG	828
Db	540	TTTTTGGGGGGGTGGCCCAAGCCAGCCTTGCTCTGGGGGGGGCCATGTGAGGCTGGAG	599
QY	827	CTGAGGACCAATGTGGGTGAGAGGTGGGTGGGTGACTACATTTGGATATATGCGAGC	886
Db	600	CTGAGGACCAATGTGGGTGAGAGGTGGGTGGGTGACTACATTTGGATATATGCGAGC	659
QY	887	ATCAAGACAGACAGCACCTTCTCCGATTTCTGGGTACTCCGACTGGACAGCTCCCA	946
Db	660	ATCAAGACAGACAGCACCTTCTCCGATTTCTGGGTACTCCGACTGGACAGCTCCCA	719
QY	947	GTCCTTTGCT 955	
Db	720	GTCCTTTGCT 728	

RESULT 4
 US-09-336-536-8
 Sequence 8, Application US/09336536
 Patent No. 6406884
 GENERAL INFORMATION:
 APPLICANT: Leiby, K.
 APPLICANT: McKay, C.
 APPLICANT: Bossone, S.
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-144
 CURRENT APPLICATION NUMBER: US/09/336,536
 CURRENT FILING DATE: 1999-06-18
 NUMBER OF SEQ. ID NOS.: 75
 SOFTWARE: PatentIn Ver. 2.0
 SEQ. ID NO. 8
 LENGTH: 1263
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-336-536-8

	Query Match	50.3%;	Score 652.8;	DB 4;	Length 1263;
	Best Local Similarity	78.0%;	Pred. No. 1.1e-130;		
	Matches 917;	Conservative	0;	Mismatches 237;	Indels 22; Gaps 6
QY	189	GAGAGACACCCGACCTCCGCGCTCCCGGTGCCAGCGCTATGAGGCCACTCTGTCTGTC	248		
Db	97	GAGAGTTCCTGGAGTCTGAGCCTCCGGGGTCCACACCATGAGCCACTTGTGCCCTTC	156		
QY	249	TGCTCTGGGACCTGGCGCGCGGCTGCCCCCACTGAGGACGACAAAGAATCCCCAGCCTCT	308		
Db	157	TGCTTCTGGGTGTGGTGTCAGGCTCTCCCTCTGTGAGACAAAGAATCCCCAGCCTGT	216		


```
QY 347 CATGACAGCCAGGCTTCCGCGGCGCGATGCGCGACGGCCGCGACGGCGCGCCGG 406
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CATGACAGCCAGGCTTCCGCGGCGCGATGCGCGACGGCCGCGACGGCGCGCCGG 180
QY 407 GCTCCGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGCTGCGGGACCTCGAGGGAGCC 466
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GCTCCGGAGAGAAAGGAGGAGGCGGAGGCGGAGCTGCGGGACCTCGAGGGAGCC 240
QY 467 GGGCGCGAGAGAGAGGCGGAGGCGCGGCGCGACCGCGCGCTGCGGAGAGTGTGCTG 526
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GGGCGCGAGAGAGAGGCGGAGGCGCGGCGCGACCGCGCGCTGCGGAGAGTGTGCTG 300
QY 527 CTTCCGGAGATCGCTTTCAGCGCGGCGCTCGAGAGCGCGGCTGCTCGCGCTGAC 586
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 CCGCGAGATGAGCTTTCAGCTGCGCGAGGATCGAGAGCGCGGATGCTCGCGCGAG 360
QY 587 GCACCTTGGCTTTCAGCGCGGCTGCTGTAAGAGAGGAGGACATTAAGAGCGCGTACC 646
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 ACACCTTACCTTTCAGCGCGGCTGCTGTAAGAGAGGAGGACATTAAGAGCGCGTACC 420
QY 647 GCGAGTTACCTTTCAGCGGCTGCTGAGGCTGCTGTAAGAGGAGGACATTAAGAGCGCGTACC 706
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Db 421 GCGAGTTACCTTTCAGCGGCTGCTGAGGCTGCTGTAAGAGGAGGACATTAAGAGCGCGTACC 480
QY 707 GCGGCGAGCTTTCAGGTTGATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 766
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Db 481 GCGGCGAGCTTTCAGGTTGATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 767 TTTTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 826
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 TTTTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 600
QY 827 CCTGAGAGACCAAGTGTGGGTGAGGTGGGTGAGTGTGGGTGAGTGTGGGTGAGTGTGG 886
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CCTGAGAGACCAAGTGTGGGTGAGGTGGGTGAGTGTGGGTGAGTGTGGGTGAGTGTGG 660
QY 887 ATCAAGACAGACAGACCTTTCGCGATTTCTGTGTAAGAGGAGGAGGAGGAGGAGG 946
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 ATCAAGACAGACAGACCTTTCGCGATTTCTGTGTAAGAGGAGGAGGAGGAGGAGGAGG 720
QY 947 GTCTTTGCT 955
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Db 721 GTCTTTGCT 729
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RESULT 8
US-09-140-804-10
Sequence 10, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Shepard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140, 804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056, 983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 729
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39
OTHER INFORMATION: polypeptide of SEQ ID NO:2.
US-09-140-804-10

Query Match 36.6%; Score 504; DB 4; Length 729;
Best Local Similarity 57.6%; Pred. No. 7.5e-93;
Matches 419; Conservative 145; Mismatches 164; Indels 0; Gaps 0;

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QY 227 ATGAGGCCACTCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGAGGCCACTCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 287 GACAACAAGATCCCAAGCTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 346
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Db 61 GAYAAAYAAARACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 347 CATGACAGCCAGGCTTCCGCGGCGCGATGCGCGACGGCCGCGACGGCGCGCCGG 406
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Db 121 CATGACAGCCAGGCTTCCGCGGCGCGATGCGCGACGGCCGCGACGGCGCGCCGG 180
QY 407 GCTCCGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGCTGCGGGACCTCGAGGGAGCC 466
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Db 181 GCTCCGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGCTGCGGGACCTCGAGGGAGCC 240
QY 467 GGGCGCGAGAGAGAGGCGGAGGCGCGGCGCGACCGCGCGCTGCGGAGAGTGTGCTG 526
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GGGCGCGAGAGAGAGGCGGAGGCGCGGCGCGACCGCGCGCTGCGGAGAGTGTGCTG 300
QY 527 CTTCCGGAGATCGCTTTCAGCGCGGCGCTCGAGAGCGCGGCTGCTCGCGCTGAC 586
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 CCGCGAGATGAGCTTTCAGCTGCGCGAGGATCGAGAGCGCGGATGCTCGCGCGAG 360
QY 587 GCACCTTGGCTTTCAGCGCGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 646
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GCNCNTNCCNTTTCAGGTTGATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 707 GCGGCGAGCTTTCAGGTTGATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 766
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 GCGGCGAGCTTTCAGGTTGATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 647 GCGAGTTACCTTTCAGCGGCTGCTGAGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAG 706
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GCGAGTTACCTTTCAGCGGCTGCTGAGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 707 TTTTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 826
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 TTTTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 600
QY 827 CCTGAGAGACCAAGTGTGGGTGAGGTGGGTGAGTGTGGGTGAGTGTGGGTGAGTGTGG 886
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CCTGAGAGACCAAGTGTGGGTGAGGTGGGTGAGTGTGGGTGAGTGTGGGTGAGTGTGG 660
QY 887 ATCAAGACAGACAGACCTTTCGCGATTTCTGTGTAAGAGGAGGAGGAGGAGGAGGAGG 946
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 ATCAAGACAGACAGACCTTTCGCGATTTCTGTGTAAGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 947 GTCTTTGCT 954
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Db 721 GTCTTTGCT 728
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RESULT 9
US-09-336-536-74
Sequence 74, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Lelby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336, 536
CURRENT FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 74
LENGTH: 601
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

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; NAME/KEY: modified_base
; LOCATION: all "n" positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-336-536-74

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Query Match	18.7%;	Score 257.8;	DB 4;	Length 601;
Best Local Similarity	72.0%;	Pred. No. 1.8e-43;		
Matches 365; Conservative	0;	Mismatches 134;	Indels 8;	Gaps 2

[illegible]

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RESULT 10
US-09-188-930-26
Sequence 26, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.101cl
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 393
TYPE: DNA
ORGANISM: Rat
US-09-188-930-26

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Query Match	10.98;	Score 149.6;	DB 3;	Length 393;
Best Local Similarity	-69.18;	Pred. No. 8.6e-22;		
Matches 250; Conservative	0;	Mismatches 104;	Indels 8;	Gaps 3

OY	66	TTGACGGCAGGGGAGGGGGCGCTGGCGCCGGGGAGAGCGCGGGGGCTGTGACGACACCAAC	125
Dd	33	TTGTACGAGGAGCGCAGGGCGCTGCCCTGGTGGGGTATGAAGTGGGAGACGAGGCCAGGAGG	92
OY	126	TGAGAGGGTCCGAGTATGACGAGCGCCCGGAGAGAGCCATTCGGGGAGCCGGGAGGGGGAC	185
Dd	93	GTCTGAGGAAGCCATTCAAAGCAGACAGCTGGGGAGAGCTGGGGAGCCGGGAAAGGCGCTAC	153
OY	186	TG-----CGAGAGGACCCCGGCGGTCCGGGCTCCCGGTGCGCAGGCGTATGAGGCGACTCC	239
Dd	153	AGACTACAAAGAGAGATCCTGGCGGTGGGCGCTCTCGGGTCAATCATTGAGGCCACTTC	212
OY	240	TGCTGTCTGCTCTCTGCGGCTTGCGGGCGCGGCTCGCCCCCACTGGAGCACAACAGTTC	299
Dd	213	TTGGCCGTGCTTTCGTGGGTCTGGGATCAGGCTCTCTCTGTGGACACACAACAAAGATTCC	273
OY	300	CCAGGCTTGTCCCGGGGGACCCCGGCGCTTCCAGGAGACCCGGGCGACCATGGAGCCAGG	358
Dd	273	CCAGGCTGTGTCCCGGGGCAAGCCGGCGCTCCGAGGACACAGGCGCACCGCAGGCCAAG	332
OY	360	GCATTGCCGGGCGCGATGSGCCGCGACGCGCGCGAGCGCGCGCCCGGGGCTTCGGGAGAGA	419
Dd	333	GCGTGGCTGGCGTGAAGGCC--TGATGGCGCGAGAGGTCACCCGGAG--TCCGGGAGAGA	390
OY	420	AA 421	
Dd	391	AA 392	

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1      RESULT 11
2      US-08-463-911-1
3      Sequence 1/, Application US/08463911
4      Patent No. 5863330
5      GENERAL INFORMATION:
6      APPLICANT: Scherer, Philipp E.
7      APPLICANT: Lodish, Harvey F.
8      TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
9      TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
10     NUMBER OF SEQUENCES: 7
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
13     STREET: Two Millita Drive
14     CITY: Lexington
15     STATE: Massachusetts
16     COUNTRY: USA
17     ZIP: 02173
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/463,911
25     FILING DATE:
26     CLASSIFICATION: 530
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Granahan, Patricia
29     REGISTRATION NUMBER: 32,227
30     REFERENCE/DOCKET NUMBER: WH95-05
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: (617) 861-6240
33     TELEFAX: (617) 861-9540
34     INFORMATION FOR SEQ. ID NO. 1:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 1276 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     MOLECULE TYPE: DNA (genomic)
41     FEATURE:
42     NAME/KEY: CDS
43     LOCATION: 46..786
44     US-08-463-911-1

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Query Match 6.6%; Score 90.6; DB 2; Length 1276;
 Best Local Similarity 51.5%; Pred. No. 7.3e-10;
 Matches 316; Conservative 0; Mismatches 279; Indels 18; Gaps 4;

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QY 333 GCACCGCGGCGCCACCATGACGACGAGGCTTCCGCGCGCGCGATGCGCGCGCGCGCGCG 392
D 170 GGATGGAGGAGGATCCGACGATCCTGCGCCACATGCGACACCGCGCGCGCGATGCGCGAG 229
QY 393 ACGCGCGCGCGCGCGCGCGCGCGAGAGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGAGC 452
D 230 ATGGCACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
QY 453 CTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 512
D 290 AGACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 349
QY 513 GGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 568
D 350 GCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
QY 569 GTGCGTCCGCGCGTGTG-----ACGACCGCTTGGCGCTTGGAGCGCGGTGTGTGTGTGT 620
D 410 TGGAGACCGCGCTACTGTTTCCCATGATGATGATGATGATGATGATGATGATGATGATGAT 469
QY 621 AGCAGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
D 470 AAGAGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 529
QY 681 ACTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
D 530 ACTTCTTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
QY 741 GCGAATCATTTGCTTTTCTTCCAGTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 800
D 590 ACAAGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 846
QY 801 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 857
D 647 CTGGCTCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
QY 858 TGGGTGACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917
D 707 ATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
QY 918 TGGGTACTCGA 930
D 767 TTCTCTACATGA 779

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RESULT 12
 US-08-463-911-6
 : Sequence 6, Application US/08463911
 : Patent No. 5869330
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 : GENERAL INFORMATION:
 : APPLICANT: Scherer, Philipp E.
 : APPLICANT: Lodish, Harvey F.
 : TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
 : NUMBER OF SEQUENCES: 7
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02173
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463, 911
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: WHI95-05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1313 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 73..804
 US-08-463-911-6

Query Match 6.0%; Score 82.2; DB 2; Length 1313;
 Best Local Similarity 50.1%; Pred. No. 3.6e-08;
 Matches 316; Conservative 0; Mismatches 303; Indels 12; Gaps 4;

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QY 321 CCGGCGCTTCCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 380
D 194 CGGCGATCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 253
QY 381 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440
D 254 CCCCTGTGAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 313
QY 441 GACTCGCGGAGACCTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
D 314 GTGAACCGGAGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
QY 501 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 560
D 374 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
QY 561 AGAGCGCGGTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 620
D 431 AGACTTACGTTACTATC---CCAACATGCCCATTCGCTTACCAAGATCTTACATC 487
QY 621 AGCAGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
D 488 AGCAAAACCACTATGATGCTCCAGTGTAATTCACATGCAACATTCCTGGGCTGACT 547
QY 681 ACTTCGCGCTCATAGCAGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
D 548 ACTTGGCTACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
QY 741 GCGAATCATTTGCTTTTCTTCCAGTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 800
D 608 ACAAGGTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 664
QY 801 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 859
D 665 CCGGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 724
QY 860 -GCTGACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917
D 725 AAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784
QY 918 TGGGTACTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 948
D 785 TTCTCTACATGACACCACTGATCACAAGT 815

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RESULT 13
 US-09-140-804-9

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 13:56:00 ; Search time 252 Seconds
(Without alignments)
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Title: US-09-944-944-41

Perfect score: 1377

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Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1377	100.0	1377	9	US-09-944-403-41
3	1377	100.0	1377	9	US-09-944-896-41
4	1377	100.0	1377	9	US-09-944-944-41
5	1377	100.0	1377	9	US-09-944-907-41
6	1377	100.0	1377	9	US-09-944-929-41
7	1377	100.0	1377	9	US-10-028-072-361
8	1377	100.0	1377	9	US-10-121-049-361
9	1377	100.0	1377	9	US-10-123-904-361
10	1377	100.0	1377	9	US-10-140-470-361
11	1377	100.0	1377	9	US-10-175-746-361
12	1377	100.0	1377	9	US-10-176-918-361
13	1377	100.0	1377	9	US-10-137-865-361
14	1377	100.0	1377	9	US-10-140-474-361
15	1377	100.0	1377	9	US-10-142-431-361
16	1377	100.0	1377	9	US-10-143-114-361
17	1377	100.0	1377	9	US-10-140-002-361
18	1377	100.0	1377	9	US-10-142-419-361
19	1377	100.0	1377	9	US-10-142-419-361

20	1377	100.0	1377	9	US-10-123-262-361	Sequence 361, App
21	1377	100.0	1377	9	US-10-142-423-361	Sequence 361, App
22	1377	100.0	1377	9	US-10-121-050-361	Sequence 361, App
23	1377	100.0	1377	9	US-10-141-755-361	Sequence 361, App
24	1377	100.0	1377	9	US-10-143-032-361	Sequence 361, App
25	1377	100.0	1377	9	US-10-123-108-361	Sequence 361, App
26	1377	100.0	1377	9	US-10-123-236-361	Sequence 361, App
27	1377	100.0	1377	9	US-10-123-261-361	Sequence 361, App
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29	1377	100.0	1377	9	US-10-140-928-361	Sequence 361, App
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31	1377	100.0	1377	9	US-10-123-292-361	Sequence 361, App
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33	1377	100.0	1377	9	US-10-124-819-361	Sequence 361, App
34	1377	100.0	1377	9	US-10-124-822-361	Sequence 361, App
35	1377	100.0	1377	9	US-10-140-925-361	Sequence 361, App
36	1377	100.0	1377	9	US-10-160-498-361	Sequence 361, App
37	1377	100.0	1377	9	US-09-944-884-41	Sequence 41, App
38	1377	100.0	1377	9	US-10-121-041-361	Sequence 361, App
39	1377	100.0	1377	9	US-10-121-043-361	Sequence 361, App
40	1377	100.0	1377	9	US-10-121-047-361	Sequence 361, App
41	1377	100.0	1377	9	US-10-123-215-361	Sequence 361, App
42	1377	100.0	1377	9	US-10-123-902-361	Sequence 361, App
43	1377	100.0	1377	9	US-10-123-908-361	Sequence 361, App
44	1377	100.0	1377	9	US-10-123-909-361	Sequence 361, App
45	1377	100.0	1377	9	US-10-123-910-361	Sequence 361, App

ALIGNMENTS

RESULT 1
US-09-944-413-41
; Sequence 41, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Batstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gertitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067, 411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694
; PRIOR FILING DATE: December 16, 1997

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1 PRIOR APPLICATION NUMBER: 60/069,702
2 PRIOR FILING DATE: December 16, 1997
3 PRIOR APPLICATION NUMBER: 60/069,870
4 PRIOR FILING DATE: December 17, 1997
5 PRIOR APPLICATION NUMBER: 60/069,873
6 PRIOR FILING DATE: December 17, 1997
7 PRIOR APPLICATION NUMBER: 60/068,017
8 PRIOR FILING DATE: December 18, 1997
9 PRIOR APPLICATION NUMBER: 60/070,440
10 PRIOR FILING DATE: January 5, 1998
11 PRIOR APPLICATION NUMBER: 60/074,086
12 PRIOR FILING DATE: February 9, 1998
13 PRIOR APPLICATION NUMBER: 60/074,092
14 PRIOR FILING DATE: February 9, 1998
15 PRIOR APPLICATION NUMBER: 60/075,945
16 PRIOR FILING DATE: February 25, 1998
17 PRIOR APPLICATION NUMBER: 60/112,850
18 PRIOR FILING DATE: December 16, 1998
19 PRIOR APPLICATION NUMBER: 60/113,296
20 PRIOR FILING DATE: December 22, 1998
21 PRIOR APPLICATION NUMBER: 60/146,222
22 PRIOR FILING DATE: July 28, 1999
23 PRIOR APPLICATION NUMBER: PCT/US98/19330
24 PRIOR FILING DATE: September 16, 1998
25 PRIOR APPLICATION NUMBER: PCT/US98/25108
26 PRIOR FILING DATE: December 1, 1998
27 PRIOR APPLICATION NUMBER: 09/216,021
28 PRIOR FILING DATE: December 16, 1998
29 PRIOR APPLICATION NUMBER: 09/218,517
30 PRIOR FILING DATE: December 22, 1998
31 PRIOR APPLICATION NUMBER: 09/254,311
32 PRIOR FILING DATE: March 3, 1999
33 PRIOR APPLICATION NUMBER: PCT/US99/12252
34 PRIOR FILING DATE: June 22, 1999
35 PRIOR APPLICATION NUMBER: PCT/US99/21090
36 PRIOR FILING DATE: September 15, 1999
37 PRIOR APPLICATION NUMBER: PCT/US99/28409
38 PRIOR FILING DATE: No. US20020136004A1ember 30, 1999
39 PRIOR APPLICATION NUMBER: PCT/US99/28313
40 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
41 PRIOR APPLICATION NUMBER: PCT/US99/28301
42 PRIOR FILING DATE: December 1, 1999
43 PRIOR APPLICATION NUMBER: PCT/US99/30095
44 PRIOR FILING DATE: December 16, 1999
45 PRIOR APPLICATION NUMBER: PCT/US00/03565
46 PRIOR FILING DATE: February 11, 2000
47 PRIOR APPLICATION NUMBER: PCT/US00/04414
48 PRIOR FILING DATE: February 22, 2000
49 PRIOR APPLICATION NUMBER: PCT/US00/05841
50 PRIOR FILING DATE: March 2, 2000
51 PRIOR APPLICATION NUMBER: PCT/US00/08439
52 PRIOR FILING DATE: March 30, 2000
53 PRIOR APPLICATION NUMBER: PCT/US00/14042
54 PRIOR FILING DATE: May 22, 2000
55 PRIOR APPLICATION NUMBER: PCT/US00/20710
56 PRIOR FILING DATE: July 28, 2000
57 PRIOR APPLICATION NUMBER: PCT/US00/32678
58 PRIOR FILING DATE: December 1, 2000
59 PRIOR APPLICATION NUMBER: PCT/US01/06520
60 PRIOR FILING DATE: February 28, 2001
61 NUMBER OF SEQ ID NOS: 120
62 SEQ ID NO 41
63 LENGTH: 1377
64 TYPE: DNA
65 ORGANISM: Homo Sapien
66 US-09-944-413-41

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Query Match          100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y      1 GACTAGTTCCTTGGAGTCGTGGAGAGAGAAACGGAGCCGCGCAGGAGCAACCAAGAC 60
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Db	61	TGGGTGACAGGACAGAGGAGGCGCTTGCCGGGAGAGCGCGGGGCTTGAGACCA	120
Qy	121	CCAACTGGAGGCTCCGGAGTAGCGAGCGCCCGGAAGAGAGCCATGGGGAGCGGGAGGG	180
Db	121	CCAACTGGAGGCTCCGGAGTAGCGAGCGCCCGGAAGAGAGCCATGGGGAGCGGGAGGG	180
Qy	181	GGAGCTGCGAGAGACCCCGCGCTCCGGGTCCGGTGCAGCGCTATGAGGCACTCT	240
Db	181	GGAGCTGCGAGAGACCCCGCGCTCCGGGTCCGGGTGCAGCGCTATGAGGCACTCT	240
Qy	241	GCTCTGCGCTCGGGGCTGGGGGGCGGGCTCGGCCCTACATGAGACAAACAATATCC	300
Db	241	GCTCTGCGCTCGGGGCTGGGGGGCGGGCTCGGCCCTACATGAGACAAACAATATCC	300
Qy	301	CAGCCTTGCCCGGGGACACCCCGGCTTTCAGAGCAAGCGGGGCAACATGGCAGCCAGG	360
Db	301	CAGCCTTGCCCGGGGACACCCCGGCTTTCAGAGCAACCGGGGCAACATGGCAGCCAGG	360
Qy	361	CTTGCCGGGCGCGCATGGCCGCGAGCGCGCGACGCGCGCCCGGGGCTCCGGAGAGA	420
Db	361	CTTGCCGGGCGCGCATGGCCGCGAGCGCGCGACGCGCGCCCGGGGCTCCGGAGAGA	420
Qy	421	AGCGAGGGGAGGAGGCGGAGCTCCGGAGACTCGAGAGGAGCCCGGGGCGCGAGAGA	480
Db	421	AGCGAGGGGAGGAGGCGGAGCTCCGGAGACTCGAGAGGAGCCCGGGGCGCGAGAGA	480
Qy	481	GCGGGGACCCCGGGGGCCACCGGGCTGCGGGGAGTGTCTGGTGCCTCGGATCCGC	540
Db	481	GCGGGGACCCCGGGGGCCACCGGGCTGCGGGGAGTGTCTGGTGCCTCGGATCCGC	540
Qy	541	CTTCAGGCGCAAGCGCTCCGAGAGCGGGGTGGCTCGCGCTGTGACGACCTTACCTT	600
Db	541	CTTCAGGCGCAAGCGCTCCGAGAGCGGGGTGGCTCGCGCTGTGACGACCTTACCTT	600
Qy	541	CTTCAGGCGCAAGCGCTCCGAGAGCGGGGTGGCTCGCGCTGTGACGACCTTACCTT	600
Db	541	CTTCAGGCGCAAGCGCTCCGAGAGCGGGGTGGCTCGCGCTGTGACGACCTTACCTT	600
Qy	601	CGACCGCTGTGTGTGAACGAGACGAGGACATTACGAGCCGTCACCGGCAAGTTACCTG	660
Db	601	CGACCGCTGTGTGTGAACGAGACGAGGACATTACGAGCCGTCACCGGCAAGTTACCTG	660
Qy	661	CCAGGTGCTGGGGCTACTACTTCGCGGTCCATGCGACCGGTCTACGGGGCAGCTGCA	720
Db	661	CCAGGTGCTGGGGCTACTACTTCGCGGTCCATGCGACCGGTCTACGGGGCAGCTGCA	720
Qy	721	GTTGATCTGTGTGAAGATGCGAATTCATTGCTCTTCTCCAGTTTTCGGGGGTG	780
Db	721	GTTGATCTGTGTGAAGATGCGAATTCATTGCTCTTCTCCAGTTTTCGGGGGTG	780
Qy	781	GCCCAAGCACAACCTCTCTCGGGGGGGGCAAGGTGAGGCTGAGAGCCTGAGAGCAAGT	840
Db	781	GCCCAAGCACAACCTCTCTCGGGGGGGGCAAGGTGAGGCTGAGAGCCTGAGAGCAAGT	840
Qy	841	GTGGGTGAGGTGGGTGTGGGTGATCTACATTGGCATCTATGCCAGCATCAAGACAGAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGTGATCTACATTGGCATCTATGCCAGCATCAAGACAGAG	900
Qy	901	CACCTTCTCGGAAATTTCTGTGTACTCCGACTGCGACAGCTCCCAAGTCTTGTAGTG	960
Db	901	CACCTTCTCGGAAATTTCTGTGTACTCCGACTGCGACAGCTCCCAAGTCTTGTAGTG	960
Qy	961	CCCACTGCAAAAGTGAAGTCAATGCTCACTCCCTGAAGAGAGGGGTGAGGTGCAACCA	1020
Db	961	CCCACTGCAAAAGTGAAGTCAATGCTCACTCCCTGAAGAGAGGGGTGAGGTGCAACCA	1020
Qy	1021	GGTCAATCCAGAGGAGGTGCGCCCTCGAATATTGTGAATGACTAGGAGGTGGGTAGA	1080
Db	1021	GGTCAATCCAGAGGAGGTGCGCCCTCGAATATTGTGAATGACTAGGAGGTGGGTAGA	1080
Qy	1081	GCACTTTCCTGCTGCTGCTGTGGCAAGAAATGGGAACAATGGCTGTCTGCGATCAAGTCTG	1140
Db	1081	GCACTTTCCTGCTGCTGCTGTGGCAAGAAATGGGAACAATGGCTGTCTGCGATCAAGTCTG	1140


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OY 1141 GCAGATGGGCGAGTGGTGGATTTCGCCAAGACAGAGAGTGTCTGTGGCGCA 1200
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DB 1141 GCAGATGGGCGAGTGGTGGATTTCGCCAAGACAGAGAGTGTCTGTGGCGCA 1200
OY 1201 GTGTAAGTCCCGCAAGTGTCTGTGGTCCAGAGACCGAGTGTCTGTGGTGC 1260
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DB 1201 GTGTAAGTCCCGCAAGTGTCTGTGGTCCAGAGACCGAGTGTCTGTGGTGC 1260
OY 1261 CTGCGCTCTGTGGTCTGTGGTCCAGACCGAGTGTCTGTGGTGTCTGTGGTGC 1320
    |||||||
DB 1261 CTGCGCTCTGTGGTCTGTGGTCCAGACCGAGTGTCTGTGGTGTCTGTGGTGC 1320
OY 1321 GATCAGCTCAATAAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAA 1377
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DB 1321 GATCAGCTCAATAAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 2
US-09-944-403-41
: Sequence 41, Application US/09944403
: Patent No. US20020165143A1
:
GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
:
FILE OF INVENTION: ACIDS ENCODING THE SAME
:
FILE REFERENCE: P2548P1C1
:
CURRENT FILING DATE: 2001-09-26
:
PRIOR APPLICATION NUMBER: 09/866,028
:
PRIOR FILING DATE: 2001-05-25
:
PRIOR APPLICATION NUMBER: 60/067,411
:
PRIOR FILING DATE: December 3, 1997
:
PRIOR APPLICATION NUMBER: 60/069,334
:
PRIOR FILING DATE: December 11, 1997
:
PRIOR APPLICATION NUMBER: 60/069,335
:
PRIOR FILING DATE: December 11, 1997
:
PRIOR APPLICATION NUMBER: 60/069,278
:
PRIOR FILING DATE: December 11, 1997
:
PRIOR APPLICATION NUMBER: 60/069,425
:
PRIOR FILING DATE: December 12, 1997
:
PRIOR APPLICATION NUMBER: 60/069,696
:
PRIOR FILING DATE: December 16, 1997
:
PRIOR APPLICATION NUMBER: 60/069,694
:
PRIOR FILING DATE: December 16, 1997
:
PRIOR APPLICATION NUMBER: 60/069,702
:
PRIOR FILING DATE: December 16, 1997
:
PRIOR APPLICATION NUMBER: 60/069,870
:
PRIOR FILING DATE: December 17, 1997
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PRIOR APPLICATION NUMBER: 60/069,873
:
PRIOR FILING DATE: December 17, 1997
:
PRIOR APPLICATION NUMBER: 60/068,017
:
PRIOR FILING DATE: December 18, 1997
:
PRIOR APPLICATION NUMBER: 60/070,440
:
PRIOR FILING DATE: January 5, 1998
:
PRIOR APPLICATION NUMBER: 60/074,086
:
PRIOR FILING DATE: February 9, 1998
:
PRIOR APPLICATION NUMBER: 60/074,092

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: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/216,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1,ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1,ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
:
NUMBER OF SEQ ID NOS: 120
:
SEQ ID NO 41
:
LENGTH: 1377
:
TYPE: DNA
:
ORGANISM: Homo Sapien
:
US-09-944-403-41
:
Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GACTAGTTCCTTGGAGTCTGGAGAGAGAAAGCGAGCCGGCAGGAGCGAACCAGGAGC 60
OY 61 TGGGCTGACGCGAGGCGAGGGGCGCTGGCGCGGGAGAAACGCGGGGCTGGAGCACCA 120
    |||||||
DB 61 TGGGCTGACGCGAGGCGAGGGGCGCTGGCGCGGGAGAAACGCGGGGCTGGAGCACCA 120
OY 121 CCAACTGAGGCTCCGAGTAGAGCGAGCCGCCGAAGAGGCAATCGGGAGACCGGAGAGG 180
    |||||||
DB 121 CCAACTGAGGCTCCGAGTAGAGCGAGCCGCCGAAGAGGCAATCGGGAGACCGGAGAGG 180
OY 181 GGGAGTGGCAGAGAGACCCCGCGTCCGGGCTCCGGGTCCAGACGCTATAGAGCCACTCT 240
    |||||||
DB 181 GGGAGTGGCAGAGAGACCCCGCGTCCGGGCTCCGGGTCCAGACGCTATAGAGCCACTCT 240

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QY 241 CGTCTGCTGCTCTCTGAGGCTGAGGCGGCTGCGCCCACTGAGCAGCAACAAGATCCC 300
DB 241 CGTCTGCTGCTCTCTGAGGCTGAGGCGGCTGCGCCCACTGAGCAGCAACAAGATCCC 300
QY 301 CAGCTCTGCGCGGAGGACCCCGGCTTCCAGGACCGCGGCAACCATGGACCCAGG 360
DB 301 CAGCTCTGCGCGGAGGACCCCGGCTTCCAGGACCGCGGCAACCATGGACCCAGG 360
QY 361 CTTGCGCGGCGCGGATGGCGCGGACCGGCGGCGCGGCGGCGGCGGCGGCGGAGAA 420
DB 361 CTTGCGCGGCGCGGATGGCGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGAGAA 420
QY 421 AGGCGAGGCGGAGGCGGCGGACTGCGGGAACCTGAGAGGAGCCCGGCGCGAGAGA 480
DB 421 AGGCGAGGCGGAGGCGGCGGACTGCGGGAACCTGAGAGGAGCCCGGCGCGAGAGA 480
QY 481 GGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 481 GGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 541 CTTGAGCGCGAAGCGCTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
DB 541 CTTGAGCGCGAAGCGCTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY 601 CGAGCGGCGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 CGAGCGGCGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CGAGGTCGCTGGGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACT 720
DB 661 CGAGGTCGCTGGGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACT 720
QY 721 GTTGTACTGTGTGAAG 780
DB 721 GTTGTACTGTGTGAAG 780
QY 781 GCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 GCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GTGGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GTGGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 CACCTTCTCGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CACCTTCTCGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 CCGACTGCAAAAGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 CCGACTGCAAAAGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GGTGATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 GGTGATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GCACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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DB 1141 GCAAGCATGGGAGAGTGGCTGATTTCTGCCCAAGAGAGAGAGAGAGAGAGAGAG 1200
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QY 1261 CTTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CTTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

QY 1321 GATCACTCATTAACCTAGAACCTCATTAACCTCATTAACCTCATTAACCTCATTA 1377
DB 1321 GATCACTCATTAACCTAGAACCTCATTAACCTCATTAACCTCATTAACCTCATTA 1377
RESULT 3
US-09-944-944-41
Sequence 41, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Balon, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998

APPLICANT: Gerdtzen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavlin, Ivan
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,944
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301

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1 PRIOR FILING DATE: December1, 1999
2 PRIOR APPLICATION NUMBER: PCT/US99/30095
3 PRIOR FILING DATE: December 16, 1999
4 PRIOR APPLICATION NUMBER: PCT/US00/03565
5 PRIOR FILING DATE: February 11, 2000
6 PRIOR APPLICATION NUMBER: PCT/US00/04414
7 PRIOR FILING DATE: February 22, 2000
8 PRIOR APPLICATION NUMBER: PCT/US00/05841
9 PRIOR FILING DATE: March 2, 2000
10 PRIOR APPLICATION NUMBER: PCT/US00/08439
11 PRIOR FILING DATE: March 30, 2000
12 PRIOR APPLICATION NUMBER: PCT/US00/14042
13 PRIOR FILING DATE: May 22, 2000
14 PRIOR APPLICATION NUMBER: PCT/US00/20710
15 PRIOR FILING DATE: July 28, 2000
16 PRIOR APPLICATION NUMBER: PCT/US00/32678
17 PRIOR FILING DATE: December 1, 2000
18 PRIOR APPLICATION NUMBER: PCT/US01/06520
19 PRIOR FILING DATE: February 28, 2001
20 NUMBER OF SEQ ID NOS: 120
21
22 SEQ ID NO 41
23 LENGTH: 1377
24 TYPE: DNA
25 ORGANISM: Homo Sapien
26
27 US-09-944-944--41

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Query Match	100.0%;	Score 1377;	DB 9;	Length 1377;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1377;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GACTAGTTCCTTGGAGTCTGGGAGAGGAAACCGAGCCCGACGGAGCGAACCGACGAC	60	
Db	1	GACTAGTTCCTTGGAGTCTGGGAGAGGAAACCGAGCCCGACGGAGCGAACCGAGC	60	
QY	61	TGGGTGACGCGACGAGGCGACGGGGCCCTCGGCCGGGAGAAAGCGCGGGGCTGAGCACC	120	
Db	61	TGGGGTACGCGACGAGGCGACGGGGCCCTCGGCCGGGAGAAAGCGCGGGGCTGAGCACC	120	
QY	121	CCAACTGAGGGTCCCGGAGTAGCGAGCGCCCGGAAAGAGAGCCATCGGGGAGCGCGGAGGG	180	
Db	121	CCAACTGAGGGTCCCGGAGTAGCGAGCGCCCGGAAAGAGAGCCATCGGGGAGCGCGGAGGG	180	
QY	181	GGGACTGGGAGAGGACCCCGGGCGTCCGGGGCTCCGGGTCCAGAGCGCTATGAGGGCCACTCT	240	
Db	181	GGGACTGGGAGAGGACCCCGGGCGTCCGGGGCTCCGGGTCCAGAGCGCTATGAGGGCCACTCT	240	
QY	241	CGTCTGCTGCTCTGGGCTCGGGGGCGCGCTCGGCCCTCCACTGAGCGAGCAACAAGATCCC	300	
Db	241	CGTCTGCTGCTCTGGGCTCGGGGGCGCGCTCGGCCCTCCACTGAGCGAGCAACAAGATCCC	300	
QY	301	CAGCCTTGCCCCGGGGCACCCTTTCAGAGCGACGCGCGGGCCACCAATGGCAGCCAGGG	360	
Db	301	CAGCCTTGCCCCGGGGCACCCTTTCAGAGCGACGCGCGGGCCACCAATGGCAGCCAGGG	360	
QY	361	CTTTCGCGGGCCGCGATGGCCCGAGAGCGCGCGGACGCGCCGGGGGCTCGGGAGAGAA	420	
Db	361	CTTTCGCGGGCCGCGATGGCCCGAGAGCGCGCGGACGCGCGGGGGCTCGGGAGAGAA	420	
QY	421	AGGCGAGGGCGGAGGCGCGGAGCTCCCGGACTTCGAGGGAAGCCCGGGCGCGAGAGAG	480	
Db	421	AGGCGAGGGCGGAGGCGCGGAGCTTCGCGGAGCTTCGAGGGAAGCCCGGGCGCGAGAGAG	480	
QY	481	GGCGGGACCGCGGGGGCCACCGGGGCGCGCGGGGAGTGCCTCGGGGCTCCCGGATCCGC	540	
Db	481	GGCGGGACCGCGGGGGCCACCGGGGCGCGCGGGGAGTGCCTCGGGGCTCCCGGATCCGC	540	
QY	541	CTTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTCTCCGCGCTGACGACACCCTTGCCCTT	600	
Db	541	CTTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTCTCCGCGCTGACGACACCCTTGCCCTT	600	
QY	601	CGACCGCGTGTGTTGAACGACGAGGACATTCAGAGCGCGTCAACGGCAAGTTCACCTG	660	
Db	601	CGACCGCGTGTGTTGAACGACGAGGACATTCAGAGCGCGTCAACGGCAAGTTCACCTG	660	

QY 661 CCAGTGGCTGGGGGCTCTACTTCTGCGGCTCCATGCCACGCTTACCGGGCCAGCTTCA 720
DB 661 CCAGTGGCTGGGGGCTCTACTTCTGCGGCTCCATGCCACGCTTACCGGGCCAGCTTCA 720
QY 721 GTTGTATCTGGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGTG 780
DB 721 GTTGTATCTGGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGTG 780
QY 781 GCCCAAGCCACCTTCGCTCTGCGGGGGGGCCATGCTGAGGCTGAGACCAAGT 840
DB 781 GCCCAAGCCACCTTCGCTCTGCGGGGGGGCCATGCTGAGGCTGAGACCAAGT 840
QY 841 GTGGGTGACAGTGGGTGGGTGACTACTATGATGCAATGCAATGCCACATCAAGACAGAG 900
DB 841 GTGGGTGACAGTGGGTGGGTGACTACTATGATGCAATGCAATGCCACATCAAGACAGAG 900
QY 901 CACCTTCTCCGGAATTTCTGTGTACTCCGACTGGCACAGCTCCCACTTTTCTTAACTG 960
DB 901 CACCTTCTCCGGAATTTCTGTGTACTCCGACTGGCACAGCTCCCACTTTTCTTAACTG 960
QY 961 CCCACTGCAAGTGAAGTCACTGCTCTGCTGCAAGAGAGAGGTGTAGGCTGACACCA 1020
DB 961 CCCACTGCAAGTGAAGTCACTGCTCTGCTGCAAGAGAGAGGTGTAGGCTGACACCA 1020
QY 1021 GGTCTATCCAGAGAGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGTAGA 1080
DB 1021 GGTCTATCCAGAGAGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGTAGA 1080
QY 1081 GCATCTCTCCCTCTGCTGCTGCTGCAAGAGATGGAACAGTGGCTGTCTGCAAGTCTG 1140
DB 1081 GCATCTCTCCCTCTGCTGCTGCTGCAAGAGATGGAACAGTGGCTGTCTGCAAGTCTG 1140
QY 1141 GCACATGAGGGGCTGAGTGTCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1200
DB 1141 GCACATGAGGGGCTGAGTGTCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1200
QY 1201 GTGTAAGTCCCCAGTTGCTCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1260
DB 1201 GTGTAAGTCCCCAGTTGCTCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1260
QY 1261 CTCGCTCTCTGCTGCTGCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1320
DB 1261 CTCGCTCTCTGCTGCTGCTGCTGCAAGAGAGAGAGTGTCTGCTGAGGCA 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 1377
DB 1321 GATCACTCAATTAACCTTAAGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 5
US-09-944-907-41
: Sequence 41, Application US/09944907
: Publication NO. US20020198147A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Batson, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fliviaroff, Ellen
: APPLICANT: Geffrisen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,907
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-944-907-41

Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTTCCTTTGAGTCTGAGAGAGAGAAAGCGAGCCGCGACGAGACCAAGAGAC 60
DB 1 GACTAGTTCCTTTGAGTCTGAGAGAGAGAAAGCGAGCCGCGACGAGACCAAGAGAC 60
QY 61 TGGGTGACAGGCGAGGCGGCGCTGCGCGGGGAGAGAGCGGGGGCTGAGACCA 120
DB 61 TGGGTGACAGGCGAGGCGGCGCTGCGCGGGGAGAGAGCGGGGGCTGAGACCA 120
QY 121 CCAACTGAGAGGCTCCGAGTAGAGAGAGCGCCCGAAGAGAGCCATCGGGAGAGCGGAGAG 180
DB 121 CCAACTGAGAGGCTCCGAGTAGAGAGAGCGCCCGAAGAGAGCCATCGGGAGAGCGGAGAG 180
QY 181 GGGACTGCGAAG 240
DB 181 GGGACTGCGAAG 240
QY 241 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CTTGCGGGGCGGAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CTTGCGGGGCGGAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AGGCGAGGCGGAG 480
DB 421 AGGCGAGGCGGAG 480
QY 481 GCGGAG 540
DB 481 GCGGAG 540
QY 541 CTTAG 600
DB 541 CTTAG 600
QY 601 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 CGAGTGGCTGGGTGCTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 CGAGTGGCTGGGTGCTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GTTGTATCTGGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGTG 780
DB 721 GTTGTATCTGGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGTG 780
QY 781 GCCCAAGCCACCTTCGCTCTGCGGGGGGGCCATGCTGAGGCTGAGACCAAGT 840
DB 781 GCCCAAGCCACCTTCGCTCTGCGGGGGGGCCATGCTGAGGCTGAGACCAAGT 840
QY 841 GTGGGTGACAGTGGGTGGGTGACTACTATGATGCAATGCAATGCCACATCAAGACAGAG 900

PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/0812030	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/0816959	PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/0818171	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/0829999	PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/0833222	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/0835455	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/0846000	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/0846277	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/0846537	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149	PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/0853333	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/0856977	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089559	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360	PRIOR FILING DATE: 1998-06-26

[illegible]

Db 1141 GCACCAATGGGGGCTGCTGATTTCTGCCCCAGACAGAGAGAGTGTGCTGTGCAAA 1200
QY 1201 GTGAATGCCCGGAGTGTCTGTGTCAGAGAGCCAGCGTGGGTCCTTCTGTC 1260
Db 1201 GTGAATGCCCGGAGTGTCTGTGTCAGAGAGCCAGCGTGGGTCCTTCTGTC 1260
QY 1261 CTCTGCTTCTGTGATGCTCCGACCCCTCTCTGCTCTGCGGGCCCTTTCTAGA 1320
Db 1261 CTCTGCTTCTGTGATGCTCCGACCCCTCTCTGCTCTGCGGGCCCTTTCTAGA 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCCCTATAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCACTCAATTAACCTTAAGAACCCCTATAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 9
US-10-123-904-361
Sequence 361, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-10-123-904-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTGTGAGTCTGTGGAGGAGAAAGCGGAGCGGAGAGGAGGAGAC 60
Db 1 GACTAGTCTCTGTGAGTCTGTGGAGGAGAAAGCGGAGCGGAGAGGAGGAGAC 60
QY 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 121 CCAACTGAGAGGAGTCCGAGAGTACGAGAGCGCCGAAAGAGAGGAGGAGGAG 180
Db 121 CCAACTGAGAGGAGTCCGAGAGTACGAGAGCGCCGAAAGAGAGGAGGAGGAG 180
QY 181 GGGAGTGCAG 240
Db 181 GGGAGTGCAG 240
QY 241 CGTCCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 CGTCCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

Db 241 CGTCCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CAGCCTCTGCCCCGGGAGACCCCGGCTTCCAGAGAGAGCCGAGGAGACCATGAGCAGAGG 360
Db 301 CAGCCTCTGCCCCGGGAGACCCCGGCTTCCAGAGAGAGCCGAGGAGACCATGAGCAGAGG 360
QY 361 CTTCGCGGAGCGAGATGAGCGGAGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAA 420
Db 361 CTTCGCGGAGCGAGATGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAA 420
QY 421 AGCGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 AGCGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GCGGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 481 GCGGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 CTTCAGGCGCAAGCGCTCCAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 541 CTTCAGGCGCAAGCGCTCCAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 601 CGAGCGGAGTCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 CGAGCGGAGTCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CCAAGTGCCTGAGGAGTCTACTACTTCCGCGTCCAGTCCAGGAGGAGGAGGAGGAG 720
Db 661 CCAAGTGCCTGAGGAGTCTACTACTTCCGCGTCCAGTCCAGGAGGAGGAGGAGGAG 720
QY 721 GTTTGATCTGTGTAAG 780
Db 721 GTTTGATCTGTGTAAG 780
QY 781 GCCAAGCGCAAGCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 GCCAAGCGCAAGCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 GTGGGTCAGAGTGTGGGTGAGTACATATGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 GTGGGTCAGAGTGTGGGTGAGTACATATGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 CACCTTCTCCGAGTCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 CACCTTCTCCGAGTCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 CCCACTGCAAGTGAAGTCTATGCTCTACTCTAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 CCCACTGCAAGTGAAGTCTATGCTCTACTCTAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GGTCAATCCAGAGAGGAGTGGCCCTCGGAATATGTAATGACTAGGAGAGTGGGTAGA 1080
Db 1021 GGTCAATCCAGAGAGGAGTGGCCCTCGGAATATGTAATGACTAGGAGAGTGGGTAGA 1080
QY 1081 GCACTCTCCGCTCTGTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 GCACTCTCCGCTCTGTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 GCAGCAATGGGAGAGTGGATGATTTCTGCCCAAGACAGAGAGAGAGAGAGAGAG 1200
Db 1141 GCAGCAATGGGAGAGTGGATGATTTCTGCCCAAGACAGAGAGAGAGAGAGAGAG 1200
QY 1201 GTGTAAGTCCCGGAGTGTCTGTGTCAGAGAGCCAGCGTGGGAGGAGGAGGAGGAG 1260
Db 1201 GTGTAAGTCCCGGAGTGTCTGTGTCAGAGAGCCAGCGTGGGAGGAGGAGGAGGAG 1260
QY 1261 CTCTGCTTCTGTGATGCTCCGACCCCTCTCTGCTCTGCGGGCCCTTTCTAGA 1320
Db 1261 CTCTGCTTCTGTGATGCTCCGACCCCTCTCTGCTCTGCGGGCCCTTTCTAGA 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCCCTATAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCACTCAATTAACCTTAAGAACCCCTATAAAAAAAAAAAAAAAAAAAAA 1377

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RESULT 10
US-10-140-470-361
; Sequence 361, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunnas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; PRIOR FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-361

Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTGAGTCTGGAGAGAGAAAGCGGACCGGACGAGGAGCGAACCAGGAC 60
DB 1 GACTAGTCTCTGAGTCTGGAGAGAGAAAGCGGACCGGACGAGGAGCGAACCAGGAC 60
QY 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CCAACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CCAACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 CGTCTGCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 CGTCTGCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 CAGCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 CAGCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 AGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 AGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
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QY 481 GCGGAGACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 GCGGAGACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 661 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 GTTGTAGTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GTTGTAGTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 CACCTTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 901 CACCTTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
QY 961 CCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 961 CCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
QY 1021 GGTATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 GGTATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GCACCTCTCGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 GCACCTCTCGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 GCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 GCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 GTGTAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1201 GTGTAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
QY 1261 CTCTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
DB 1261 CTCTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 GATCAGCTAATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1377
DB 1321 GATCAGCTAATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1377

RESULT 11
US-10-175-746-361
; Sequence 361, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
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? CURRENT FILING DATE: 2002-06-20
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 361
? LENGTH: 1377
? TYPE: DNA
? ORGANISM: Homo Sapien
? OS-10-176-918-361

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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1377;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	IACIAGTCTCTTGAGAGCTGGAGAGSAGAAAGCGACCCGAGGGAGCCAAACAGAC	60
Db	1	GACIAGTCTCTTGAGAGCTGGAGAGSAGAAAGCGAGCCGACBAGGAGCCAAACAGAC	60
OY	61	TGGGGTGACGCGCAGGGGCAGGGGGCCCTTGCCCGGGGAGAGCGCGGGGGCTTGAGCACC	120
Db	61	TGGGGTGACGCGCAGGGGCAGGGGGCCCTTGCCCGGGGAGAAACCGCGGGGGCTTGAGCACC	120
OY	121	CCAACTGAGAGGCTCGCAGTAGCCAGCGCCCCCGGAAGCGAGCCATCGGGGAGCCGGAGGG	180
Db	121	CCAACTGAGAGGCTCGCAGTAGCGAGCGCCCCCGGAAGCGAGCCATCGGGGAGCCGGAGGG	180
OY	181	GGGAGCTGGAGAGAGACCCCGGGCGTCGCCGGGGCTCCCGGTCCAGAGCGCTAAGAGCCACT	240
Db	181	GGGAGCTGGAGAGAGACCCCGGGGCTCCGGGGCTCCCGGTCCAGAGCGCTAAGAGCCACTCT	240
OY	241	CGTCTGCTGCTCTTGAGGCTTGCGGGCCGGGCTCGCCCCACTGAGCAGCAACAAAGATCCC	300
Db	241	CGTCTGCTGCTCTTGAGGCTTGCGGGCCGGGCTCGCCCCACTGAGCAGCAACAAAGATCCC	300
OY	301	CAGCCTTGCCCGGGGGGCACCCCGGGCTTCACAGGCAGCGCGGGGCACACATGAGCAGCAGGG	360
Db	301	CAGCCTTGCCCGGGGGGCACCCCGGGCTTCACAGGCAGCGCGGGGCACACATGAGCAGCAGGG	360
OY	361	CTTGCGGGGGCGCGATGCGCGCGAGAGCGCGGAGCGCGCGCGGGGGCTCCGGGGAGAGA	420
Db	361	CTTGCGGGGGCGCGATGCGCGCGAGAGCGCGGAGCGCGCGCGGGGGCTCCGGGGAGAGA	420
OY	421	AGGGAGAGGGCGGAGAGCGGGGAGCTGCCGGAGCTCGAGAGGAGACCCCGGGCGCGAGAGA	480
Db	421	AGGGAGAGGGCGGAGAGCGGGGAGCTGCCGGAGCTCGAGAGGAGACCCCGGGCGCGAGAGA	480
OY	481	GGCGGGACCCGCGGGGGCCACCGGGCTTGCCGGGGAGTGTCTGGGTGCTTCGCGAGTCCGC	540
Db	481	GGCGGGACCCGCGGGGGCCACCGGGCTTGCCGGGGAGTGTCTGGGTGCTTCGCGAGTCCGC	540
OY	541	CTTGAGCGCCCAAGCGCTCCGAGAGCGCGGGTACCCTCGCGCTGACGACCTTACCTCTT	600
Db	541	CTTGAGCGCCCAAGCGCTCCGAGAGCGCGGGTACCCTCGCGCTGACGACCTTACCTCTT	600
OY	601	CGACCCGCGTGGTGGAGACGAGAGAGGACATTAGACGCCCGTACACCGCAAGTTACCTG	660
Db	601	CGACCCGCGTGGTGGAGACGAGAGAGGACATTAGACGCCCGTACACCGCAAGTTACCTG	660
OY	661	CCAGGTGCTGGGGGTCTACTACTTTCGCGCTCCATCCACCGCTTACCGGGCCAGCTCACA	720
Db	661	CCAGGTGCTGGGGGTCTACTACTTTCGCGCTCCATCCACCGCTTACCGGGCCAGCTCACA	720
OY	721	GTTTGATCTGTTGAAGATGCGCATTCATTCGCTTCTTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTTGAAGATGCGCATTCATTCGCTTCTTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCAAGCGACCTCGCTCGGGGGGGGGGCAATGGTAGAGGTGAGAGCCCTGAGAGACCACT	840
Db	781	GCCCAAGCGACCTCGCTCGGGGGGGGGGCAATGGTAGAGGTGAGAGCCCTGAGAGACCACT	840
OY	841	GTGGGTGACAGTGGGTGTGGGTGACTACATTGGCATTTGCGACAGCATCAAGACAGACG	900
Db	841	GTGGGTGACAGTGGGTGTGGGTGACTACATTGGCATTTGCGACAGCATCAAGACAGACG	900

QY	901	TAACCTTCACCGAATTTCTGGATGCTACGACGTGGGACAGACGTCGCCAGCTTTGGCTATAG	960
Db	901	CACCTTCACCGAATTTCTGGATGCTACGACGTGGGACAGACGTCGCCAGCTTTGGCTATAG	960
QY	961	CCCACTGCAAAAGTAGCTATGCTCTCACTCTAGAGAGAGGTGTAGGCTGACACCA	1024
Db	961	CCCACTGCAAAAGTAGCTATGCTCTCACTCTAGAGAGAGGTGTAGGCTGACACCA	1024
QY	1021	GATCATCCAGAGAGGCTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGGTAGA	1080
Db	1021	GATCATCCAGAGAGGCTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGGTAGA	1080
QY	1081	GCACATCCCGTCTGCTGTGGCAAGATGGAGACATGGCTGTCTCGATCAGATCAGTGTG	1144
Db	1081	GCACATCCCGTCTGCTGTGGCAAGATGGAGACATGGCTGTCTCGATCAGATCAGTGTG	1144
QY	1141	GCAGATGGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGATGTCTGTGGCTGGCAG	1200
Db	1141	GCAGATGGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGATGTCTGTGGCTGGCAG	1200
QY	1201	GTTGTAAGTCCCCAGTGTCTGTGGTCAGAGACCCAGCGTGGGGTGCTCTTCTCCGTGTC	1260
Db	1201	GTTGTAAGTCCCCAGTGTCTGTGGTCAGAGACCCAGCGTGGGGTGCTCTTCTCCGTGTC	1260
QY	1261	CTGTACTTCTCGAATGCTCCGCCACCCGCTGCTGCTCGGGGGCGGGCCCTTTTCTCAGA	1320
Db	1261	CTGTACTTCTCGAATGCTCCGCCACCCGCTGCTGCTCGGGGGCGGGCCCTTTTCTCAGA	1320
QY	1321	GATCAGCTAATTAACCTTAAGAACCTCGATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA	1377
Db	1321	GATCAGCTAATTAACCTTAAGAACCTCGATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA	1377

RESULT 13
US-10-176-921-361

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/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Flvlaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330P1C288
/ CURRENT APPLICATION NUMBER: US/10/176,921
/ CURRENT FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 361
/ LENGTH: 1377
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-176-921-361

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Best Local	Similarity	100.0%	Pred. No. 0;		
Matches 1377;	Conservative	0;	Mismatches	0;	Gaps

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QY	1141	GCAGATGGGGCAGTGGCTGGATTTCTCTCCCAAGACAGACAGTCTCTGTCGGCA	1200
Db	1141	GCAGATGGGGCAGTGGCTGGATTTCTCTCCCAAGACAGACAGTCTCTGTCGGCA	1200
QY	1201	GTTGTAAGTCCCCCAGTTTCTCTGTGTCAGAGACCAGCGTGGGTGTCTCTCTGTCG	1260
Db	1201	GTTGTAAGTCCCCCAGTTTCTCTGTGTCAGAGACCAGCGTGGGTGTCTCTCTGTCG	1260
QY	1261	CTGTGCTTCTGTGGATTCCTCCCAACCCCTCTGTCTGTGGGCGCGCCCTTTTCTCAGA	1320
Db	1261	CTGTGCTTCTGTGGATTCCTCCCAACCCCTCTGTCTGTGGGCGCGCCCTTTTCTCAGA	1320
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; Sequence 361, Application US/10137865			
; Publication No. US20030032155A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: Deforge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zhenli			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3330R1C154			
; CURRENT FILING DATE: 2002-05-03			
; Prior Application removed - See Palm or File Wrapper			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 361			
; LENGTH: 1377			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-137-865-361			
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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	GACTAGTCTCTGTGAGTCTGTGGAGAGGAAGCGAGCCGGACAGGAGCGAACCAGAGAC	60
QY	61	TGGGGTACGGCAGCGCAGGGGGCGCTGTGCGGGAGAAAGCGGGGGCTGTGAGCACCA	120
Db	61	TGGGGTACGGCAGCGCAGGGGGCGCTGTGCGGGAGAAAGCGGGGGCTGTGAGCACCA	120
QY	121	CCAACTGAGAGGTCGGAGTAGACGAGCGCCCAAGAGAGGCGCATCGGGAGACCGGAGGG	180
Db	121	CCAACTGAGAGGTCGGAGTAGACGAGCGCCCAAGAGAGGCGCATCGGGAGACCGGAGGG	180
QY	181	GGGACTCGAGAGACCCCGCGCTCGCGGGCTCCCGGTGACAGCGCTATGAGCCACTCTCT	240
Db	181	GGGACTCGAGAGACCCCGCGCTCGCGGGCTCCCGGTGACAGCGCTATGAGCCACTCTCT	240

OY	241	GTCTCTGTGCTCTCGGGGCTCGGGGGGCGGCTGCGCCCACTGGAGCAACAAGATCCC	300
Db	241	CTCTCTGTGCTCTCTG888CTTGGGCGGCGGCTGCGCCCACTGGAGCAACAAGATCCC	300
OY	301	CAGCCTCTGCCCCGGGCGCAACCCCGGCTTCCAGGACAGCGCGGGCCACCATGGGACCCAGGG	360
Db	301	CAGCCTCTGCCCCGGGCGGCAACCCCGGCTTCCAGGACAGCCGGGCGCACCATGGGACCCAGGG	360
OY	361	CTTCGCGGGGCGCGCATGGGCGCGGACAGGGCGGCGGCGCGCGGGGCTCCGGGAGGAA	420
Db	361	CTTCGCGGGGCGCGCATGGGCGCGGACAGGGCGGCGGCGCGGGGCTCCGGGAGGAA	420
OY	421	AGGCGAGGGCGGAGAGCCGGGAGCTCCGGGACCTCGAGGGGACCCCGGGCGGAGAGA	480
Db	421	AGGCGAGGGCGGAGAGCCGGGAGCTCCGGGAGCTCGAGGGGACCCCGGGCGGAGAGA	480
OY	481	GGGGGAGCCCGCGGGGGGCCACCGGGGCTCGCGGGGAGAGCTCGGGTGGCTCCGCGATCCG	540
Db	481	GGGGGAGCCCGCGGGGGGCCACCGGGGCTCGCGGGGAGAGCTCGGGTGGCTCCGCGATCCG	540
OY	541	CTTCAGGCGCCAGGCGCTCCGAGAGCCGGGGTCCCTCCGCGCTGTAGAGCACCTTGGCCCTT	600
Db	541	CTTCAGGCGCCAGGCGCTCCGAGAGCCGGGGTCCCTCCGCGCTGTAGAGCACCTTGGCCCTT	600
OY	601	CGACCGCGCTGTGGGGAACGAGAGGAGCATTTAGAGCGCTGTACCGGGCAAGTTCACTGT	660
Db	601	CGACCGCGCTGTGGGGAACGAGAGGAGCATTTAGAGCGCGCTGTACCGGGCAAGTTCACTGT	660
OY	661	CCAGGTGCTTGGGCTTACTACTTTCGCCCTCCATATGCCACCGTCTTACCGGGCGAGCTGCA	720
Db	661	CCAGGTGCTTGGGCTTACTACTTTCGCCCTCCATATGCCACCGTCTTACCGGGCGAGCTGCA	720
OY	721	GTTTGATCTGTGTAAGAAATGCGAGATCCATATGCTCTTCTTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTGTAAGAAATGCGAGATCCATATGCTCTTCTTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCCAAGGCAACCTCCTCTCGGGGGGGGGCCATGTAGAGGTGAGAGCTGAGACCAAGT	840
Db	781	GCCCCAAGGCAACCTCCTCTCGGGGGGGGGCCATGTAGAGGTGAGAGCTGAGACCAAGT	840
OY	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGGATCATTCATCCAGACATCAAGACAGAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGGATCATTCATCCAGACATCAAGACAGAG	900
OY	901	CACCTTCTCCGGATTTCTGTGTACTCCGACTGGGACAGCTCCCAAGCTTTGGCTTAGTG	960
Db	901	CACCTTCTCCGGATTTCTGTGTACTCCGACTGGGACAGCTCCCAAGCTTTGGCTTAGTG	960
OY	961	CCCACTGCAAAAGTGAAGCTCATGCTCACTCCTTGAAGAGAGGAGGTGAGGCTGACAAACA	1020
Db	961	CCCACTGCAAAAGTGAAGCTCATGCTCACTCCTTGAAGAGAGGAGGTGAGGCTGACAAACA	1020
OY	1021	GGTCAATCAGAGAGGGCTGGCCCCCTGGGAATATTGTGAATACTAAGGAGGTGGGATAGA	1080
Db	1021	GGTCAATCAGAGAGGGCTGGCCCCCTGGGAATATTGTGAATACTAAGGAGGTGGGATAGA	1080
OY	1081	GCACCTCTCCGCTCTGCTGTGGCAAGAGAAATGGGAACAGTGGCTGCTCAGATCAGAGTGTG	1140
Db	1081	GCACCTCTCCGCTCTGCTGTGGCAAGAGAAATGGGAACAGTGGCTGCTCAGATCAGAGTGTG	1140
OY	1141	GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACACAGAGAGTGTGCTGCTGGGCA	1200
Db	1141	GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACACAGAGAGTGTGCTGCTGGGCA	1200
OY	1201	GTTGAAGTCCCCCAGTTGCTCTGTGCTCAGAGAGCCAGGTGGGGGTGCTCTTCCCTGGTCT	1260
Db	1201	GTTGAAGTCCCCCAGTTGCTCTGTGCTCAGAGAGCCAGGTGGGGGTGCTCTTCCCTGGTCT	1260
OY	1261	CTGTGCTTCTCTGGATCTCTCCCAACCCCTCTGTCTCTGGGGCGCGGCTTTTCTCAGA	1320
Db	1261	CTGTGCTTCTCTGGATCTCTCCCAACCCCTCTGTCTCTGGGGCGCGGCTTTTCTCAGA	1320

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 11:25:35 ; Search time 251 Seconds
(without alignments)
8050.387 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1. gactagttctcttgagctc.....aaaaaaaaaaaaaaaa 1377

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues 2085038

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1377	100.0	1377	9	US-09-944-896-41 Sequence 41, Appl
4	1377	100.0	1377	9	US-09-944-944-41 Sequence 41, Appl
5	1377	100.0	1377	9	US-09-944-907-41 Sequence 41, Appl
6	1377	100.0	1377	9	US-09-944-929-41 Sequence 41, Appl
7	1377	100.0	1377	9	US-10-028-072-361 Sequence 361, App
8	1377	100.0	1377	9	US-10-121-049-361 Sequence 361, App
9	1377	100.0	1377	9	US-10-123-904-361 Sequence 361, App
10	1377	100.0	1377	9	US-10-140-470-361 Sequence 361, App
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16	1377	100.0	1377	9	US-10-142-431-361 Sequence 361, App
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25	1377	100.0	1377	9	US-10-123-108-361	Sequence 361, App
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35	1377	100.0	1377	9	US-10-140-925-361	Sequence 361, App
36	1377	100.0	1377	9	US-10-160-498-361	Sequence 361, App
37	1377	100.0	1377	9	US-09-944-884-41	Sequence 41, Appl
38	1377	100.0	1377	9	US-10-121-041-361	Sequence 361, App
39	1377	100.0	1377	9	US-10-121-043-361	Sequence 361, App
40	1377	100.0	1377	9	US-10-121-047-361	Sequence 361, App
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ALIGNMENTS

RESULT 1

US-09-944-413-41

Sequence 41, Application US/09944413

Patent No. US20020156004A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerlitsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kljavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548P1

CURRENT APPLICATION NUMBER: US/09/944,413

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

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1 PRIOR APPLICATION NUMBER: 60/069,702
2 PRIOR FILING DATE: December 16, 1997
3 PRIOR APPLICATION NUMBER: 60/069,870
4 PRIOR FILING DATE: December 17, 1997
5 PRIOR APPLICATION NUMBER: 60/069,873
6 PRIOR FILING DATE: December 17, 1997
7 PRIOR APPLICATION NUMBER: 60/068,017
8 PRIOR FILING DATE: December 18, 1997
9 PRIOR APPLICATION NUMBER: 60/070,440
10 PRIOR FILING DATE: January 5, 1998
11 PRIOR APPLICATION NUMBER: 60/074,086
12 PRIOR FILING DATE: February 9, 1998
13 PRIOR APPLICATION NUMBER: 60/074,092
14 PRIOR FILING DATE: February 9, 1998
15 PRIOR APPLICATION NUMBER: 60/075,945
16 PRIOR FILING DATE: February 25, 1998
17 PRIOR APPLICATION NUMBER: 60/112,850
18 PRIOR FILING DATE: December 16, 1998
19 PRIOR APPLICATION NUMBER: 60/113,296
20 PRIOR FILING DATE: December 22, 1998
21 PRIOR APPLICATION NUMBER: 60/146,222
22 PRIOR FILING DATE: July 28, 1999
23 PRIOR APPLICATION NUMBER: PCT/US98/19330
24 PRIOR FILING DATE: September 16, 1998
25 PRIOR APPLICATION NUMBER: PCT/US98/25108
26 PRIOR FILING DATE: December 1, 1998
27 PRIOR APPLICATION NUMBER: 09/216,021
28 PRIOR FILING DATE: December 16, 1998
29 PRIOR APPLICATION NUMBER: 09/218,517
30 PRIOR FILING DATE: December 22, 1998
31 PRIOR APPLICATION NUMBER: 09/254,311
32 PRIOR FILING DATE: March 3, 1999
33 PRIOR APPLICATION NUMBER: PCT/US99/12252
34 PRIOR FILING DATE: June 22, 1999
35 PRIOR APPLICATION NUMBER: PCT/US99/21090
36 PRIOR FILING DATE: September 15, 1999
37 PRIOR APPLICATION NUMBER: PCT/US99/28409
38 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
39 PRIOR APPLICATION NUMBER: PCT/US99/28313
40 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
41 PRIOR APPLICATION NUMBER: PCT/US99/28301
42 PRIOR FILING DATE: December 1, 1999
43 PRIOR APPLICATION NUMBER: PCT/US99/30095
44 PRIOR FILING DATE: December 16, 1999
45 PRIOR APPLICATION NUMBER: PCT/US00/03555
46 PRIOR FILING DATE: February 11, 2000
47 PRIOR APPLICATION NUMBER: PCT/US00/04414
48 PRIOR FILING DATE: February 22, 2000
49 PRIOR APPLICATION NUMBER: PCT/US00/05841
50 PRIOR FILING DATE: March 2, 2000
51 PRIOR APPLICATION NUMBER: PCT/US00/08439
52 PRIOR FILING DATE: March 30, 2000
53 PRIOR APPLICATION NUMBER: PCT/US00/14042
54 PRIOR FILING DATE: May 22, 2000
55 PRIOR APPLICATION NUMBER: PCT/US00/20710
56 PRIOR FILING DATE: July 28, 2000
57 PRIOR APPLICATION NUMBER: PCT/US00/32678
58 PRIOR FILING DATE: December 1, 2000
59 PRIOR APPLICATION NUMBER: PCT/US01/06520
60 PRIOR FILING DATE: February 28, 2001
61 NUMBER OF SEQ ID NOS: 120
62 SEQ ID NO 41
63 LENGTH: 1377
64 TYPE: DNA
65 ORGANISM: Homo Sapien
66 US-09-944-413--41

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			Indels	0
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D	b	1	GACTAGTCTCTTGGAGAGTCTGGGAGAGGAAAGCGAGCCGCGACAGGACGAAACCAAGAC	60
Q	y	61	TGGGTGACGGCAGGGGCGCTGGCCGGGAGAGCGCGGGGCTGGAGCACCA	120
D	b	61	TGGGTGACGGCAGGGGCGCTGGCCGGGAGAGCGCGGGGCTGGAGCACCA	120
Q	y	121	CCAATTGAGAGGTCCGGAGTAGCCGAGCGCCCGAAGAGAGCCATGGGGAGCGCCGGAGG	180
D	b	121	CCAATTGAGAGGTCCGGAGTAGCCGAGCGCCCGAAGAGAGCCATGGGGAGCGCCGGAGG	180
Q	y	181	GGAGCTGGAGAGAGACCCGGGCTCCGGGATCCGGTGACAGCGCTATGAGGCCACTCT	240
D	b	181	GGAGCTGGAGAGAGACCCGGGCTCCGGGATCCGGTGACAGCGCTATGAGGCCACTCT	240
Q	y	241	CGTCTGCTGCTCTGGGCTTGGGCGCGGCGCGCTCGCCCACTGACGACAAACAAATGCC	300
D	b	241	CGTCTGCTGCTCTGGGCTTGGGCGCGGCGCGCTCGCCCACTGACGACAAACAAATGCC	300
Q	y	301	CAGCTCTGCCCCGGGGCACCCCGGCTTCCAGGACAGCGCGGGCCACCATGGCAGCAAGG	360
D	b	301	CAGCTCTGCCCCGGGGCACCCCGGCTTCCAGGACAGCGCGGGCCACCATGGCAGCAAGG	360
Q	y	361	CTTGGCGGGGCGCGATGGGCGCGAGAGCGCGAGCGCGCGCGCGCGCGCGCGCGAGAGA	420
D	b	361	CTTGGCGGGGCGCGATGGGCGCGAGAGCGCGAGCGCGCGCGCGCGCGCGCGCGAGAGA	420
Q	y	421	AGCGAGGCGCGGAGCGCGGAGCTGCCGAGACTTGAGGGGACCCCGGGCGCGAGAGA	480
D	b	421	AGCGAGGCGCGGAGCGCGGAGCTGCCGAGACTTGAGGGGACCCCGGGCGCGAGAGA	480
Q	y	481	GGCGGGACCCCGGGGGCCACCGGGGCTGGCGGGGAGTGTGGGTGGCTCCGGCGATCCGC	540
D	b	481	GGCGGGACCCCGGGGGCCACCGGGGCTGGCGGGGAGTGTGGGTGGCTCCGGCGATCCGC	540
Q	y	541	CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCCGCGTCTGACGACCCCTTGCCCTT	600
D	b	541	CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCCGCGTCTGACGACCCCTTGCCCTT	600
Q	y	601	CGACCGCGTGTGTGAAGAGACGAGAGACATTACAGACGCGCTCACCGGCAAGTTACCTG	660
D	b	601	CGACCGCGTGTGTGAAGAGACGAGAGACATTACAGACGCGCTCACCGGCAAGTTACCTG	660
Q	y	661	CCAGTGGCTGGGCTACTACTTCCGCTCCATGCCACCGCTTACCGGGGACGCTGCA	720
D	b	661	CCAGTGGCTGGGCTACTACTTCCGCTCCATGCCACCGCTTACCGGGGACGCTGCA	720
Q	y	721	GTTTGATCTGGGAAGATGGGAAATCCATTGCGCTCTTCCAGTTTTCGGGGGCTG	780
D	b	721	GTTTGATCTGGGAAGATGGGAAATCCATTGCGCTCTTCCAGTTTTCGGGGGCTG	780
Q	y	781	GCCCAAGCAGACCTCGCTCTCGGGGGGGGCCATGGTGAAGGCTGAGACCTGAGACCAAGT	840
D	b	781	GCCCAAGCAGACCTCGCTCTCGGGGGGGGCCATGGTGAAGGCTGAGACCTGAGACCAAGT	840
Q	y	841	GTGGGTGAGAGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGACAG	900
D	b	841	GTGGGTGAGAGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGACAG	900
Q	y	901	CACGCTCCGGAATTTCTGTACTCCGACTCGGAGACAGCTCCCAAGCTTTGGCTTAGTG	960
D	b	901	CACGCTCCGGAATTTCTGTACTCCGACTCGGAGACAGCTCCCAAGCTTTGGCTTAGTG	960
Q	y	961	CCCACTGCAAAAGTAGCTCATGCTCTCACTCTAGAAAGAGAGGTGTAGAGCTGACAAACA	1020
D	b	961	CCCACTGCAAAAGTAGCTCATGCTCTCACTCTAGAAAGAGAGGTGTAGAGCTGACAAACA	1020
Q	y	1021	GGTCATCCAGAGAGGCTGGCCCCCTGGGAATTTGTGATGATGAGGAGGCTGGGCTAGA	1080
D	b	1021	GGTCATCCAGAGAGGCTGGCCCCCTGGGAATTTGTGATGATGAGGAGGCTGGGCTAGA	1080
Q	y	1081	GCACCTCCCGCTCGCTGCTGCTGGGCAAGAAATGGGAAACAGTGGCTCTGTCGCAATCAGTCTG	1140
D	b	1081	GCACCTCCCGCTCGCTGCTGCTGGGCAAGAAATGGGAAACAGTGGCTCTGTCGCAATCAGTCTG	1140

OY	241	CGTCTGCTGGTCCMGGGGCTGGGGGGCCGGGTCGGCCCTGACTGAGCAGCAACAATATCC	300
Db	241	CGTCTGCTGGTCCMGGGGCTGGGGGGCCGGGTCGGCCCTGACTGAGCAGCAACAATATCC	300
OY	301	CAGCCTTCGCCCCGGGGGCACCCCGGCTTCCAGGCAAGCCGGGGCCACATATGCGAGCCAGG	360
Db	301	CAGCCTTCGCCCCGGGGGCACCCCGGCTTCCAGGCAAGCCGGGGCCACATATGCGAGCCAGG	360
OY	361	CTTCCCGGGGGCCCATGGGCCCCGAGAGGGCCGAGCGGGCCGCCGGGGCTCCGGGGAGAA	420
Db	361	CTTCCCGGGGGCCCATGGGCCCCGAGAGGGCCGAGCGGGCCGCCGGGGCTCCGGGGAGAA	420
OY	421	AGGGGAGGGGGGAGGCGGGGACTGCCGGAGCTTCGAGGGGACCCCGGGGCCGCGAGAGA	480
Db	421	AGGGGAGGGGGGAGGCGGGGACTGCCGGAGCTTCGAGGGGACCCCGGGGCCGCGAGAGA	480
OY	481	GGCGGGACCCGCGGGGGCCACCGGGCTTCGCGGGGAGTCTCGTGCTCCGCGATCCG	540
Db	481	GGCGGGACCCGCGGGGGCCACCGGGCTTCGCGGGGAGTCTCGTGCTCCGCGATCCG	540
OY	541	CTTCAAGCGCCAAAGGGCTCCGAGAGCGGGGTGCTCCGCGCTGAGCGACCTTGCCCT	600
Db	541	CTTCAAGCGCCAAAGGGCTCCGAGAGCGGGGTGCTCCGCGCTGAGCGACCTTGCCCT	600
OY	601	CGACCGCGTGTGGTGAACGAGCAGAGGGACATTACAGACCGCTCACCGGCAATGTACCTG	660
Db	601	CGACCGCGTGTGGTGAACGAGCAGAGGGACATTACAGACCGCTCACCGGCAATGTACCTG	660
OY	661	CCAGGTGCTGGGGGCTCTACTACTTCGCGCTGCATGCCACCGCTACCGGGGCCAGCTCA	720
Db	661	CCAGGTGCTGGGGGCTCTACTACTTCGCGCTGCATGCCACCGCTACCGGGGCCAGCTCA	720
OY	721	GTTTGATCTGGTGAAGAATGCGAATTCATTGCCCTTCTTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGGTGAAGAATGCGAATTCATTGCCCTTCTTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCAAGCCACCTTCGCTCTCGGGGGGGGCCATGCTGAGGCTGGAAGCTTGAGAGCAAGT	840
Db	781	GCCCAAGCCACCTTCGCTCTCGGGGGGGGCCATGCTGAGGCTGGAAGCTTGAGAGCAAGT	840
OY	841	GTGGGTGAGGTGGGTGTGGGGTGAATTAATTGGCACTATGCGACATCAAGACAGACAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGGTGAATTAATTGGCACTATGCGACATCAAGACAGACAG	900
OY	901	CACCTTCTCCGGATTTCTGTGTACTCCGACTGCGACAGCTCCCGAGTCTTTCCTTAAGT	960
Db	901	CACCTTCTCCGGATTTCTGTGTACTCCGACTGCGACAGCTCCCGAGTCTTTCCTTAAGT	960
OY	961	CCCACTGCAAGTATGACTCATGCTCCTCACTCCTTAAGAGAGGTGTGAGGCTGACAAACA	1020
Db	961	CCCACTGCAAGTATGACTCATGCTCCTCACTCCTTAAGAGAGGTGTGAGGCTGACAAACA	1020
OY	1021	GGTATATCCAGAGGGCTGGCCCCCTGGAAATATTGTGATACTATGAGAGGTGGGGTAGA	1080
Db	1021	GGTATATCCAGAGGGCTGGCCCCCTGGAAATATTGTGATACTATGAGAGGTGGGGTAGA	1080
OY	1081	GCACTTCTCCGTCTGCTGCTGGCAAGGAATGGGAACAAGTGGCTGTCTCGATCAGGTCTG	1140
Db	1081	GCACTTCTCCGTCTGCTGCTGGCAAGGAATGGGAACAAGTGGCTGTCTCGATCAGGTCTG	1140
OY	1141	GCACGATGGGGCAGGGGTGGATTTTCGCCCAAGACGAGAGAGTGTCTGTGCTGGGCA	1200
Db	1141	GCACGATGGGGCAGGGGTGGATTTTCGCCCAAGACGAGAGAGTGTCTGTGCTGGGCA	1200
OY	1201	GTTGAAGTCCCGCCAGTTTCTGTGGTCCAGAGACCCACGATGGGGGTCTCTCTTCCTGGT	1260
Db	1201	GTTGAAGTCCCGCCAGTTTCTGTGGTCCAGAGACCCACGATGGGGGTCTCTCTTCCTGGT	1260
OY	1261	CTGTGCTTCTGTGATCTCTCCCAACCCCTCTGTCTCTGGGGCCGGGCCCTTTTCTCAGA	1320
Db	1261	CTGTGCTTCTGTGATCTCTCCCAACCCCTCTGTCTCTGGGGCCGGGCCCTTTTCTCAGA	1320

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09      1321 GATCACTCAATAAACCTTAGAAGACCTCATTAATTTTTTTTTTTTTTTTTTTTTTTT 1377
Db      1321 GATCAGCTCAATAAAACTTAGAACCTCATTAATTTTTTTTTTTTTTTTTTTTTTTT 1377

RESULT 3
US-09-944-896-41
; Sequence 41, Application US/09944896
; Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 564
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCY/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCY/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998

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Query Match	Similarity	100.0%	Score 1377	DB 9	Length 1377
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					Gaps
					0
QY	1	GACTAGTTCCTTGTGGAGTCTGGGAGAGGAAAGCCGAGCCCGGACAGGAGCGGAAACCAAGGAC	60		
Db	1	GACTAGTTCCTTGTGGAGTCTGGGAGAGGAAAGCCGAGCCCGGACAGGAGCGGAAACCAAGGAC	60		
QY	61	TGGGGTGACGGCAGGAGGAGGGGGGCGCTTGGCCGGGGAAGCGCGGGGGCTTGGAGCACCA	120		
Db	61	TGGGGTGACGGCAGGAGGAGGGGGGCGCTTGGCCGGGGAAGCGCGGGGGCTTGGAGCACCA	120		
QY	121	CCAACGTGAGGGTCCGGAGTAGCGAGCGACCCCGAAGGAGAGGCCATCGGGGAGCGGGGAGGG	180		
Db	121	CCAACGTGAGGGTCCGGAGTAGCGAGCGACCCCGAAGGAGAGGCCATCGGGGAGCGGGGAGGG	180		
QY	181	GGGACTCGAGAGGACCCCGCGTCCCGGACTCCCGGTCCCAAGCCCTATGAGGCGCACTCT	240		
Db	181	GGGACTCGAGAGGACCCCGCGTCCCGGACTCCCGGTCCCAAGCCCTATGAGGCGCACTCT	240		
QY	241	CGTCTGCTGCTCCTGGGCGCTTGGGCGCGGCGTCCGCCCTCTGAGCGACACAGATGCC	300		
Db	241	CGTCTGCTGCTCCTGGGCGCTTGGGCGCGGCGTCCGCCCTCTGAGCGACACAGATGCC	300		
QY	301	CAGCCTCGCCCGGGGGGACCCCGGCGTTCGAGGCGAGCGCGGGGCGACCATGCGAGCGAGGG	360		
Db	301	CAGCCTCTGCCCCGGGGGACCCCGGCGTTCGAGGCGAGCGCGGGGCGACCATGCGAGCGAGGG	360		
QY	361	CTTCCCGGGCGCGCATGCGCGAGCGCGCGAGCGCGCGCCCGGGGGCTCCGGAGAGAGA	420		
Db	361	CTTCCCGGGCGCGCATGCGCGAGCGCGCGAGCGCGCGCCCGGGGGCTCCGGAGAGAGA	420		
QY	421	AGGCGAGGGCGGAGGCGCGGAGCTTCCGGGACCTTCGAGGGGAGCCCGGGCGCGGAGAGA	480		
Db	421	AGGCGAGGGCGGAGGCGCGGAGCTTCCGGGACCTTCGAGGGGAGCCCGGGCGCGGAGAGA	480		

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RESULT 4
US-09-944-944-41
; Sequence 41, Application US/0944944
; Patent NO. US20020173463A1
; GENERAL INFORMATION:
;
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

```


QY 1081 GCACCTCCGTCCTCTGCTGAGATGGAGAGAGGCTGCTGAGATCAGTCTG 1140
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QY 1141 GCAGATGGGAGTGGTGGATTTCTGCCAGACAGAGAGTCTGTCGGCAA 1200
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DB 1261 CTCTCTCTCTGTCGTCCTCCACCCCTCTCTCTCTGCGGCGGCTTCCTCAGA 1320
QY 1321 GATCAGTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAA 1377
DB 1321 GATCAGTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAA 1377

RESULT 7
US-10-028-072-361
: Sequence 361, Application US/10028072
: Publication No. US20030004311A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang
: TITLE OF INVENTION:
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/10/028,072
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
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: PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-03-27

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PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360	PRIOR FILING DATE: 1998-06-26

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;
; PRIOR FILING DATE: 1998-07-01
;
; PRIOR APPLICATION NUMBER: 60/091519
;
; PRIOR FILING DATE: 1998-07-02
;
; PRIOR APPLICATION NUMBER: 60/091982
;
; PRIOR FILING DATE: 1998-07-07
;

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Query Match	100.0%	Score 1377	DB 9	Length 1377
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1377	0	Mismatches	0	Gaps 0

QY	1	GACTACTTCTCTGGAGTCTGGGAGAGAGAAAGCCGACCCGGAGGGAGGCAACACAGAC	60
Dp	1	GACTACTTCTCTGGAGTCTGGGAGAGAGAAAGCGAGACCGGAGGGAGGCAACACAGAC	60
QY	61	TGGGGTGACGGCAGAGGGCAGGGGGCCCTTGCGCGGGGAGAGACCGCGGGGCTGTGAGCACCA	120
Dp	61	TGGGGTGACGGCAGAGGGCAGGGGGCCCTTGCGCGGGGAGAGACCGCGGGGCTGTGAGCACCA	120
QY	121	CCAACTGGAGGGTCCGGAGTACCGAGGCCCCGAAAGGAGGCAATCGGGGAGCGGGAGGG	180
Dp	121	CCAACTGGAGGGTCCGGAGTACCGAGGCCCCGAAAGGAGGCAATCGGGGAGCGGGAGGG	180
QY	181	GGGACTGCGAGAGAGACCCCGCGCTCCGGGCTCCGGGTCCACGCGCTATGAGGCCACTCT	240
Dp	181	GGGAGCTGGAGAGAACCCCGCGCTCCGGGCTCCGGGTCCACGCGCTATGAGGCCACTCT	240
QY	241	CGTCTGCTGCTCTTGgggCTTGGGCGCGGCTCGCCCCACATGGAGCACAAGATCCC	300
Dp	241	CGTCTGCTGCTCTTGgggCTTGGGCGCGGCTCGCCCCACATGGAGCACAAGATCCC	300
QY	301	CAGCCTCTGCCCCGGGGGCAACCAGGCTTCCAGAGCAGCGCCGGGCGACATGGCAGCAGGG	360
Dp	301	CAGCCTCTGCCCCGGGGGCAACCAGGCTTCCAGAGCAGCGCCGGGCGACATGGCAGCAGGG	360
QY	361	CTTGGCGGGCCCGATGAGCGCGGAGCGCGCGAGCGCGCGCGGGGCTCCGGAGAGAA	420
Dp	361	CTTGGCGGGCCCGCATGAGCGCGGAGCGCGCGAGCGCGCGCGGGGCTCCGGAGAGAA	420
QY	421	AGCGAGGGCGGGAGCGCGGGAATTGCGGGGACTTGGAGGGAGCCCGGGCGCGAGAGA	480
Dp	421	AGCGAGGGCGGGAGCGCGGGAATTGCGGGGACTTGGAGGGAGCCCGGGCGCGAGAGA	480
QY	481	GGCGGGAGCCCGGGGGGCCACCGGGCTTGCGGGGAGTGGCTCGGGTGGCTCCGGATCCG	540
Dp	481	GGCGGGAGCCCGGGGGGCCACCGGGCTTGCGGGGAGTGGCTCGGGTGGCTCCGGATCCG	540
QY	541	CTTCAAGCGCAAGGCTCCGAGAGGCGGGGTGCTCGCGCGTCAAGCACCCTTGGCCCTT	600
Dp	541	CTTCAAGCGCGAAGGCTCCGAGAGGCGGGGTGCTCGCGCGTCAAGCACCCTTGGCCCTT	600
QY	601	CGACCGCGTGTGTGAAGCAGACAGGAGCATTTACGAGCGCGTCACCGGCAAGTTCACCTG	660
Dp	601	CGACCGCGTGTGTGAAGCAGACAGGAGCATTTACGAGCGCGTCACCGGCAAGTTCACCTG	660
QY	661	CCAGGTGCTTGGGGGTCTACTACTTGGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA	720
Dp	661	CCAGGTGCTTGGGGGTCTACTACTTGGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA	720
QY	721	GTTTATATCTGGTGAAGATATGGCGAATCATTTGGCTCTTCTTCCAGTTTTTCGGGGGGGTG	780
Dp	721	GTTTATATCTGGTGAAGATATGGCGAATCATTTGGCTCTTCTTCCAGTTTTTCGGGGGGGTG	780
QY	781	GGCCAAAGCAGAGCTGCTCTCGGGGGGGGGCCATGTAGAGCTGTAGAGCAACAAGT	840
Dp	781	GGCCAAAGCAGAGCTGCTCTCGGGGGGGGGCCATGTAGAGCTGTAGAGCAACAAGT	840
QY	841	GTTGGGTGCAAGTGGGTGTGGGTGTACTACTATTGGCATTTATGCCAGCATCAAGACAGAC	900
Dp	841	GTTGGGTGCAAGTGGGTGTGGGTGTACTACTATTGGCATTTATGCCAGCATCAAGACAGAC	900
QY	901	CACCTTCTCGGAGATTTCTGGTGTACTCCGACTGGCAGACGTCCCCAGCTTTTGTAGTG	960
Dp	901	CACCTTCTCGGAGATTTCTGGTGTACTCCGACTGGCAGACGTCCCCAGCTTTTGTAGTG	960

Db 1141 GCACATGAGGAGTGGCTGATTTCTGCCCCAAGACAGAGAGTGTGCTGTGCGCA 1200
QY 1201 GTGTAAGTCCCGCAGATTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGCGTC 1260
Db 1201 GTGTAAGTCCCGCAGATTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGCGTC 1260
QY 1261 CTCTGCTTCTCTGATGATCTCCCAACCCCTCTCTCTGCGGCGGCTTTTCTCAGA 1320
Db 1261 CTCTGCTTCTCTGATGATCTCCCAACCCCTCTCTCTGCGGCGGCTTTTCTCAGA 1320
QY 1321 GATACATCAATAAAGCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATACATCAATAAAGCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 9
US-10-123-904-361
; Sequence 361, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGTGAGTCTGGAGAGAGAAAGCGGAGCCGGAGCGAGCAACAGAC 60
Db 1 GACTAGTCTCTTGTGAGTCTGGAGAGAGAAAGCGGAGCCGGAGCGAGCAACAGAC 60
QY 61 TGGGGTACGCGAGGAGGAGGGGGGCTGGCGGGGAGAGCGGGGGCTGTGAGACCA 120
Db 61 TGGGGTACGCGAGGAGGAGGGGGGCTGGCGGGGAGAGCGGGGGCTGTGAGACCA 120
QY 121 CCAACTGAGAGGTCGCGAGTAGAGAGCGCCCGAAGAGAGCCATCGGGAGCGGAGGG 180
Db 121 CCAACTGAGAGGTCGCGAGTAGAGAGCGCCCGAAGAGAGCCATCGGGAGCGGAGGG 180
QY 181 GGGAGTCCGAGAGAGAGCCCGGCGTCCGGGTCCCGGTGTGAGAGCCACTCT 240
Db 181 GGGAGTCCGAGAGAGAGCCCGGCGTCCGGGTCCCGGTGTGAGAGCCACTCT 240
QY 241 CGTCTGCTGCTCTCTGGGCTGGCGGGGCTGGCCCCCACTGAGACAAAGATCCC 300
Db 241 CGTCTGCTGCTCTCTGGGCTGGCGGGGCTGGCCCCCACTGAGACAAAGATCCC 300

Db 241 CGTCTGCTGCTCTCTGGGCTGGCGGGGCTGGCCCCCACTGAGACAAAGATCCC 300
QY 301 CAGCCTGTGCGCGGGGAGACCCCGGCTTTCAGAGAGCCCGGGACCATGGACCAAGG 360
Db 301 CAGCCTGTGCGCGGGGAGACCCCGGCTTTCAGAGAGCCCGGGACCATGGACCAAGG 360
QY 361 CTTCGCGGGCGGATGAGCGCGGAGCGCCGAGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 CTTCGCGGGCGGATGAGCGCGGAGCGCCGAGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 AGGCGAGGGGGGAGGGCGGAGCTGCGGGGACCTCGAGGGGAGCCCGGGGCGGAGAGA 480
Db 421 AGGCGAGGGGGGAGGGCGGAGCTGCGGGGACCTCGAGGGGAGCCCGGGGCGGAGAGA 480
QY 481 GGGCGAGCCCGCGGGGAGCCAGCCGGGCTGCGGGGAGTGTCTGCTGCTCGCGATCCG 540
Db 481 GGGCGAGCCCGCGGGGAGCCAGCCGGGCTGCGGGGAGTGTCTGCTGCTCGCGATCCG 540
QY 541 CTTCAGCGCAAGCGCTCCGAGAGCGGGGTGCTCGCGCGCTGAGCGCACCTTGCCCTT 600
Db 541 CTTCAGCGCAAGCGCTCCGAGAGCGGGGTGCTCGCGCGCTGAGCGCACCTTGCCCTT 600
QY 601 CGACCGGCTGCTGTGAGAGAGAGAGGAGACATTAAGAGCGCGGTACCGGCAAGTCACTG 660
Db 601 CGACCGGCTGCTGTGAGAGAGAGGAGAGACATTAAGAGCGCGGTACCGGCAAGTCACTG 660
QY 661 CCAAGTCTGAGGCTACTACTTCCGCGTCCATGACCGCTACCGGCGGCGGCGGCGCA 720
Db 661 CCAAGTCTGAGGCTACTACTTCCGCGTCCATGACCGCTACCGGCGGCGGCGGCGCA 720
QY 721 GTTTGATCTGCTGAGAGATGAGGAGATTCATTCCTCTTTTCCAGTTTTCGGGGGCTG 780
Db 721 GTTTGATCTGCTGAGAGATGAGGAGATTCATTCCTCTTTTCCAGTTTTCGGGGGCTG 780
QY 781 GCCCAAGCGAGCGCTGCTCGGGGGGGGAGCATGTGAGGCTGAGGCTGAGGACCAAGT 840
Db 781 GCCCAAGCGAGCGCTGCTCGGGGGGGGAGCATGTGAGGCTGAGGCTGAGGACCAAGT 840
QY 841 GTGGGTGAGAGTGGGTGGGTGAGTACATTTGGATGATGAGGAGGAGGAGGAGGAGG 900
Db 841 GTGGGTGAGAGTGGGTGGGTGAGTACATTTGGATGATGAGGAGGAGGAGGAGGAGG 900
QY 901 CACCTTCCGAGTCTGTGCTGAGTACGAGTCCGAGCGTCCCACTCTTCTGTTAGTG 960
Db 901 CACCTTCCGAGTCTGTGCTGAGTACGAGTCCGAGCGTCCCACTCTTCTGTTAGTG 960
QY 961 CCAAGTCAAGAGAGTCAATGCTCACTCACTAGAGAGGAGGAGGAGGAGGAGGAGG 1020
Db 961 CCAAGTCAAGAGAGTCAATGCTCACTCACTAGAGAGGAGGAGGAGGAGGAGGAGG 1020
QY 1021 GGTATCCAGAGAGGCTGGCCCGCTGGAATATTGTGATGACTAGGAGAGTGGGTAGA 1080
Db 1021 GGTATCCAGAGAGGCTGGCCCGCTGGAATATTGTGATGACTAGGAGAGTGGGTAGA 1080
QY 1081 GCACTCTCCGCTCTGCTGCTGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Db 1081 GCACTCTCCGCTCTGCTGCTGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 GCAAGATGGGAGAGTGGATTTTGGCCCAAGAGACAGAGAGGAGGAGGAGGAGGAGG 1200
Db 1141 GCAAGATGGGAGAGTGGATTTTGGCCCAAGAGACAGAGAGGAGGAGGAGGAGGAGG 1200
QY 1201 GTGTAAGTCCCGCAGTTGCTCTGTCCAGAGAGCCAGGAGGAGGAGGAGGAGGAGG 1260
Db 1201 GTGTAAGTCCCGCAGTTGCTCTGTCCAGAGAGCCAGGAGGAGGAGGAGGAGGAGG 1260
QY 1261 CTCTGCTTCTCTGATCTCTCCCAACCCCTCTCTGCTCTGCGGCGGCGCTTTTCTCAGA 1320
Db 1261 CTCTGCTTCTCTGATCTCTCCCAACCCCTCTCTGCTCTGCGGCGGCGCTTTTCTCAGA 1320
QY 1321 GATCACTCAATAAAGCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCACTCAATAAAGCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377

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RESULT 10
US-10-140-470-361
; Sequence 361, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P333081C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-470-361

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	Query Match	Similarity	100.0%	Score 1377;	DB 9;	Length 1377;	
	Best Local	Similarity	100.0%	Pred. No. 0;			
	Matches 1377;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
QY	1	GACTAGTTCCTTTGGAGCTGTGGAGAGGAAACCGAGCCGAGCAGAGAGCGAACCCAGAGC	60				
Db	1	GACTAGTTCCTTTGGAGCTGTGGAGAGGAAAGCGGAGCCGAGAGCGAACCCAGAGC	60				
QY	61	TGGGGTACCGCAGAGGCAAGGGGGGCGCTGGCGCGGGGAGAAACCGCGGGGGCTGAGACACA	120				
Db	61	TGGGGTACCGCAGAGGCAAGGGGGGCGCTGGCGCGGGGAGAAAGCGCGGGGGCTGAGACACA	120				
QY	121	CCAACCTGAGAGGTCGCGAGTAGCAGACGCCCCGAAAGAGAGGCATCTGGGGAGCCGCGAGAGG	180				
Db	121	CCAACCTGAGAGGTCGCGAGTAGCAGACGCCCCGAAAGAGAGGCATCTGGGGAGCCGCGAGAGG	180				
QY	181	GGGACTCGCAGAGGACCCCGGCGTCGCCGGGTCCCGGTCCAGAGCTATGAGGCCACTCT	240				
Db	181	GGGACTCGCAGAGGACCCCGGCGTCGCCGGGTCCCGGTCCAGAGCTATGAGGCCACTCT	240				
QY	241	CGTCTCGCTGTCTCTGGGCTTGAGGCGCGCGCTCGGCCCCCACTGAGCAGCAACAAGATCCC	300				
Db	241	CGTCTCGCTGTCTCTGGGCTTGAGGCGCGCGCTCGGCCCCCACTGAGCAGCAACAAGATCCC	300				
QY	301	CAGGCTCTGCCCGGGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGGCCACATGGCAGCCAGGG	360				
Db	301	CAGGCTCTGCCCGGGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGGCCACATGGCAGCCAGGG	360				
QY	361	CTTTCGCCGGGCGCATGGCCCGCGAGAGCGCGCCCGCGGGGCTCCGGGAGAGAA	420				
Db	361	CTTTCGCCGGGCGCATGGCCCGCGAGAGCGCGCCCGCGGGGCTCCGGGAGAGAA	420				
QY	421	AGGCGAGGCGCGGAGGCCGGGACTGCGGGAGACTTGGAGGGAGACCCCGGGCGCGAGGAGA	480				
Db	421	AGGCGAGGCGCGGAGGCCGGGACTGCGGGAGACTTGGAGGGAGACCCCGGGCGCGAGGAGA	480				

QY	481	GGGGGAAACCCGGGGGGCCACCGGGGCTGGCGGGGAAGTGCCTGGGCTCCGGATCCG	540
Dp	481	GGGGGAAACCCGGGGGGCCACCGGGGCTGGCGGGGAAGTGCCTGGGCTCCGGATCCG	540
QY	541	CTTTCAGCGCAAGCGCTCCGAGAGCGGGGTGCCTCCGCGCTCAAGCACCTTGGCCCTT	600
Dp	541	CTTTCAGCGCAAGCGCTCCGAGAGCGGGGTGCCTCCGCGCTCAAGCACCTTGGCCCTT	600
QY	601	CGACCGGTGTCTGTGTATGAGAGCAGGGACATTAGACGCGCTCACCGGCAATTCACTG	660
Dp	601	CGACCGGTGTCTGTGTATGAGAGCAGGGACATTAGACGCGCTCACCGGCAATTCACTG	660
QY	661	CCAGGTGCTGGGGGTCTACTACTTGGCGCTCATGCCACGCTTACGGGGCACCTGCA	720
Dp	661	CCAGGTGCTGGGGGTCTACTACTTGGCGCTCATGCCACGCTTACGGGGCACCTGCA	720
QY	721	GTTTGTATGTGTGTAGATGGCAATGCCAATTGCCTCTTCTTCCAGTTTTCGGGGGTG	780
Dp	721	GTTTGTATGTGTGTAGATGGCAATGCCAATTGCCTCTTCTTCCAGTTTTCGGGGGTG	780
QY	781	GCCCAAGCAGAGCTCGCTCGGGGGGGGGCCATGGTGTAGGCTGTGAGGCTGTGAGCAAGT	840
Dp	781	GCCCAAGCAGAGCTCGCTCGGGGGGGGGCCATGGTGTAGGCTGTGAGGCTGTGAGCAAGT	840
QY	841	GTTGGGTGAGTGGGTGTGGGTGAGTACATTGGCATCTATGCCACGATCAAGACAGACAG	900
Dp	841	GTTGGGTGAGTGGGTGTGGGTGAGTACATTGGCATCTATGCCACGATCAAGACAGACAG	900
QY	901	CACCTTCTCCGGATTTCTGTGTACTCCGACGTGGACAGCTCCCACTTTTGGTTAGTG	960
Dp	901	CACCTTCTCCGGATTTCTGTGTACTCCGACGTGGACAGCTCCCACTTTTGGTTAGTG	960
QY	961	CCCACTGCAAAAGTAGAGCTATGCTCTCACTCTGTAGAAAGAGGTGAGGCTGCACAACA	1020
Dp	961	CCCACTGCAAAAGTAGAGCTATGCTCTCACTCTGTAGAAAGAGGTGAGGCTGCACAACA	1020
QY	1021	GGTATCCAGAGAGGCTGGCCCCCTGGAAATTTGTGAATACCTAGAGGAGGTGGGGTAGA	1080
Dp	1021	GGTATCCAGAGAGGCTGGCCCCCTGGAAATTTGTGAATACCTAGAGGAGGTGGGGTAGA	1080
QY	1081	GCACCTCTCCGCTCTGCTGTGSCAAGAAATGGGAAACAATGCTCTTGCATCAGAGCTG	1140
Dp	1081	GCACCTCTCCGCTCTGCTGTGSCAAGAAATGGGAAACAATGCTCTTGCATCAGAGCTG	1140
QY	1141	GCAGCATGGGGGAGTGGCTGATTTCTGCCAAGACAGAGAGAGTGTCTGTGTGGCAA	1200
Dp	1141	GCAGCATGGGGGAGTGGCTGATTTCTGCCAAGACAGAGAGAGTGTCTGTGTGGCAA	1200
QY	1201	GTTGTAGTCCCCCAGTTGCTGTGTGTGTCAGAGAGCCACAGTGGGGTGTCTTCTCTGTGTC	1260
Dp	1201	GTTGTAGTCCCCCAGTTGCTGTGTGTGTCAGAGAGCCACAGTGGGGTGTCTTCTCTGTGTC	1260
QY	1261	CTGTGCTTCTGTGATCTTCCCCACCCCTCTGCTCTGTGGGCGGGCCCTTTTCTAGA	1320
Dp	1261	CTGTGCTTCTGTGATCTTCCCCACCCCTCTGCTCTGTGGGCGGGCCCTTTTCTAGA	1320
QY	1321	GATCATCATATAACTTAAGAACCTCATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1377
Dp	1321	GATCATCATATAACTTAAGAACCTCATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1377

US-RESULT 11
US-10-175-746-361
Sequence 361, Application US/1015746A
Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.

CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-918-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGAGCCGGCAGAGGACCAACAGAGC 60
DB 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGAGCCGGCAGAGGACCAACAGAGC 60
QY 61 TGGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 61 TGGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 GGTCTGTCTCTCTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 GGTCTGTCTCTCTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 CAGCTCTGCTCTCTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 CAGCTCTGCTCTCTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 CTTGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 CTTGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 CGACGCGCTGCTGTGTAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CGACGCGCTGCTGTGTAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CCAAGTGGCTGGGAGTCTACTTTCGCGTCCATCCACCGCTACCGGAGGAGGAGGAGGAG 720
DB 661 CCAAGTGGCTGGGAGTCTACTTTCGCGTCCATCCACCGCTACCGGAGGAGGAGGAGGAG 720
QY 721 GTTGTATCTGTGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GTTGTATCTGTGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
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QY 901 CACTTCTCCGAGTCTTGTGTAAGTCCGAGTGGACAGACAGTCCCAAGTCTTGTAGTG 960
DB 901 CACTTCTCCGAGTCTTGTGTAAGTCCGAGTGGACAGACAGTCCCAAGTCTTGTAGTG 960
QY 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCTACTCTCTAGAAAGAGGAGGAGTGAAGTCAACCA 1020
DB 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCTACTCTCTAGAAAGAGGAGGAGTGAAGTCAACCA 1020
QY 1021 GGTCAATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 GGTCAATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GCATCTCCGCTCTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 GCATCTCCGCTCTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 GCAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 GCAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 GTGTAGTCCGCTCTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1201 GTGTAGTCCGCTCTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
QY 1261 CTCTGCTCTCTGTAATCTCTCCACCCCTCTGCTGCTGGGAGGAGGAGGAGGAGGAGG 1320
DB 1261 CTCTGCTCTCTGTAATCTCTCCACCCCTCTGCTGCTGGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377
DB 1321 GATCACTCAATTAACCTTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 13
US-10-176-921-361
; Sequence 361, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-176-921-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGAGCCGGCAGAGGACCAACAGAGC 60
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[illegible]

QY	1321	GATCAGCTCAATAAACCTTAGAACCCTCATTTTTTTTTTTTTTTTTTTTTTTTAAAAAAA	1377
Dd	1321	GATCAGCTCAATAAACCTTAGAACCCTCATTTTTTTTTTTTTTTTTTTTTTTTAAAAAAA	1377
 RESULT 15 US-10-140-474-361			
/	Sequence 361,	Application US/10140474	
/	Publication No.	US20030032156a1	
/	GENERAL INFORMATION:		
/	APPLICANT:	Baker, Kevin P.	
/	APPLICANT:	Beresini, Maureen	
/	APPLICANT:	DeForge, Laura	
/	APPLICANT:	Desnoyers, Luc	
/	APPLICANT:	Filvaroff, Ellen	
/	APPLICANT:	Gao, Wei-Qiang	
/	APPLICANT:	Gerritsen, Mary E.	
/	APPLICANT:	Goddard, Audrey	
/	APPLICANT:	Godowski, Paul J.	
/	APPLICANT:	Gurney, Austin L.	
/	APPLICANT:	Sherwood, Steven	
/	APPLICANT:	Smith, Victoria	
/	APPLICANT:	Stewart, Timothy A.	
/	APPLICANT:	Tunas, Daniel	
/	APPLICANT:	Watanabe, Colin K	
/	APPLICANT:	Wood, William	
/	APPLICANT:	Zhang, Zhenlin	
/	TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC		
/	FILE REFERENCE: P3330R1C162		
/	CURRENT APPLICATION NUMBER: US/10/140,474		
/	PRIORITY FILING DATE: 2002-05-06		
/	Prior Application removed - See Palm or File Wrapper		
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/	SEQ ID NO 361		
/	LENGTH: 1377		
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Dd	61	TGGGGTGACGCAGGAGGAGGAGGGGGCCCTGTGCCGGGGAGAAAGCGCGGGGCTGTGAGCACCA	120
QY	121	CCAAGTCGAGGGGTCCGGAGTAGCGAGGCGCCCCGAAAGAGAGGCGCATCGGGGAGCGGAGG	180
Dd	121	CCAAGTCGAGGGGTCCGGAGTAGCGAGGCGCCCCGAAAGAGAGGCGCATCGGGGAGCGGAGG	180
QY	181	GGGAGCTGGAGAGAGNACCCCGGCGTTCGGGGCTCCCGGTGCACAGCGCTATGAGGCGCACTCT	240
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Dd	241	CGTCCGTGCTGCTCTGTGGGCTGTGGGCGCGGCGCTCGCCCTCATGTGACGACACACAGATCCC	300
QY	301	CAGCCTGTGCCCCGGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGGCAACATGGAGGCAAGG	360
Dd	301	CAGCCTGTGCCCCGGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGGCAACATGGAGGCAAGG	360
QY	361	CTTGGCGGGGCGCGATGTGCGCGAGAGGCGCGGAGCGGCGCGCCGGGGGCTCCGGGAGAGAA	420
Dd	361	CTTGGCGGGGCGCGATGTGCGCGAGAGGCGCGGAGCGGCGCGCCGGGGGCTCCGGGAGAGAA	420
QY	421	AGCGGAGGGCGGAGGCGCGGAGCTTGCAGGACCTTCAGAGGAGACCCCGGGGCGCGAGAGAA	480

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 11:27:14 ; Search time 367 Seconds
(without alignments)
8449.596 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1377	100.0	20	AAx87258
2	1377	100.0	20	AAx80052
3	1377	100.0	21	AAAD01241
4	1377	100.0	21	AAx46907
5	1377	100.0	21	AAx49560
6	1377	100.0	22	AAx21424
7	1326	96.3	21	AAx38626
8	1305	94.8	20	AAx24684
9	1119	81.3	22	AAx44970

10	1068	77.6	1338	22	AAx44998	Human secreted pro
11	1068	77.6	1338	22	AAx44999	Human secreted pro
12	1068	77.6	1338	22	AAx45000	Human secreted pro
13	1068	77.6	1338	22	AAx45001	Human secreted pro
14	912	66.2	3248	24	AAx39624	Human secreted pro
15	763	55.4	764	24	AAx62228	CDNA sequence #15
16	638	46.3	1082	23	AAx76911	DNA encoding novel
17	608	44.2	728	22	AAx49971	Human TANGO 253 OR
18	608	44.2	728	22	AAx49972	Human secreted pro
19	557	40.5	728	22	AAx44994	Human secreted pro
20	557	40.5	728	22	AAx44995	Human secreted pro
21	557	40.5	728	22	AAx44996	Human secreted pro
22	544	39.5	602	22	AAx34447	Human colon cancer
23	305	22.1	536	23	AAx98154	Human signal pepti
24	247	17.9	536	23	AAx76910	DNA encoding novel
25	60	4.4	60	24	ABN0870	Human spliced tran
26	51	3.7	51	20	AAx24695	Linker primer ZC15
27	51	3.7	51	20	AAx24703	Linker primer ZC15
28	50	3.6	50	20	AAx24696	Linker primer ZC15
29	50	3.6	50	20	AAx24704	Linker primer ZC15
30	45	3.3	45	20	AAx80088	Human PRO344 probe
31	45	3.3	45	21	AAx58514	Human PRO344 (UNQ3
32	45	3.3	45	21	AAx01258	Hybridisation prob
33	45	3.3	45	21	AAx46913	Probe used to scre
34	45	3.3	45	21	AAx49494	Probe for CDNA enc
35	45	3.3	65	20	AAx24697	Linker primer ZC15
36	43	3.1	68	20	AAx24705	Linker primer ZC15
37	39	2.8	63	20	AAx24702	Linker primer ZC15
38	35	2.5	729	22	AAx44973	Murine TANGO 253 c
39	35	2.5	729	22	AAx45038	Murine secreted pr
40	35	2.5	729	22	AAx45039	Murine secreted pr
41	35	2.5	729	22	AAx45040	Murine secreted pr
42	35	2.5	729	22	AAx45041	Murine secreted pr
43	35	2.5	1263	22	AAx44972	Human TANGO 253 O
44	35	2.5	1263	22	AAx45006	Murine secreted pr
45	35	2.5	1263	22	AAx45007	Murine secreted pr

ALIGNMENTS

RESULT 1	
AAx87258	AAx87258 standard; CDNA; 1377 BP.
ID	AAx87258; (first entry)
AC	27-SEP-1999
XX	CDNA clone encoding human PRO344, amplified in tumour cells.
DT	PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human; ss.
DE	Homo sapiens.
XX	
OS	
XX	
FH	Key
FT	CDs
FT	sig_peptide
FT	mat_peptide
FT	Location/Qualifiers
XX	/*tag= a
XX	227..271
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XX	272..955
XX	/*tag= c
PN	WO9935170-A2.
XX	
PD	15-JUL-1999.
XX	
PF	05-JAN-1999;
XX	99WO-US00106.
PR	20-NOV-1998;
PR	05-JAN-1998;
PR	29-APR-1998;
PR	22-MAY-1998;
PR	98US-0109304.
PR	98US-0070440.
PR	98US-0083500.
PR	98US-0086414.

PD 10-JUN-1999.
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 PF 01-DEC-1998; 98WO-US25108.
 XX
 PR 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069425.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069696.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX
 PA (GENENTECH INC.)
 XX
 PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;
 DR WPI; 1999-371118/31.
 DR P-PSDB; AAY17827.
 XX
 PT Nucleic acids encoding PRO secreted and transmembrane proteins
 XX
 PS Claim 2; Fig 20; 123pp; English.
 PS
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cyostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 CC
 XX Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;
 SQ

Query Match 100.0%; Score 1377; DB 20; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 181 GGGAGTGGAG 240
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 QY 301 CAGCCTCTGAGGAG 360
 DB 301 CAGCCTCTGAGGAG 360
 QY 361 CTGGCGGGGCGAG 420
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DB 361 CTGGCGGGGCGAG 420
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 QY 781 GCGGAG 840
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RESULT 3
 AAD01241
 ID AAD01241 standard; cdna; 1377 BP.
 XX
 AC AAD01241;
 XX

DT		08-NOV-2000	(first entry)
XX			
DE	Human PRO344 protein encoding cDNA clone, DNA40592-1242.		
XX			
KM	PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative;		
KM	neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;		
KW	breast; prostate; colon; lung; renal; ovarian; central nervous system;		
KM	CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;		
XX	extracellular domain; ECD; ss.		
XX			
OS	Homo sapiens.		
FT			
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XX			
PN			
PD	WO20032778-AZ.		
XX			
XX	08-JUN-2000.		
XX			
PF	30-NOV-1999; 99WO-US28409.		
XX			
PR	01-DEC-1998; 98MO-US25108.		
PR	16-DEC-1998; 98US-0112850.		
PR	22-DEC-1998; 98US-0113296.		
PR	20-JUL-1999; 99US-0144738.		
XX	26-JUL-1999; 99US-0145698.		
PA	(GETH) GENENTECH INC.		
PI	Chen J, Goddard A, Gurney AL, Hillian K, Napier M, Wood WI;		
DR	WP1: 2000-412325/35.		
DR	P-PSDB; AAY71468.		
PT	New composition useful for inhibiting neoplastic cell growth and for		
PT	treatng cancers, comprises PRO655, PRO344 or PRO364 polypeptide or		
PT	their antagonists -		
XX			
PS	Claim 20; Fig 5; 108pp; English.		
XX			
CC	The present sequence is the cDNA clone, designated as DN40592-1242,		
CC	encoding the human PRO344 polypeptide. It is isolated from human foetal		
CC	Lung tissue cDNA library, identified using probes based on a consensus		
CC	sequence DN434398, derived from secreted protein extracellular domain		
CC	(ECD) Expressed Sequence Tag (EST). This clone is assigned ATCC deposit		
CC	No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and		
CC	is used for treating tumours, using an effective amount of PRO655, PRO364		
CC	and PRO344. This composition is especially useful for treatment of human		
CC	cancers such as breast, prostate, colon, lung, renal, ovarian and CNS,		
CC	leukemia and melanoma.		
SQ	Sequence 1377 BP: 251 A; 422 C; 472 G; 232 T; 0 other:		
OY	Query Match	100.0%; Score 1377; DB 21; Length 1377;	
OY	Best Local Similarity	100.0%; Pred. No. 0;	
Db	Matches 1377; Conservative	0; Mismatches	0; Indels
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QY	121	CCAACTGGAGGGTCCGGAGTACCGAGCCGCCGGAAGAGAGCCATGGGGAGACCCGGAGGG	180
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Db	241	CGTCTGCTGCTCTGCGGCGTGGCGGCGGCGCTCGCCCGCCACTGAGAGACACAAAGATCCC	300
QY	301	CAGCCTCTGCCCCGGGGCACCCCGGCTTCCAGGCACGCCGGGCCACATGGCAGCAGGG	360
Db	301	CAGCCTCTGCCCCGGGGCACCCCGGCTTCCAGGCACGCCGGGCCACATGGCAGCAGGG	360
QY	361	CTTGCCGGGGCCGAGATGGGCGCGAGGGCGGCGGAGGGCGCCCGGGGGCTCCGGAGAGA	420
Db	361	CTTGCCGGGGCCGAGATGGGCGCGAGGGCGGCGGAGGGCGCCCGGGGGCTCCGGAGAGA	420
QY	421	AGGCGAGGGCGGGAGGCCGGGACTCCGGGACCTTCGAGGGGACCCCGGGCCGCGAGAGA	480
Db	421	AGGCGAGGGCGGGAGGCCGGGACTCCGGGACCTTCGAGGGGACCCCGGGCCGCGAGAGA	480
QY	481	GGCGGGAGACCCCGGGGGCCACCGGGGCTGCGGGGAGTGTCTGGTGCCTCCCGATCCGC	540
Db	481	GGCGGGAGACCCCGGGGGCCACCGGGGCTGCGGGGAGTGTCTGGTGCCTCCCGATCCGC	540
QY	541	CTTCAGCGCCAAAGCCTCGAGAGCGGGGTGCTCGCGCGTGTGAGCGCACCTTCCTCT	600
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QY	721	GTTTATCTGGGAAGATGGGAGATTCATTCGCTTCTTCCAGTTTTCGGGGGGTG	780
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QY	901	CACCTTCGCGAATTCGTGTGACTTCGACAGGGACAGCTCCCAAGCTTGTGCTTAGTG	960
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QY	1081	GCACCTTCGCGTCTGCTGCTGGCAAGAAATGGGAACAATGGCTGTCTCGATCAAGTGTG	1140
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QY	1141	GCACCATGGGAGAGGCTGTGATTTCTCCCAAGACAGAGAGAGTCTGTGTCGCA	1200
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QY 1321 GATCAGTCATTAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCAGTCATTAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377
RESULT 4
ID AAA46907 standard; cDNA: 1377 BP.
AC AAA46907;
XX 03-OCT-2000 (first entry)
XX cDNA encoding novel polypeptide PRO344.
XX PRO201; PRO322; PRO1265; PRO344; PRO343; PRO347; PRO357;
KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
XX Homo sapiens.
XX OS
FH Key Location/Qualifiers
FT CDS 227..958
FT tag- a
PN MO200037640-A2.
XX 29-JUN-2000.
XX 16-DEC-1999; 99WO-US30095.
XX 22-DEC-1998; 98US-0113296.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 02-DEC-1999; 99WO-US28565.
XX (GETH) GENENTECH INC.
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
PI Wood WT;
XX WPI: 2000-452188/39.
XX P-PSDB: AAY93688.
XX New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation -
XX Claim 50; Fig 9; 220pp; English.
XX The present sequence encodes a novel human polypeptide. The
XX specification describes novel polypeptides designated PRO201, PRO292,
XX PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,
XX PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
XX the genome of tumour cells. The polypeptides are believed to contribute
XX to tumorigenesis. The polypeptides are useful target for the
XX identification of certain cancers, and may act as predictors of the
XX prognosis of tumour treatment. Antibodies against these polypeptides
XX are useful in the treatment and diagnosis of neoplastic cell growth
XX and proliferation in mammals.
XX Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

Query Match 100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 301 CAGCGCTGCGCGGGGCGACCCCGGCGTTCAGAGGAGCGCGGGCCACCATGGCGAGCGG 360
QY 361 CTTCGCGGCGCGAGTGGCGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGAGAA 420
Db 361 CTTCGCGGCGCGAGTGGCGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGAGAA 420
QY 421 AGCGAGGCGGCGAGGCGCGGAGCTGCCGAGCTTGAGGAGACCCCGGCGCGAGAGA 480
Db 421 AGCGAGGCGGCGAGGCGCGGAGCTGCCGAGCTTGAGGAGACCCCGGCGCGAGAGA 480
QY 481 GGGCGGAGCCCGGGGGGCCACCGGGGAGTGGCGGAGTGGCTCCGCGATCCGC 540
Db 481 GGGCGGAGCCCGGGGGGCCACCGGGGAGTGGCGGAGTGGCTCCGCGATCCGC 540
QY 541 CTTCAGCGCCAAAGCGCTCCAGAGAGCGGGGTGCTCGCGCTGACGACCCCTTCCCT 600
Db 541 CTTCAGCGCCAAAGCGCTCCAGAGAGCGGGGTGCTCGCGCTGACGACCCCTTCCCT 600
QY 601 CGACCGGCTGCTGGAACGAGCAGGAGCATTTAGAGCGCGTACCGGCAAGTTACTG 660
Db 601 CGACCGGCTGCTGGAACGAGCAGGAGCATTTAGAGCGCGTACCGGCAAGTTACTG 660
QY 661 CCAGGTGCTGGGGGTCTACTTCTGCGGCTCCAGTCCAGCGTACCGGGCGAGCTGCA 720
Db 661 CCAGGTGCTGGGGGTCTACTTCTGCGGCTCCAGTCCAGCGTACCGGGCGAGCTGCA 720
QY 721 GTTGATCTGTGGAAGATGCGAATTCATTCCTTCTTCCAGTTTTCGGGGGTG 780
Db 721 GTTGATCTGTGGAAGATGCGAATTCATTCCTTCTTCCAGTTTTCGGGGGTG 780
QY 781 GCCCAAGCAGCTTCGCTCTGCGGGGGGCGATGAGGCTGAGAGCTGAGAGCAAGT 840
Db 781 GCCCAAGCAGCTTCGCTCTGCGGGGGGCGATGAGGCTGAGAGCTGAGAGCAAGT 840
QY 841 GTGGGTGAGGTGGGTGGGTGAGTACATTTGGCATATGACAGCATCAAGAGACAG 900
Db 841 GTGGGTGAGGTGGGTGGGTGAGTACATTTGGCATATGACAGCATCAAGAGACAG 900
QY 901 CACCTTCCGGAATTTCTGTACTCCGAGCTGGCAGACGCTCCCAAGTCTTGTCTAGTG 960
Db 901 CACCTTCCGGAATTTCTGTACTCCGAGCTGGCAGACGCTCCCAAGTCTTGTCTAGTG 960
QY 961 CCCACTGCAAGTAGCTCATAGCTCTTCACTCTTAGAAGAGAGGCTGAGGCTGACACCA 1020
Db 961 CCCACTGCAAGTAGCTCATAGCTCTTCACTCTTAGAAGAGAGGCTGAGGCTGACACCA 1020


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Db      841 GTGGGTGACAGTGGGTGTGGGTGACTACATGATGGCATATATGCGACAGATCAAGACAGACAG 900
Qy      901 CACCTTCCCGGATTTTCGTGTGTACTCCGACTGGACAGCTCCCAAGTCTTGCTTAGTG 960
Db      901 CACCTTCCCGGATTTTCGTGTGTACTCCGACTGGACAGCTCCCAAGTCTTGCTTAGTG 960
Qy      961 CCCACTGGAAGTGAAGTCAATGCTCTCACTCTACCTCTAGAGAGAGGTGTGAGGGCTGACAAACA 1020
Db      961 CCCACTGGAAGTGAAGTCAATGCTCTCACTCTACCTCTAGAGAGAGGTGTGAGGGCTGACAAACA 1020
Qy      1021 GGTCAATCCAGAGAGGGCTGCCCCCCTCGAATATTTGTGAATGATGAGGAGGTGGGTAGA 1080
Db      1021 GGTCAATCCAGAGAGGGCTGCCCCCCTCGAATATTTGTGAATGATGAGGAGGTGGGTAGA 1080
Qy      1081 GCACATCCGCTCTCTCTCTCTGCGAAGGATGGAGACTGCTGTCTGCTGATCAGCTCTG 1140
Db      1081 GCACATCCGCTCTCTCTCTCTGCGAAGGATGGAGACTGCTGTCTGCTGATCAGCTCTG 1140
Qy      1141 GCAGCATGGGCGAGTGGCTGTGATTTCTGCCAAGACAGAGAGAGTGTCTGTGTCGCA 1200
Db      1141 GCAGCATGGGCGAGTGGCTGTGATTTCTGCCAAGACAGAGAGAGTGTCTGTGTCGCA 1200
Qy      1201 GTGTAGTCCCGCACTGCTCTGTGTCAGAGAGCCACGCGTGGGTGCTCTCTCTGTC 1260
Db      1201 GTGTAGTCCCGCACTGCTCTGTGTCAGAGAGCCACGCGTGGGTGCTCTCTCTGTC 1260
Qy      1261 CTCTGCTCTCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db      1261 CTCTGCTCTCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Qy      1321 GATCACTCAATTAACCTTAAGAACCTCTATTAATAAAAAAAAAAAAAAAAAAAAAA 1377
Db      1321 GATCACTCAATTAACCTTAAGAACCTCTATTAATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 6
AAS21424
ID      AAS21424 standard; cDNA; 1377 BP.
AC      AAS21424;
DT      24-OCT-2001 (first entry)
XX      Human cDNA sequence encoding for PRO344 polypeptide.
DE      Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW      breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW      cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW      adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX      Homo sapiens.
OS      Homo sapiens.
PN      WO200140466-A2.
XX      07-JUN-2001.
PD      01-DEC-2000; 2000WO-US32678.
PE      01-DEC-1999; 99WO-US28301.
XX      01-DEC-1999; 99WO-US28634.
PR      02-DEC-1999; 99WO-US28551.
XX      02-DEC-1999; 99WO-US28564.
PR      02-DEC-1999; 99WO-US28565.
XX      09-DEC-1999; 99US-0170262.
PR      16-DEC-1999; 99WO-US30095.
XX      20-DEC-1999; 99WO-US30911.
PR      20-DEC-1999; 99WO-US30999.
XX      30-DEC-1999; 99WO-US31243.
PR      06-JAN-2000; 2000WO-US00277.
XX      06-JAN-2000; 2000WO-US00376.
PR      11-FEB-2000; 2000WO-US03565.
XX      18-FEB-2000; 2000WO-US04341.
PR      24-FEB-2000; 2000WO-US04342.

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PR      22-FEB-2000; 2000WO-US04414.
PR      24-FEB-2000; 2000WO-US04914.
PR      24-FEB-2000; 2000WO-US05004.
PR      01-MAR-2000; 2000WO-US05601.
PR      20-MAR-2000; 2000WO-US07377.
PR      21-MAR-2000; 2000WO-US07532.
PR      30-MAR-2000; 2000WO-US08439.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15264.
PR      10-NOV-2000; 2000WO-US30873.
PA      (GENTH ) GENENTECH INC.
XX      Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI      Gerlitsen ME, Goddard A, Godowski PJ, Gunney AU, Sherwood S;
PI      Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
DR      WPI: 2001-408281/43.
DR      P-PSDB: AAU12352.
XX      Isolated, secretory and transmembrane PRO polypeptide used to detect
PT      other PRO polypeptides, link bioactive molecules to cells expressing
PT      PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT      lung, breast, prostate, cervical.
XX      Claim 3; Fig 361; 813pp; English.
PS      AAS21244-AAS21518 encode for novel human secretory and transmembrane
XX      PRO polypeptides. The PRO polypeptides are useful to detect other
XX      PRO polypeptides, to link bioactive molecules to cells expressing
XX      PRO polypeptides, to modulate biological activities of cells expressing
XX      PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX      breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX      polypeptide expression in a cell sample to that in a control sample.
XX      Some of the 275 sequences are also useful to stimulate the release of
XX      tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX      proliferation or differentiation of chondrocytes, the proliferation or
XX      gene expression in pericyte cells, the release of proteoglycans from
XX      cartilage, the proliferation of inner ear utricular supporting cells or
XX      of T-lymphocytes, or the release of a cytokine from peripheral blood
XX      monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX      the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX      skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX      to factor VIIA. The PRO polypeptides can be used in assays to identify
XX      molecules involved in binding interactions. The polynucleotides encoding
XX      PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX      transgenic or knock out animals and can be used in gene therapy.
SQ      Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other:
Query Match      100.0%; Score 1377; DB 22; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GACTAGTCTCTTTGAGTCTGGAGAGAGAAAGCCGAGCCGACGAGAGCAACAGAGC 60
Db      1 GACTAGTCTCTTTGAGTCTGGAGAGAGAAAGCCGAGCCGACGAGAGCAACAGAGC 60
Qy      61 TGGGCTGACGCGAGGCGAGGGGCGCTTGGCGCGGAGAGAGCGGGGCTTGACACCA 120
Db      61 TGGGCTGACGCGAGGCGAGGGGCGCTTGGCGCGGAGAGAGCGGGGCTTGACACCA 120
Qy      121 CCACTGAGGAGTCCGAGTACGAGAGCCGCCGAAAGAGAGCCATCGGGAGCGGGAGG 180
Db      121 CCACTGAGGAGTCCGAGTACGAGAGCCGCCGAAAGAGAGCCATCGGGAGCGGGAGG 180
Qy      181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db      181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy      241 GGTCTGTCTCTCTGAGGCTGGGCGGCGGCTGCGCCCACTGAGACAGACAAGATCCC 300

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Db 241 CGTCTCTGCTCTCTGAGCCCTGAGCGCGGCTCCGCCCTCATGGAGCAACAAGATCCC 300
QY 301 CAGCCTTGCCCGGGGACACCCGGGCTTCCAGGACCCGGGACCACCATGAGCAGCAGG 360
Db 301 CAGCCTTGCCCGGGGACACCCGGGCTTCCAGGACCCGGGACCACCATGAGCAGCAGG 360
QY 361 CTTCGCGGGCGCGATGAGCCGCGAGCGGCGCGGCGCGGCGGCGCTCCGGGAGAA 420
Db 361 CTTCGCGGGCGCGATGAGCCGCGAGCGGCGCGGCGCGGCGGCGCTCCGGGAGAA 420
QY 421 AGCGGAGGGGGGAGGGGCGGAGCTGCGGGAGCTTCGAGGGGAGACCCCGGGCGCGAGAGA 480
Db 421 AGCGGAGGGGGGAGGGGCGGAGCTGCGGGAGCTTCGAGGGGAGACCCCGGGCGCGAGAGA 480
QY 481 GGGGGAGACCCGGGGGCGCCACCGGGGCTGCGGGGAGTGCCTCGGTCCTCCGAGTCCG 540
Db 481 GGGGGAGACCCGGGGGCGCCACCGGGGCTGCGGGGAGTGCCTCGGTCCTCCGAGTCCG 540
QY 541 CTTCAGCGCCAAAGCGCTCCAGAGACCGGGTGCCTCCGCGTTCGAGCGACCTTGCCCTT 600
Db 541 CTTCAGCGCCAAAGCGCTCCAGAGACCGGGTGCCTCCGCGTTCGAGCGACCTTGCCCTT 600
QY 601 CGACCGGCTGCTGGTGAAGAGAGAGGACATTAAGAGCGCGTCAACGGCAAGTTCACCTG 660
Db 601 CGACCGGCTGCTGGTGAAGAGAGAGGACATTAAGAGCGCGTCAACGGCAAGTTCACCTG 660
QY 661 CCAAGTGCCTGGGGTCTACTACTTGGCGTCCATGCAACCGCTTACCGGGCGCACCTGCA 720
Db 661 CCAAGTGCCTGGGGTCTACTACTTGGCGTCCATGCAACCGCTTACCGGGCGCACCTGCA 720
QY 721 GTTTGATCTGGTGAAGATGCGGATTCATTCCTTTCTTCCAGTTTTTCGGGGGGTG 780
Db 721 GTTTGATCTGGTGAAGATGCGGATTCATTCCTTTCTTCCAGTTTTTCGGGGGGTG 780
QY 781 GCCCAAGCCAGCCTCGCTCTCGGGGGGCGCATGCTGAGCCTGAGGACCAAGT 840
Db 781 GCCCAAGCCAGCCTCGCTCTCGGGGGGCGCATGCTGAGCCTGAGGACCAAGT 840
QY 841 GTGGGTCAGAGTGGGTGGGTGACTATTCATTTGGCATTTATGCCAGATCAAGACAGACAG 900
Db 841 GTGGGTCAGAGTGGGTGGGTGACTATTCATTTGGCATTTATGCCAGATCAAGACAGACAG 900
QY 901 CACCTTCTCCGGAATTTCTGCTGTAATCTCGAAGTGGACAGCTCCCACTTTTGTATG 960
Db 901 CACCTTCTCCGGAATTTCTGCTGTAATCTCGAAGTGGACAGCTCCCACTTTTGTATG 960
QY 961 CCCACTGCAAGAGAGCTCATGCTCATGCTCATGCTCATGAGGAGGGGTGAGGCTGACACCA 1020
Db 961 CCCACTGCAAGAGAGCTCATGCTCATGCTCATGCTCATGAGGAGGGGTGAGGCTGACACCA 1020
QY 1021 GGTTCATTCAGAGAGGCTGGCCGCCCTGGAATATTTGTAATGACTAGGAGGTGGGTAGA 1080
Db 1021 GGTTCATTCAGAGAGGCTGGCCGCCCTGGAATATTTGTAATGACTAGGAGGTGGGTAGA 1080
QY 1081 GCACCTCTCCCTCTGCTGCTGCTGCGAAGAAATGGGAAAGTGGCTGTCGATCAGGCTG 1140
Db 1081 GCACCTCTCCCTCTGCTGCTGCTGCGAAGAAATGGGAAAGTGGCTGTCGATCAGGCTG 1140
QY 1141 GCAGCATGAGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGAGTGGCTGCTGGTGGCAA 1200
Db 1141 GCAGCATGAGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGAGTGGCTGCTGGTGGCAA 1200
QY 1201 GTGTAAGTCCCGCAGTTGCTGCTGCTGCTGCGAAGCCACGAGTGGGGTGTCTCTTCTG 1260
Db 1201 GTGTAAGTCCCGCAGTTGCTGCTGCTGCTGCGAAGCCACGAGTGGGGTGTCTCTTCTG 1260
QY 1261 CTCTGCTTCTCTGAGATCTCCCAACCCCTCTGCTCTGAGGCGCGGCTTTTCTCAGA 1320
Db 1261 CTCTGCTTCTCTGAGATCTCCCAACCCCTCTGCTCTGAGGCGCGGCTTTTCTCAGA 1320
QY 1321 GATCACTCATATAACTAGAACCTCTATATATATATATATATATATATATATATATATAT 1377
Db 1321 GATCACTCATATAACTAGAACCTCTATATATATATATATATATATATATATATATATAT 1377

Db 1321 GATCACTCATATAACTAGAACCTCTATATATATATATATATATATATATATATATATAT 1377
RESULT 7
AAC58626
ID AAC58626 standard; cDNA: 1377 BP.
XX AAC58626;
XX 29-JAN-2001 (first entry)
XX
DE Human PRO344 protein UNQ303 encoding cDNA SEQ ID NO:240.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; anthraxitic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;
KW antineoplastic; hepatotropic; virucide; antiparasitic; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
OS Homo sapiens.
XX
XX W0200053758-A2.
XX
PD 14-SEP-2000.
PD
PE 02-MAR-2000; 2000WO-US05841.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99WO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145638.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 03-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 XX
 PA (GENTECH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI: 2000-572271/53.
 DR P-PSDB: AAB33461.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 PS Claim 23: Fig 95; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 1377 BP; 251 A; 423 C; 471 G; 232 T; 0 other;
 Query Match 96.3%; Score 1326; DB 21; Length 1377;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1376; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 421 AGGGAGGCGCGGAGGCGGAGCTCGCGGAGCACTCGAGGGAGACCCCGGCGCGAGGAGA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 GCGGAGACCCCGCGGGGCCACCGGCGCTCGCGGGAGTGTCTGGTCCCTCCGCATCCG 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 GCGCGGACCCCGCGGGGCCACCGGCGCTCGCGGGAGTGTCTGGTCCCTCCGCATCCG 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 CTTGAGGCGCAAGGCGTCCGAGAGCCGGGTGCTCCGCGCGCTGACGACCCCTTGCCCTT 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 541 CTTGAGGCGCAAGGCGTCCGAGAGCCGGGTGCTCCGCGCGCTGACGACCCCTTGCCCTT 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 CGACCGGTGTGTGTAAGAGAGGAGCAATTAAGAGCCGTCAACCGGCAAGTTACCTG 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 601 CGACCGGTGTGTGTAAGAGAGGAGCAATTAAGAGCCGTCAACCGGCAAGTTACCTG 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 CCAGGTGCTGGGGTCTACTACTTCCGCGTCAATGCCAGCTTACCGGGCCAGCTGCA 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 661 CCAGGTGCTGGGGTCTACTACTTCCGCGTCAATGCCAGCTTACCGGGCCAGCTGCA 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 721 GTTGTATCTGTGTAAGAGAGGCAATCCATTCCTTCTCCAGTTTTCGGGGGGTG 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 721 GTTGTATCTGTGTAAGAGAGGCAATCCATTCCTTCTCCAGTTTTCGGGGGGTG 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 781 GCCCAAGCCAGCTCTGCTCTGCGGGGGGCCATGCTGAGAGCTGAGCAACCAAGT 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 781 GCCCAAGCCAGCTCTGCTCTGCGGGGGGCCATGCTGAGAGCTGAGCAACCAAGT 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 841 GTGGGTGAGGTGGGTGTGGGTGACTACATATTGGCATTCAGCCATCAAGACAGAG 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 841 GTGGGTGAGGTGGGTGTGGGTGACTACATATTGGCATTCAGCCATCAAGACAGAG 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 901 CACCTTCGCCGATTTTCGTGCTACTCCGACTGGCAGAGTCCCGAGCTTGTGTTAGTG 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 901 CACCTTCGCCGATTTTCGTGCTACTCCGACTGGCAGAGTCCCGAGCTTGTGTTAGTG 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 961 CCCACTGCAAGTAGCTCATGCTCTACATCTCTGAAGAGAGGTTGAGGCTGCAACCA 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 961 CCCACTGCAAGTAGCTCATGCTCTACATCTCTGAAGAGAGGTTGAGGCTGCAACCA 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1021 GGTATATCCAGAGAGGCGTGGGCGCCCGCTGGAAATATGTGAATACATAGGAGGTGGGTAGA 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1021 GGTATATCCAGAGAGGCGTGGGCGCCCGCTGGAAATATGTGAATACATAGGAGGTGGGTAGA 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1081 GCACCTTCGCTGCTGCTGCTGCTGCAAGAGATGGAACAGTGTCTCTGATCAGGTCG 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1081 GCACCTTCGCTGCTGCTGCTGCTGCAAGAGATGGAACAGTGTCTCTGATCAGGTCG 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1141 GCAGCATGAGGCGAGTGGCTGATTTCTGCCAAGACAGAGAGTGTGCTGCGCAA 1200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1141 GCAGCATGAGGCGAGTGGCTGATTTCTGCCAAGACAGAGAGTGTGCTGCGCAA 1200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1201 GTGTAAGTCCCGCAGTGTCTGTGTCAGAGAGCCAGAGTGGGTGCTCTTCTCTGTC 1260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1201 GTGTAAGTCCCGCAGTGTCTGTGTCAGAGAGCCAGAGTGGGTGCTCTTCTCTGTC 1260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1261 CTTGCTTCTCTGATTCCTCCCAACCCCTCTCTGCTCTGAGGCGGCGCTTTTCTCAGA 1320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1261 CTTGCTTCTCTGATTCCTCCCAACCCCTCTCTGCTCTGAGGCGGCGCTTTTCTCAGA 1320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 8
 AAX24684 standard; cDNA; 1347 BP.
 AAX24684;
 21-JUN-1999 (first entry)
 Human adipocyte-specific protein zs1g39 cDNA.

KW	Adipocyte-specific protein; zslg39; human; fatty acid metabolism;
KW	energy balance; nutrition; antimicrobial; ss.
OS	Homo sapiens.
FH	Key
FH	CDS
FT	Location/Qualifiers
FT	/tag= a
FT	198..929
FT	s1g-peptide
FT	198..251
FT	/tag= b
FT	/note= "alternatively nucleotides 198-242"
FT	mat_peptide
FT	252..926
FT	/tag= c
FT	/note= "alternatively nucleotides 243-926"
PN	WO9910492-A1.
PD	04-MAR-1999.
XX	
PE	26-AUG-1998; 98WO-US17724.
XX	
PR	26-AUG-1997; 97US-0056983.
PA	(ZIMO) ZIMOGENTICS INC.
XX	
PI	Humes JM, Shepard FO;
DR	WPI: 1999-204665/17.
XX	P-PSDB: AAM97984.
PT	Zslg39 protein - used to modulate fatty acid metabolism
PS	Claim 16; 109-111; 132pp; English.
XX	
CC	This isolated polynucleotide encodes human adipocyte-specific
CC	protein zslg39 (AAM97984). Claimed polynucleotides comprise
CC	nucleotides 243-962, 252-962, 285-482, 285-485, 285-485,
CC	285-491, 285-491, 491-926 of this isolated polynucleotide.
CC	Novel zslg39 polypeptides were initially identified by querying an
CC	EST database for secretory signal sequences characterised by an
CC	upstream methionine start site, a hydrophobic region of approximately
CC	13 amino acids and a cleavage site. A single EST sequence was
CC	discovered, and the novel polypeptide encoded by the full-length
CC	cDNA allowed the identification of a homologue relationship with
CC	adipocyte complement related protein Acrp30 and adipocyte secreted
CC	protein apml. A full-length clone was obtained from a lung tissue
CC	library. The zslg39 gene maps to the 11q23.3 region. Expression
CC	vectors, cultured cells and a method of producing zslg39 polypeptide
CC	are claimed, as well as probes and primers (useful in diagnostic
CC	applications), and a method for modulating free fatty acid
CC	metabolism by administering a zslg39 polypeptide. The zslg39
CC	polypeptide may also be used in organ preservation, for
CC	cryopreservation, for surgical pretreatment to prevent injury due
CC	to ischaemia and/or inflammation, and as an antimicrobial agent,
CC	promoting lysis or phagocytosis of infectious agents.
CC	
SQ	Sequence 1347 BP: 235 A; 421 C; 465 G; 226 T; 0 other:
QY	Query Match 94.8%; Score 1305; DB 20; Length 1347;
Db	Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
44 AGGAGCAACACAGACTGGGTGCAGCGCAGAGGCCAGGGGCGCTGGCCGGGAGAAGG 103	
15 AGGAGCCAAACAGACTGGGTGCAGCGCAGAGGCCAGGGGCGCTGGCCGGGAGAAGG 74	
104 CGGGGCTGAGACACCACCACTGAGAGGTCCGAGTAGCAGCGCCCCGAAGAGGCCA 163	
Db 75 CGGGGCTGAGACACCACCACTGAGAGGTCCGAGTAGCAGCGCCCCGAAGAGGCCA 134	
QY 164 TCGGGGAACCCGGGAGGGGGAATGCGAAGAACCCCGCGTCCGGGCTCCGGTCCACG 223	

DE	Human secreted protein related coding sequence SEQ ID NO: 105.
KX	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW	INTERCEPT 258; coronary disorder; olfactory disorder;
KM	neurolept disorder; pulmonary disorder; immunological disorder;
KW	developmental disorder; kidney disorder; ss.
KX	Homo sapiens.
OS	
XX	MO200078808-A1.
PN	
PD	28-DEC-2000.
PX	19-JUN-2000; 2000WO-US16883.
PF	
XX	18-JUN-1999; 99US-0336536.
PR	
XX	(MILL-) MILLENNIUM PHARM INC.
PA	
PI	Leiby KR, McKay C, Bossone S;
XX	WI; 2001-050109/06.
DR	
XX	New nucleic acids for treating diseases and disorders, e.g.
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT	sclerosis and asthma -
XX	
PS	Disclosure; Page 272; 332pp; English.
XX	
CC	The present invention provides the protein and coding sequences of the
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC	coronary, pulmonary, olfactory, immunological, neurological,
CC	developmental and kidney disorders.
XX	
SQ	Sequence 1338 BP; 229 A; 422 C; 460 G; 227 T; 0 other;
Query Match	77.6%; Score 1068; DB 22; Length 1338;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 1288; Conservative	0; Mismatches 2; Indels 1; Gaps 1
QY	57 GGACTGGGCTACGGCAGCGAGGGGGCGCTGGGCCGGAGAGCGCGGGGGCTGAGAC 116
Db	18 GGACTGGGGTACCGCAGCGCAGGGGGCGCTGGGCCGGAGAGCGCGGGCTGAGAC 77
QY	117 ACCACCAACGTGAGGGGTCCGAGTAGTAGGAGGGCCCCGAAGAAGAGGCATTCGGGAGCCGG 176
Db	78 ACCACCAACGTGAGGGGTCCGAGTAGTAGGAGGGCCCCGAAGAAGAGGCATTCGGGAGCCGG 137
QY	177 AGGGGGGACTCGAGAGAGACCCTCGGCTTCGCGGCTCCGAGTSCAGGCTATGAGGCCAC 236
Db	138 AGGGGGGACTCGAGAGAGACCCTCGGCTTCGCGGCTCCGAGTSCAGGCTATGAGGCCAC 197
QY	237 TCCTGTCTCTGCTCTGCTCTGCGGCTTGCGGGCCGCGCTCGCCCACTGAGCAGCAACAAGA 296
Db	198 TCCTGTCTCTGCTCTGCTCTGCGGCTTGCGGGCCGCGCTCGCCCACTGAGCAGCAACAAGA 257
QY	297 TCCCCAGCTCTGCCCCGGGGGACCCCGGCTTTCCAGGACGACCGGGCCACCATGTGCGAGCC 356
Db	258 TCCCCAGCTCTGCCCCGGGGGACCCCGGCTTTCCAGGACGACCGGGCCACCATGTGCGAGCC 317
QY	357 AGGCTTGTCCGGGCGCGCATGGCCGCGAGCGCGGCGGAGCGGGCGCGCGGGGCTCGGGGAG 416
Db	318 AGGCTTGTCCGGGCGCGCATGGCCGCGAGCGCGGCGGAGCGGGCGCGGGGCTCGGGGAG 377
QY	417 AGAAGCGGAGGGGGGAGGCGCGGACTTCGGGAGCTTCGAGGGGAGCCCGGGCCGCGAG 476
Db	378 AGAAGCGGAGGGGGGAGG--CGGAGCTTCGGGAGCTTCGAGGGGAGCCCGGGCCGCGAG 436
QY	477 GAGAGGCGGAGCCCGCGGGGCCACCGGGCTTCCGGGAGTGTCTGCTTCCGCGAT 536
Db	437 GAGAGGCGGAGCCCGCGGGGCCACCGGGCTTTCGGGAGTGTCTGCTTCCGCGAT 496

OY	533	CCGCGCTTCAGGCGCAACGCGTCCGAGACCGGGGCGCTCCGCGCTGACGACACCCCTTGC	596
Db	497	CCGCGCTTCAGGCGCAACGCGTCCGAGACCGGGGCGCTCCGCGCTGACGACACCCCTTGC	556
OY	597	CCTTCGACACGGGTGCTGGTGAACAGACAGGAGACATTATGACAGCGCGTACCGGGCAAGTCA	656
Db	557	CCTTCGACACGGGTGCTGGTGAACAGACAGGAGACATTATGACAGCGCGTACCGGGCAAGTCA	616
OY	657	CCTGCCAGGTGCGTGGGGTCTACTACTTTCGCGGTCAATGCGACCGTGTACCGGGCCAGCC	716
Db	617	CCTGCCAGGTGCGTGGGGTCTACTACTTTCGCGGTCAATGCGACCGTGTACCGGGCCAGCC	676
OY	717	TGCACTTTCGATCTGCTGTGAAGAAATGGCAATTCATATGCGCTCTTCTTTCACATTTTTCGGGG	776
Db	677	TGCACTTTCGATCTGCTGTGAAGAAATGGCAATTCATATGCGCTCTTCTTTCACATTTTTCGGGG	736
OY	777	GGTGGCCCAAGCCAGCCCTCGCTCTCGGGGGGGGCGCATATGATGAGGCTGAGCGCTGAGAGCC	836
Db	737	GGTGGCCCAAGCCAGCCCTCGCTCTCGGGGGGGGCGCATATGATGAGGCTGAGAGCTGAGAGCC	796
OY	837	AAGTGTGGGTGACAGGTGGGTGGGTGACTATATGCAATTCATATGCAATTCATCCAGCATCAAGACAG	896
Db	797	AAGTGTGGGTGACAGGTGGGTGGGTGACTATATGCAATTCATATGCAATTCATCCAGCATCAAGACAG	856
OY	897	ACACACCTCTCTCCGGAAATTCCTGGTGTACCTCCGACCTGGGACAGTGTCCCGAGTCTTTCCTT	956
Db	857	ACACACCTCTCTCCGGAAATTCCTGGTGTACCTCCGACCTGGGACAGTGTCCCGAGTCTTTCCTT	916
OY	957	AGTGCACCACTGCAAAAGTAGACTCATGTGCTTCATCTCATCTAGAAAGAGAGGGTGTAGAGCTGACA	1016
Db	917	AGTGCACCACTGCAAAAGTAGACTCATGTGCTTCATCTCATCTAGAAAGAGAGGGTGTAGAGCTGACA	976
OY	1017	ACCAAGTTCATCAGAGAGGGGTGGCCCCCTGGGAATATTGTGAAATGACTAAGGAGGTGGGG	1076
Db	977	ACCTGTGTATTCAGAGAGGGGTGGCCCCCTGGGAATATTGTGAAATGACTAAGGAGGTGGGG	1036
OY	1077	TAGAGCACTCTCCGCTCCCTGGTGCCTGGGAAGGAATGGGAACAGTGGCGTGTGGCATCAGG	1136
Db	1037	TAGAGCACTCTCCGCTCCCTGGTGCCTGGGAAGGAATGGGAACAGTGGCGTGTGGCATCAGG	1096
OY	1137	TCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCCAAGACAGACAGAGGATGTGCTGTCTGT	1196
Db	1097	TCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCCAAGACAGACAGAGGATGTGCTGTCTGT	1156
OY	1197	GCAAGTGTAACTCCCCCAATGCTCTGTGTCCAGAGAGCCACAGGGTGGGTCTCTCTCTCT	1256
Db	1157	GCAAGTGTAACTCCCCCAATGCTCTGTGTCCAGAGAGCCACAGGGTGGGTCTCTCTCTCTCT	1216
OY	1257	GGTCTCTGCTTCTCTGGATCTCTCCGACACCCCTCGTGCCTCTGGGGGCGGGCCCTTTTCT	1316
Db	1217	GGTCTCTGCTTCTCTGGATCTCTCCGACACCCCTCGTGCCTCTGGGGGCGGGCCCTTTTCT	1276
OY	1317	CAGAGATCACTCAATAAACCCTAAGAACCCCTC	1347
Db	1277	CAGAGATCACTCAATAAACCCTAAGAACCCCTC	1307
RESULT 12			
AAAF45000			
ID ID AAF45000 standard; cDNA; 1338 BP.			
XX AAF45000;			
XX AC			
XX DT 28-MAR-2001. (first entry)			
XX DE			
XX Human secreted protein related coding sequence SPO ID NO: 107.			
XX			
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;			
KW INTERCEPT 256; coronary disorder; olfactory disorder;			
KW neurological disorder; pulmonary disorder; immunological disorder;			
KW developmental disorder; kidney disorder; ss.			

PR 08-NOV-2000; 2000US-247505P.
 PR 09-NOV-2000; 2000US-248642P.
 PR 16-NOV-2000; 2000US-249824P.
 PR 21-NOV-2000; 2000US-252824P.
 PR 08-DEC-2000; 2000US-254305P.
 PR 18-DEC-2000; 2000US-256448P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Yue H, Yao MG, Gandhi AR, Baughn MR, Swarnakar A, Walla NK;
 PI Sanjambala M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burford N;
 PI Ding L, Hafalia Aja, Tang YT, Bandman O, Warren BA, Honchell CD;
 PI Lu DM, Thangavelu K, Lee S, Xu Y, Yang J, Lai PG, Tran B;
 PI Ison CH, Duggan BM, Sapperstein SK;
 XX
 DR WPI: 2002-519296/55.
 DR P-PSDB; AAO21663.
 XX
 PT Human secreted proteins and polynucleotides for diagnosing, treating or
 PT preventing disorders of cell proliferative, cardiovascular,
 PT developmental, neurological and autoimmune/inflammatory disorders -
 PT
 PS Claim 5; Page 194-195; 229pp; English.
 XX
 CC The invention relates to an isolated human secreted protein (SECP)
 CC polypeptide from 63 fully defined protein sequences given in the
 CC specification. The polypeptide is useful for the diagnosing/treating of a
 CC disease with decreased/overexpression of SECP. Examples of disorders
 CC associated with abnormal expression of SECP include a cell proliferative
 CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory
 CC disorder, AIDS, allergies, anemia, asthma, cardiovascular disease e.g.
 CC congestive heart failure, ischemic heart disease; developmental disorder
 CC e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.
 CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.
 CC The SECP polynucleotide and polypeptide are further useful for analysing
 CC the proteome of a tissue or a cell type. The polynucleotide is useful for
 CC creating knockin humanised animals (pigs) or transgenic animals (mice or
 CC rats) to model human disease, and for somatic or germ-line gene therapy,
 CC and further for generating hybridisation probes useful in mapping the
 CC naturally occurring genomic sequence. This polynucleotide sequence
 CC represents the DNA of a human secreted protein of the invention.
 CC
 XX
 SQ Sequence 3248 BP; 565 A; 1058 C; 946 G; 679 T; 0 other;
 Query Match 66.28; Score 912; DB 24; Length 3248;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2689 CTCTCGGGGGGGGGGCTGAGGCTGAGGCTGAGGCCAAGTGTGGTCCAGGTGGGT 2748
 QY GTGGGTGACATCATTTGGATCTATGCCAGCATCAAGACAGACACACCTTCGCGATT 916
 DB 2749 GTGGGTGACATCATTTGGATCTATGCCAGCATCAAGACAGACACACCTTCGCGATT 2808
 QY CTGGTGTACCTCCAGCTGCGACAGCTCCCGACTTGTGTAGTCCCACTGCAAGTGA 976
 DB 2809 CTGGTGTACCTCCAGCTGCGACAGCTCCCGACTTGTGTAGTCCCACTGCAAGTGA 2868
 QY 977 CTGATGCTCTGATCTCTAGAAAGAGGTGTAGGCTGACAAACAGTTCATCAGAGAGGC 1036
 DB 2869 CTGATGCTCTGATCTCTAGAAAGAGGTGTAGGCTGACAAACAGTTCATCAGAGAGGC 2928
 QY 1037 TGGCCCCCCTGGATATTGTGAATGACTAGAGGAGTGGGGTGAAGACACTCCGCTGC 1096
 DB 2929 TGGCCCCCCTGGATATTGTGAATGACTAGAGGAGTGGGGTGAAGACACTCCGCTGC 2988
 QY 1097 TGTGCGAAGGAATGGGAACAGTGTCTGTGCGATCAGTCTGCGACATGGGCGAGTG 1156
 DB 2989 TGTGCGAAGGAATGGGAACAGTGTCTGTGCGATCAGTCTGCGACATGGGCGAGTG 3048
 QY 1157 GCTGATTTCTGCCCAAGACAGAGAGTGTCTGTGCGAAGTGAAGTCCCAAGT 1216
 DB 3049 GCTGATTTCTGCCCAAGACAGAGAGTGTCTGTGCGAAGTGAAGTCCCAAGT 3108
 QY 1217 TGTCTGTGTCAGAGAGCCAGCGGGGTGCTCTTCGTCGCTGCTGCTCTGCTGAT 1276
 DB 3109 TGTCTGTGTCAGAGAGCCAGCGGGGTGCTCTTCGTCGCTGCTGCTGCTGCTGAT 3168
 QY 1277 CTTCCACACCCCT 1336
 DB 3169 CTTCCACACCCCT 3228
 QY 1337 TAAGAACCTCA 1348
 DB 3229 TAAGAACCTCA 3240
 RESULT 15
 AAS62228
 ID AAS62228 standard; cDNA: 764 BP.
 AC AAS62228;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE cDNA sequence #15 encoding novel human secreted protein.
 KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
 KW immune deficiency disorder; blood disorder; inflammatory disorder;
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
 KW immunosuppressive; antirheumatic; ss.
 OS Homo sapiens.
 XX
 PN WO20017291-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 29-MAR-2001; 2001WO-US10485.
 XX
 PR 06-APR-2000; 2000US-195604P.
 XX
 PA (GEMT) GENETICS INST INC.
 XX
 PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
 PI Gulinko K, Graham JR;
 XX
 DR WPI: 2002-010900/01.
 XX
 PT New polynucleotides encoding secreted proteins useful for treating e.g.

PT asthma, HIV and Crohn's disease -
 XX
 PS Claim 1; Page 79; 391pp; English.
 CC The present invention relates to the isolation of novel cDNA sequences
 CC which encode human secreted proteins. The cDNA sequences have been
 CC derived from a variety of human tissues. The invention also provides
 CC a method for producing proteins from these polynucleotide sequences.
 CC The proteins are useful for identifying compounds that modulate their
 CC activity and production, and the cell is also useful for identifying
 CC compounds that modulate expression of the polynucleotide sequences
 CC encoding the secreted proteins. The sequences of the invention are
 CC useful for treating diseases such as hyperproliferative disorders
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
 CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
 CC The polynucleotide sequences of the invention are also useful in gene
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
 CC invention that encode for novel human secreted proteins.
 XX
 SO Sequence 764 BP; 136 A; 225 C; 229 G; 174 T; 0 other;

Query Match 55.4%; Score 763; DB 24; Length 764;
 Best Local Similarity 100.0%; Pred. No. 1.5e-275;
 Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 ACGACCCCTTGCCTTGACCGCGCTGCTGTAACGACGACGACATTACGACGCCCTCA 644
 DB 1 ACGACCCCTTGCCTTGACCGCGCTGCTGTAACGACGACGACATTACGACGCCCTCA 60
 QY 645 CCGGCAAGTTACCTGCGAGGTGGGTGCTACTACTTCCGCGCTCCACCGCT 704
 DB 61 CCGGCAAGTTACCTGCGAGGTGGGTGCTACTACTTCCGCGCTCCACCGCT 120
 QY 705 ACCGGGCCAGCCTGAGTTGATGTAAGAAATGGCAATTCCTTCTTCC 764
 DB 121 ACCGGGCCAGCCTGAGTTGATGTAAGAAATGGCAATTCCTTCTTCC 180
 QY 765 AGTTTTGGGGGGTGGCCCAAGCAGCTGCTCGGGGGGGCCATGGTAGGCTGG 824
 DB 181 AGTTTTGGGGGGTGGCCCAAGCAGCTGCTCGGGGGGGCCATGGTAGGCTGG 240
 QY 825 AGCTGAGGACCAAGTGGGTGAGGTGGGTGAGTACATTCATTCATATGCA 884
 DB 241 AGCTGAGGACCAAGTGGGTGAGGTGGGTGAGTACATTCATTCATATGCA 300
 QY 885 GCATCAAGACAGACAGCACTTCCGGAATTCGCTACTCCGACTGCGACAGCTCC 944
 DB 301 GCATCAAGACAGACAGCACTTCCGGAATTCGCTACTCCGACTGCGACAGCTCC 360
 QY 945 CAGTCTTTGCTTACTGCTCACTGCAAAAGTCACTGCTCACTCTACAGAGAGGT 1004
 DB 361 CAGTCTTTGCTTACTGCTCACTGCAAAAGTCACTGCTCACTCTACAGAGAGGT 420
 QY 1005 GTGAGGCTGACACACAGTCAATCCAGAGGGGCTGGCCCTGGAAATTTGTAATGACT 1064
 DB 421 GTGAGGCTGACACACAGTCAATCCAGAGGGGCTGGCCCTGGAAATTTGTAATGACT 480
 QY 1065 AGGAGAGTGGGTAGAGCACTCTCCGCTCTCTGCTGCAAGAAATGGGAACAGTGGCTG 1124
 DB 481 AGGAGAGTGGGTAGAGCACTCTCCGCTCTCTGCTGCAAGAAATGGGAACAGTGGCTG 540
 QY 1125 TCTGCGATCAGGCTGCGACATGGGGCAGTGGCTGATTTCTGCCAAGACAGAGAG 1184
 DB 541 TCTGCGATCAGGCTGCGACATGGGGCAGTGGCTGATTTCTGCCAAGACAGAGAG 600
 QY 1185 TGTGCTGTGCTGCAAGTGAAGTCCCAAGTGTCTGTGTCAGAGAGCCACAGTGGGG 1244
 DB 601 TGTGCTGTGCTGCAAGTGAAGTCCCAAGTGTCTGTGTCAGAGAGCCACAGTGGGG 660
 QY 1245 TGTCTCTTCTCTGCTCTCTCTCTCTGATCTCCACACCCCTCTGCTCTGAGGGC 1304

DB 661 TGTCTCTTCTCTGCTCTCTCTCTCTGATCTCCACACCCCTCTGCTCTGAGGGC 720
 QY 1305 CGGCCCTTTCTCAGAGATCACTCAATTAACCTTAAGAACCTC 1347
 DB 721 CGGCCCTTTCTCAGAGATCACTCAATTAACCTTAAGAACCTC 763

Search completed: June 21, 2003, 12:53:40
 Job time : 373 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 11:35:55 ; Search time 3716 Seconds

(without alignments)
10784.328 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1 gactagctctcttgagctc.....aaaaaaaaaaaaaaaaaa 1377

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
1: gb_da:
2: gb_hcg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_da:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rtd:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1377	100.0	1377	6	AX464228
2	1305	94.8	1337	6	AR329841
3	1305	94.8	1347	6	AR138193
4	1136	82.5	1370	9	BC029485
5	1050	76.3	1068	9	HSMB009283
6	908	65.9	191362	9	AP003396
7	908	65.9	219574	9	AP002956
8	736	53.4	182429	2	AP001557
9	562	40.8	198902	2	AP001156
10	432	31.4	441	9	HMM2092F04
11	274	19.9	173038	2	AP001003
12	139	10.1	2288	9	AK055132
13	73	5.3	144	6	AR138211
14	72	5.2	144	6	AR138212
15	72	5.2	144	6	AR138214
16	54	3.9	147	6	AR138213
17	51	3.7	51	6	AR138218
18	51	3.7	51	6	AR138226
19	50	3.6	50	6	AR138219
20	50	3.6	50	6	AR138227
21	45	3.1	65	6	AR138220
22	43	3.3	68	6	AR138228
23	39	2.8	63	6	AR138225
24	38	2.8	62	6	AR138216
25	35	2.5	1234	10	BC025174
26	35	2.5	1271	10	BC023068
27	35	2.5	1929	3	LETD01
28	35	2.5	3025	10	AF002705
29	35	2.5	4220	10	AF469650
30	35	2.5	110000	2	AC096324_0
31	35	2.5	125544	2	AC095139
32	35	2.5	156869	2	AP002888
33	35	2.5	249283	2	AC124577
34	34	2.5	1587	9	HSMB02589
35	34	2.5	116289	10	AL691484
36	34	2.5	205044	2	AC024453
37	33	2.4	746	6	AR137703
38	33	2.4	814	3	AR483742
39	33	2.4	1237	8	AF255795
40	33	2.4	1305	5	NCMETADEN
41	33	2.4	1321	5	AB085669
42	33	2.4	1494	9	HSB420600
43	33	2.4	1522	9	BC001131
44	33	2.4	1629	3	AY119018
45	33	2.4	1743	9	BC022272

ALIGNMENTS

RESULT 1
AX464228
LOCUS
DEFINITION Sequence 361 from Patent WO0140466.
ACCESSION AX464228
VERSION
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, Y., Stewart, T.A., Tamas, D., Watanabe, C.K.,


```

Db      315 CACCATGACAGCCAGGCTTCCCGGCGCCGATGCGCCGACGCGCCCGCGAGCGCGCCG 374
OY      404 GGGGCTCCGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGACGCGGGAGCTCGAGGGGAG 463
Db      375 GGGGCTCCGGAGAGAAAGGAGGAGGCGGAGGCGCGGAGACGCGGGAGCTCGAGGGGAG 434
OY      464 CCGGCGCGGAGAGAGAGGCGGAGCCCGGGGGCCCAACCGGCGCTGCGGGAGTGCCTG 523
Db      435 CCGGCGCGGAGAGAGGCGGAGCCCGGGGGCCCAACCGGCGCTGCGGGAGTGCCTG 494
OY      524 GTGCTCCGGAGATCCGCTTCAGGGCCCAAGGCTCCAGAGGCGGGTGCCTCCGCTCT 583
Db      495 GTGCTCCGGAGATCCGCTTCAGGGCCCAAGGCTCCAGAGGCGGGTGCCTCCGCTCT 554
OY      584 GAGCAGCCCTTGCCCTTCGACCGCGGTGCTGGTGAAGAGAGGAGACATTAAGAGCGGCTC 643
Db      555 GAGCAGCCCTTGCCCTTCGACCGCGGTGCTGGTGAAGAGAGGAGACATTAAGAGCGGCTC 614
OY      644 ACCGGAAGTTCACCTCCAGAGGCTCGGGGGTCTACTTCCGCTTCATGCCAGCGCTC 703
Db      615 ACCGGAAGTTCACCTCCAGAGGCTCGGGGGTCTACTTCCGCTTCATGCCAGCGCTC 674
OY      704 TACCGGCGCAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
Db      675 TACCGGCGCAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 734
OY      764 CAGTTTTTCGGGGGGTGGCCCAAGCCAGCCCTGCTCGGGGGGGGCGCATGATGATGATG 823
Db      735 CAGTTTTTCGGGGGGTGGCCCAAGCCAGCCCTGCTCGGGGGGGGCGCATGATGATGATG 794
OY      824 GAGCCTAGAGACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 883
Db      795 GAGCCTAGAGACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 854
OY      884 AGCATCAAGACAGACACACCTCTCGGATTTCTGGTGTACTGCTGCTGCTGCTGCTGCTG 943
Db      855 AGCATCAAGACAGACACACCTCTCGGATTTCTGGTGTACTGCTGCTGCTGCTGCTGCTG 914
OY      944 CCAATCTTCTTCTAGTCCCACTGCAAGTGAAGTCAATGCTCACTCACTAGAGAGGG 1003
Db      915 CCAATCTTCTTCTAGTCCCACTGCAAGTGAAGTCAATGCTCACTCACTAGAGAGGG 974
OY      1004 TGTGAGGCTCAACAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
Db      975 TGTGAGGCTCAACAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1034
OY      1064 TAGGAGAGTGGGGAGAGCACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
Db      1035 TAGGAGAGTGGGGAGAGCACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
OY      1124 GTCTGAGATAGGTCTGGGAGCATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 1183
Db      1095 GTCTGAGATAGGTCTGGGAGCATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 1154
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Db      1215 GTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1274
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RESULT 4
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 LOCUS
 DEFINITION
 1370 bp. mRNA. linear. PRI 16-MAY-2002
 Homo sapiens, C1q and tumor necrosis factor related protein 5,
 clone MGC:32938 IMAGE:5278184, mRNA, complete cds.

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ACCESSION BC029485
VERSION BC029485.1 GI:20810468
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 1370)
JOURNAL Strausberg, R.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAC Plate: 48 Row: h Column: 14
This clone was selected for full length sequencing because it
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Matches 1336; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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OY 69 CCGGAGGAGAGGGGGGCGCTGGCGGGGAGAAACCGGGGCTGGAGACACCAACTGG 128
Db 76 CCGGAGGAGAGGGGGGCGCTGGCGGGGAGAAACCGGGGCTGGAGACACCAACTGG 135
OY 129 AGGTCGGAGTACGAGAGCCCGCGAAGAGGCGCATCGGGAGAGCCGGAGAGGGGACTGC 188
Db 136 AGGTCGGAGTACGAGAGCCCGCGAAGAGGCGCATCGGGAGAGCCGGAGAGGGGACTGC 195
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Db      196 GAGAGACCCCGGCGTCCGGGCTCCCGGAGGCTATGAGGCGACTCGTCTC 255
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QY      429 GCGGAGGCGCGGAGATGCCGGGAGCTCGAGGAGACCCGGGCGGAGAGAGCGG 488
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QY      489 GCGGAGGCGCGGAGATGCCGGGAGTGTCTCGGAGTGTCTCGGAGTGTCTCAG 548
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QY      789 CAGGCTGCTGCTCGGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
Db      796 CAGGCTGCTGCTCGGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855
QY      849 AGGTGGTGTGGGTGACTACTATTCATTCATTCATTCATTCATTCATTCATTC 908
Db      856 AGGTGGTGTGGGTGACTACTATTCATTCATTCATTCATTCATTCATTCATTC 915
QY      909 CCGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
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QY      969 AAGAGAGCTCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1028
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LOCUS      HSM800923      1068 bp      mRNA      linear      PRI 18-FEB-2000
DEFINITION Homo sapiens mRNA; CDNA DKFZp586B0621 (from clone DKFZp586B0621).
ACCESSION AL110261
VERSION    AL110261.1 GI:5817222
KEYWORDS
SOURCE
ORGANISM  Homo sapiens.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1068)
            Ottenwelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
            Direct Submission
            Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by Medigenomix (Martinsried/Germany) within the CDNA
            sequencing consortium of the German Genome Project. This clone
            (DKFZp586B0621) is available at the RZPD in Berlin. Please contact
            the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cdna/.
FEATURES
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QY      359 GCGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 418
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Db	181	GAGGCGGAGACCCGCGGGGGCCACCGGGGCTGGCCGGGGAGTGTGTGGTGTCTCCGGATCC	240
OY	539	GCCTTCAAGCCCAAGCGCTCCGAGAGCCGGGTGCTCCGCGCTGACGACCACTTTCGCC	598
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OY	599	TTGCGACGCGGCTGTGTGAAGAGAGGAGGAATTGACAGCGCCGTCACCGGCAAGTTCAAC	658
Db	301	TTTGCACCGCGGTGTGTGAAGAGAGGAGGAATTGACAGCGCGCTACCGGCAAGTTCAAC	360
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Db	481	TGGCCCAAGCCAGAGCTGCTCTCCGGGGGGGGGCATATGAGAGGCTGAGACCTGAGGACCAA	540
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OY	959	TGCCCCATGCAAAAGTGAAGTATGCTCTCATCTCTCTAAGAAAGAGGTTGAGAGCTACAAAC	1018
Db	661	TGCCCCATGCAAAAGTGAAGTATGCTCTCATCTCTCTAAGAAAGAGGTTGAGAGCTACAAAC	720
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OY	1079	GAGCACTTCCGCTCCTGCTGTGCGAAGAAATGGGAACAGTGGCTGTGTGCAATCAGGTC	1138
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OY	1139	TGGGAGCATGGGGGAGTGGGTGGAATTTGTGCCAAGACAAAGAGTGTGCTGTGCTGGC	1198
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OY	1199	AAGTGAATGTCGCCAGTTGTCTGTGTCAGAGAGCCACGGTGGGGTCTCTCTTCCTGAG	1258
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Source	Organism	Hom sapiens DNA, clone:RP11-334B6.
REFERENCE	ORGANISM	Hom sapiens DNA, clone:RP11-334B6.
REFERENCE	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	TITLE	1. Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
REFERENCE	JOURNAL	Hom sapiens genomic DNA
REFERENCE	AUTHORS	2 (bases 1 to 191362)
REFERENCE	TITLE	Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
REFERENCE	JOURNAL	Direct Submission
REFERENCE	AUTHORS	Submitted (12-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Shukho-Chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@esc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
REFERENCE	JOURNAL	This work was done in collaboration with Arai, Y., Kubo, T. and Ohki, M.
REFERENCE	AUTHORS	National Cancer Center Research Institute
REFERENCE	JOURNAL	Cancer Genomic Division
REFERENCE	AUTHORS	5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN
REFERENCE	JOURNAL	zip: 104-0045
REFERENCE	AUTHORS	phone: 81-3-3542-2511 ex 4752, fax: 81-3-3542-0688 e-mail: yarai@nc.ccr.go.jp.
REFERENCE	JOURNAL	Location/Qualifiers
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REFERENCE	JOURNAL	500 ACCGGGCGTGGCGGGGAGTGTCTGGTGGCTTCGGGATCGCGCTTCAGCGCAAGCGCTCC 559
REFERENCE	AUTHORS	6322 ACCGGGCGTGGCGGGGAGTGTCTGGTGGCTTCGGGATCGCGCTTCAGCGCAAGCGCTCC 6263
REFERENCE	JOURNAL	560 GAGAGCGGGGTGCTCCGCGCTCTGAGCCACCTTCGCTTCGAGCGCGGTCTGTGAAC 619
REFERENCE	AUTHORS	6262 GAGAGCGGGGTGCTCCGCGCTCTGAGCCACCTTCGCTTCGAGCGCGGTCTGTGAAC 6203
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REFERENCE	AUTHORS	6202 GAGAGGAGACATTACAGAGCGGTACCGGCAAGTTACCTTCAGAGTCTGTGGGTCTAC 6143
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REFERENCE	AUTHORS	6142 TACTTCGCGGTACATGCCACCGGTACCGGGGCCAGCTTCAGATTGATGTGTGAAGAT 6083
REFERENCE	JOURNAL	740 GGGCAATTCATGGCTCTTTTCTTCAGTTTTCGGGGGGTGGCCCAAGCTCGTC 799
REFERENCE	AUTHORS	6082 GGGCAATTCATGGCTCTTTTCTTCAGTTTTCGGGGGGTGGCCCAAGCTCGTC 6023
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Db      5902 GTGACTCCGACGTGGACAGAGTCCCACTGTTCTTCTAGTCCCACTGCAAGAGGACTC 5843
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QY      1220 TCTGCTCCAGAGAGCCAGAGTGGGGTGTCTCTCTCCGTGCTGCTGCTGCTGCTGCT 1279
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RESULT 7
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DEFINITION
ACCESSION AP002956
VERSION    AP002956.1 GI:22255355
KEYWORDS   HTG.
SOURCE      Homo sapiens DNA, clone:R1105h09.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1
            Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Totori,Y., Watanabe,H. and Sakaki,Y.
            Homo sapiens 219,574 genomic DNA of 11q
            Published Only in Database (2002)
            2 (bases 1 to 219574)
            Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Totori,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsr.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Overlapping Clones: pd71a4, PQ3868
            Cytogenetic Position: 21q22.1, region:D21S226-AML
            STR Markers (ePCR): stSG53747, SHGC-16045, D11S2450, SHGC-7143,
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            stSG31054, sts-X57110, WT-8978, GDB:1198117, stSG29284, SHGC-130657,
            D11S1941E, WT-14589, stSG60191, stSG50535, A002048, stSG26946,
            stSG41092,
            TIGR-A005D38, Bdaa7902, D11S69E, RH80030
            Contamination: none detected
            non-ACGT bases: none
            Additional author information
            Arai,Y., Kudo,T., Ohki,M.
            National Cancer Center Research Institute,
            Cancer Genomic Division
            5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN

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zip: 104-0045
phone: +81-3-3542-2511 ex4752, fax: +81-3-3542-0688 e-mail:
yatal@nci.go.jp.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      680 TACTTGGCGCTGCATGCGACCGCTCTACCGGGCCAGCTGCAAGTTGATCTGTGTAAGAT 739
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QY      740 GCGCAATTCATTTGCTCTTTCTTCCAGTTTTCGGGGGGTGGCCCAAGCCAGCCCTGCTC 799
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QY      800 TCGGGGGGGGCGCATGTGAGGCTGAGAGCTGAGAGCAAGTGTGGGTGACAGTGGGTG 859
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QY      860 GGTGACTACATTTGGCATCTATGCGAGATCAAGACAGACAGACACCTTCTCGGATTTCTG 919
Db      208700 GGTGACTACATTTGGCATCTATGCGAGATCAAGACAGACAGACACCTTCTCGGATTTCTG 208641
QY      920 GTGACTCCGACGTGGCAGAGTCCCGCAGTCTTTGCTTAGTGTCCACATGCAAGTGTGAGCTC 979
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QY      980 ATGCTCTACCTCTAGAGAGAGGTGTGAGGCTGACACACAGTCTATCCAGAGGCTGG 1039
Db      208580 ATGCTCTACCTCTAGAGAGAGGTGTGAGGCTGACACACAGTCTATCCAGAGGCTGG 208521
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QY      1100 TGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGTCTGCGACATGGGAGAGTGGCT 1159
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QY      1220 TCTGCTCCAGAGAGCCAGAGTGGGGTGTCTCTTCTGCTGCTGCTGCTGCTGCTGCT 1279
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OY      1280 CCCCACCCCTGCTGCTGCGGCGCCCTTTCTCAGAGATCACTAATAAACCCTAA 1339
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OY      1340 GAACCCGC 1347
Db      208220 GAACCCGC 208213

RESULT 8
LOCUS   AP001557
DEFINITION Homo sapiens chromosome 11 clone RP11-680A7 map 11q23, WORKING
ACCESSION AP001557
VERSION   AP001557.3 GI:11094164
KEYWORDS  HTG: HTGS, PHASE1; HTGS, DRAFT.
SOURCE    Homo sapiens DNA, clone:RP11-680A7.
ORGANISM  Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 182429)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
          Homo sapiens 182,429 genomic DNA of 11q23
          Published Only in DataBase (2000)
          2 (bases 1 to 182429)
          Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
          Direct Submission
          Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel:81-45-503-9111, Fax:81-45-503-9170
          On Nov 3, 2000 this sequence version replaced gi:8117391.

COMMENT  ----- Genome Center
          Center: RIKEN Genomic Sciences Center(GSC)
          Center code: RIKEN
          Web site: http://hgp.gsc.riken.go.jp/
          Contact: hattori@gsc.riken.go.jp
          ----- Project Information
          Center project name: Humdrft11
          Center clone name: RP11-680A7
          ----- Summary Statistics
          Sequencing vector: PCR products; 100% of reads
          Chemistry: Dye-terminator ET-amersham; 100% of reads
          Assembly program: Phrap; version 0.990329
          Consensus quality: 175597 bases at least Q40
          Consensus quality: 178555 bases at least Q30
          Consensus quality: 179768 bases at least Q20
          Insert size: 180429; sum-of-ctngs
          Quality coverage: 9.01x in Q20 bases; sum-of-ctngs

NOTE: This is a 'working draft' sequence. It currently consists of
21 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1
30107 contig of 30107 bp in length
30208 54357 contig of 24150 bp in length
54458 69839 contig of 15382 bp in length
69940 84048 contig of 14109 bp in length
84149 95177 contig of 11029 bp in length
95278 107763 contig of 12486 bp in length
107864 119057 contig of 11194 bp in length
119158 128134 contig of 8977 bp in length
128335 136903 contig of 8669 bp in length
137004 145887 contig of 8884 bp in length
145988 153199 contig of 7212 bp in length
153300 159565 contig of 6266 bp in length

```

```

159666 163580 contig of 3915 bp in length
163681 165152 contig of 1472 bp in length
165253 166901 contig of 1649 bp in length
167002 170460 contig of 3459 bp in length
170561 172761 contig of 2201 bp in length
172862 175605 contig of 2744 bp in length
175706 178308 contig of 2603 bp in length
178409 180918 contig of 2510 bp in length
180919 182429 contig of 1411 bp in length.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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54358 54457 gap of 100 bp
54458 69839 contig of 15382 bp in length
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69940 84048 contig of 14109 bp in length
84049 84148 gap of 100 bp
84149 95177 contig of 11029 bp in length
95178 95277 gap of 100 bp
95278 107763 contig of 12486 bp in length
107764 107863 gap of 100 bp
107864 119057 contig of 11194 bp in length
119058 119157 gap of 100 bp
119158 128134 contig of 8977 bp in length
128135 128334 gap of 100 bp
128335 136903 contig of 8669 bp in length
136904 137003 gap of 100 bp
137004 145887 contig of 8884 bp in length
145888 145987 gap of 100 bp
145988 153199 contig of 7212 bp in length
153200 153299 gap of 100 bp
153300 159565 contig of 6266 bp in length
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159666 163580 contig of 3915 bp in length
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163681 165152 contig of 1472 bp in length
165153 165252 gap of 100 bp
165253 166901 contig of 1649 bp in length
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167002 170460 contig of 3459 bp in length
170461 170560 gap of 100 bp
170561 172761 contig of 2201 bp in length
172762 172861 gap of 100 bp
172862 175605 contig of 2744 bp in length
175606 175705 gap of 100 bp
175706 178308 contig of 2603 bp in length
178309 178408 gap of 100 bp
178409 180918 contig of 2510 bp in length
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181019 182429 contig of 1411 bp in length.

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/chromosome="11"
/map="11q23"
/clone="RP11-680A7"
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69940..84048
/note="assembly_fragment"

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Consensus quality: 171788 bases at least Q40
Consensus quality: 184443 bases at least Q30
Consensus quality: 191295 bases at least Q20
Insert size: 194802: sum-of-contigs
Quality coverage: 4.12x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 20627 contig of 20627 bp in length
20728 31817 contig of 11090 bp in length
31918 41131 contig of 9214 bp in length
41232 49745 contig of 8514 bp in length
49846 59457 contig of 9612 bp in length
59358 66804 contig of 7247 bp in length
66905 73970 contig of 7066 bp in length
74071 81007 contig of 6937 bp in length
81108 87320 contig of 6213 bp in length
87421 93250 contig of 5830 bp in length
93351 97965 contig of 4615 bp in length
98066 102941 contig of 4876 bp in length
103042 109017 contig of 5976 bp in length
109118 113391 contig of 4274 bp in length
113492 118783 contig of 5292 bp in length
118784 124241 contig of 5358 bp in length
124242 124341 contig of 100 bp in length
124342 129766 contig of 5425 bp in length
129767 129866 contig of 5607 bp in length
129867 135473 contig of 5607 bp in length
135474 135573 contig of 5012 bp in length
135574 140585 contig of 5012 bp in length
140586 140685 contig of 100 bp in length
140686 144027 contig of 3342 bp in length
144028 144127 contig of 100 bp in length
144128 147923 contig of 3796 bp in length
147924 148023 contig of 4038 bp in length
148024 152461 contig of 4438 bp in length
152462 152561 contig of 100 bp in length
152562 155444 contig of 2883 bp in length
155445 155544 contig of 100 bp in length
155545 158721 contig of 3177 bp in length
158722 158821 contig of 100 bp in length
158822 162903 contig of 4082 bp in length
162904 163003 contig of 100 bp in length
163004 166121 contig of 3118 bp in length
166122 166221 contig of 100 bp in length
166222 169851 contig of 3630 bp in length
169852 169951 contig of 100 bp in length
169952 172048 contig of 2097 bp in length
172049 172148 contig of 100 bp in length
172149 175332 contig of 3184 bp in length
175333 175432 contig of 100 bp in length
175433 177914 contig of 2482 bp in length
177915 178014 contig of 100 bp in length
178015 179875 contig of 1861 bp in length
179876 179975 contig of 100 bp in length
179976 181604 contig of 1629 bp in length
181605 181704 contig of 100 bp in length
181705 183951 contig of 2247 bp in length
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184052 185927 contig of 1876 bp in length
185928 186027 contig of 100 bp in length
186028 187870 contig of 1843 bp in length
187871 187970 contig of 100 bp in length
187971 189591 contig of 1621 bp in length
189592 189691 contig of 100 bp in length
189692 191169 contig of 1478 bp in length
191170 191269 contig of 100 bp in length
191270 192527 contig of 1258 bp in length
192528 192627 contig of 100 bp in length
192628 194288 contig of 1661 bp in length
194289 194388 contig of 100 bp in length
194389 195658 contig of 1270 bp in length
195659 195758 contig of 100 bp in length
195759 197707 contig of 1949 bp in length
197708 197807 contig of 100 bp in length

Sequence updated (26-May-2000).

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 20627 contig of 20627 bp in length
20628 20727 gap of 100 bp
20728 31817 contig of 11090 bp in length
31818 31917 gap of 100 bp
31918 41131 contig of 9214 bp in length
41132 41231 gap of 100 bp
41232 49745 contig of 8514 bp in length
49746 49845 gap of 100 bp
49846 59457 contig of 9612 bp in length

59458 59557 gap of 100 bp
59558 66804 contig of 7247 bp in length
66805 66904 gap of 100 bp
66905 73970 contig of 7066 bp in length
73971 74070 gap of 100 bp
74071 81007 contig of 6937 bp in length
81008 81107 gap of 100 bp
81108 87320 contig of 6213 bp in length
87321 87420 gap of 100 bp
87421 93250 contig of 5830 bp in length
93251 93350 gap of 100 bp
93351 97965 contig of 4615 bp in length
97966 98065 gap of 100 bp
98066 102941 contig of 4876 bp in length
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124242 124341 gap of 100 bp
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166122 166221 gap of 100 bp
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177915 178014 gap of 100 bp
178015 179875 contig of 1861 bp in length
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181705 183951 contig of 2247 bp in length
183952 184051 gap of 100 bp
184052 185927 contig of 1876 bp in length
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186028 187870 contig of 1843 bp in length
187871 187970 gap of 100 bp
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189692 191169 contig of 1478 bp in length
191170 191269 gap of 100 bp
191270 192527 contig of 1258 bp in length
192528 192627 gap of 100 bp
192628 194288 contig of 1661 bp in length
194289 194388 gap of 100 bp
194389 195658 contig of 1270 bp in length
195659 195758 gap of 100 bp
195759 197707 contig of 1949 bp in length
197708 197807 gap of 100 bp

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Best Local Similarity 99.8%; Pred. No. 9.7e-291;
Matches 612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 795 CGCTCTCGGGGGGGGCGCATGAGTGAAGCTGAGACCAAGTGTGGGTGCGAGGTGG 854
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QY 855 GTGTGGGTGACTACATTGGACATCTATGCGACATCAAGACAGACACCTTCTCCGAT 914
DB 194509 GTGTGGGTGACTACATTGGACATCTATGCGACATCAAGACAGACACCTTCTCCGAT 194568
QY 915 TTCTGTGTACTCCGACATGCGACAGCTCCCAAGTCTTTGCTTATGTCCTCACTGCAAGTG 974
DB 194569 TTCTGTGTACTCCGACATGCGACAGCTCCCAAGTCTTTGCTTATGTCCTCACTGCAAGTG 194628
QY 975 AGCTCATGCTCTCACTCTAGAAAGAGGAGTGTGAGCTGACACCAAGGTCATCCAGAGG 1034
DB 194629 AGCTCATGCTCTCACTCTAGAAAGAGGAGTGTGAGCTGACACCAAGGTCATCCAGAGG 194688
QY 1035 GCTGGCCCCCTGGAATATTTGTAATGACTAGAGAGTGGGGTAGAGCACTCTCCGCTCT 1094
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QY 1095 GCTGTGGCAAGATGGGAACAGTGTCTGTGATCAGTGTGCGACATGCGAGCAGTGGGCGAG 1154
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DB 194809 TGGCTGATTTCTGCGCAAGACAGAGAGTGTGCTGTGCGCAAGTGAAGTCCGCCA 194868
QY 1215 GTTGTCTGTGTCCAGAGACCCAGAGTGGGGTGTCTCTCTGCTCTCTGCTTCTGCG 1274
DB 194869 GTTGTCTGTGTCCAGAGACCCAGAGTGGGGTGTCTCTCTGCTCTCTGCTTCTGCG 194928
QY 1275 ATCTCTCCCCACCTCTCTGCTCTGCGGGGGGGCCCTTTTCTCAAGATCACTCAATATA 1334
DB 194929 ATCTCTCCCCACCTCTCTGCTCTGCGGGGGGGCCCTTTTCTCAAGATCACTCAATATA 194988
QY 1335 CCTAAGAACCTCT 1347
DB 194989 CCTAAGAACCTCT 195001

RESULT 10
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DEFINITION Homo sapiens full length insert cDNA clone ZD92F04.
ACCESSION AF086482.1 GI:3483827
KEYWORDS FLI_CDNA.

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                  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE         1 (bases 1 to 441)
AUTHORS           Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
                  Marsh,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
                  Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
                  Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
                  Schurk,R., Ritter,E., Kohn,S., Swaller,T., Beyhmer,K., Hillier,L.,
                  Wilson,R. and Waterston,R.
TITLE             Full Clone Sequencing of the Longest Available Member from Each
                  Unigene Cluster
JOURNAL           2 (bases 1 to 441)
REFERENCE         Waterston,R.
AUTHORS           Direct Submission
JOURNAL           Submitted (24-AUG-1998) Department of Genetics, Washington
                  University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT           SUBMITTED BY:
                  Genome Sequencing Center
                  Department of Genetics
                  Washington University
                  St. Louis MO 63108, USA
                  http://genome.wustl.edu/gsc
                  mailto:est@watson.wustl.edu

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NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.

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Best Local Similarity 100.0%; Pred. No. 8.4e-221;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 977 CTGATGCTCTACTCTTGAAGAGGAGGTGAGCTGACAAACAGAGTATCCAGAGGCC 1036
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QY 1097 TGCTGCAAGATGGGAACAGTGTCTGTGCATCAGTCTGCGACATGCGGCGAGTG 1156
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QY 1157 GCTGATTTCTGCGCAAGACAGAGAGTGTGCTGTGCGCAAGTGAAGTCCCGCAGT 1216
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* 163685 163784: gap of 100 bp
* 163785 165216: contig of 1432 bp in length
* 165217 165316: gap of 100 bp
* 165317 166657: contig of 1341 bp in length
* 166658 166757: gap of 100 bp
* 166758 168307: contig of 1550 bp in length
* 168308 168407: gap of 100 bp
* 168408 170030: contig of 1623 bp in length
* 170031 170130: gap of 100 bp
* 170131 171725: contig of 1595 bp in length
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FEATURES

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 Matches 394; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 166779 GCACATTACGAGCGCGGTACCGGCAAGTTACCTCCAGGTCCTGGGGTCTACTACTTC 166838
QY 686 GCCGTCATGCGACCGGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGATGGCGAA 745
    |||||||
DB 166839 GCCGTCATGCGACCGGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGATGGCGAA 166898
QY 746 TCACATGCTCTCTTTTCTTCCAGTTTTC-6GGGGGTGGGCCCAAGCCAGCCTGCTTCGGG 804
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DB 166899 TCACATGCTCTCTTTTCTTCCAGTTTTC-6GGGGGTGGGCCCAAGCCAGCCTGCTTCGGG 166958
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    |||||||
DB 167019 CTACATTTGGCATCTATGCGCAGCATCAGACAGACAGACACCTTCTCCGATTTCTGGTGA 167078
QY 925 CTCGACATGCGACACACTCCCGAGTCTTGTCTTAGTCCCGCATGCGAAATGAGCTATGCT 984
    |||||||
DB 167079 CTCGACATGCGACACACTCCCGAGTCTTGTCTTAGTCCCGCATGCGAAATGAGCTATGCT 167138
QY 985 CTCACCTCCTAGAGAGAGGAGGTGTGAGGCTGACAAAC 1019
    |||||||
DB 167139 CTCACCTCCTAGAGAGAGGAGGTGTGAGGCTGACAAAC 167173

```

RESULT 12
 AK055132
 LOCUS
 DEFINITION Homo sapiens cDNA FLJ30570 fis, clone BRAHW2005998, weakly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BC 3.4.24.-).
 ACCESSION AK055132
 VERSION AK055132.1 GI:16549793
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens brain cDNA to mRNA, clone_11b:BRAHW2 clone:BRAHW2005998.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshiikawa,Y., Matsumura,Y., Moriya,S., Chida,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Katoaka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuko,Y., Nagai,K. and Isogai,T.

TITLE NED0 human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2288)
 AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
 JOURNAL Direct Submission

COMMENT
 Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp. Tel:81-438-52-3975, Fax:81-438-52-3986)
 NED0 human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

FEATURES
 Location/Qualifiers

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/db_xref="taxon:9606"
/clone="BRAMH2005998"
/tissue_type="brain"
/clone_lib="BRAMH2"
/note="cloning vector: pME18SFL3"
161. 1900
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB70859.1"
/db_xref="GI:16549794"
/translation="MKDRSDVILCMETSESKTEFCNPAPFEPESGPPPPVEDAS
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PDPPPTHCVMHIOVADHAIOLKIALIESVASCLFDELSPPEPLRVCR
VPPPTLNTNASHLVFVSDSVSEGEFHMYQAMRGSCAHDEFRCOLICLPD
SYVDGFRANCADSDERINCSKFSGCGNLGLGTFSTPTLQYPPHQLCTHHSVP
AGHSIELQHNESLEADDECKFDVEYETSSGAGLLRFGCAEPPLVSSHBL
SVLEKRDHGISSGFSATYLAFNATNPCCPSLSCAGCKGQVMDMWRDCTDS
DDNCSGLPEPPELACEPVEMCIGISYWTAFINIMVGMTQEEVVEVLSYKSLT
SLPCYOHFRLLCGLVPRCTPLGSVLPQRSVQEAHEHCQSGIALLTGPWFNCR
LPEADLENAQP"

BASE COUNT      405 a      773 c      626 g      484 t
ORIGIN

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Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1185 TGTGCTGTGCTGGCACTGTAAGTCCCAAGTGTCTGTCTCCAGAGCCACGCGTGGG 1244
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DB 2126 TGTGCTGTGCTGGCACTGTAAGTCCCAAGTGTCTGTCTCCAGAGCCACGCGTGGG 2185
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QY 1245 TGTGCTGTGCTGTGCTGTCTGTGATCTCCCAAGCCCTCTGTCTGTGGGG 1304
      |||||||
DB 2186 TGTGCTGTGCTGTGCTGTCTGTGATCTCCCAAGCCCTCTGTCTGTGGGG 2245
      |||||||

QY 1305 CGGCCCTTTTCTCAGAGAT 1323
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DB 2246 CGGCCCTTTTCTCAGAGAT 2264
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RESULT 13
ARI38211 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 28 from patent US 6197930.
DEFINITION ARI38211
ACCESSION ARI38211
VERSION ARI38211.1 GI:14479720
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 28 06-MAR-2001;
FEATURES
source location/Qualifiers
1. 144
/organism="unknown"

BASE COUNT      38 a      41 c      36 g      29 t
ORIGIN

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Best Local Similarity 5.3%; Score 73; DB 6; Length 144;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 ACTGACGACACAAAGATCCCAAGCTCTGCGCGGGGACACCGGCTTCCAGGACGCC 339
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QY 340 GGGCCACCATGGC 352
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```
DB 132 GGGCCACCATGGC 144

RESULT 14
ARI38212 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 29 from patent US 6197930.
DEFINITION ARI38212
ACCESSION ARI38212
VERSION ARI38212.1 GI:14479721
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 29 06-MAR-2001;
FEATURES
source location/Qualifiers
1. 144
/organism="unknown"

BASE COUNT      41 a      40 c      43 g      20 t
ORIGIN

Query Match
Best Local Similarity 5.2%; Score 72; DB 6; Length 144;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 CTGACGACACAAAGATCCCAAGCTCTGCGCGGGGACACCGGCTTCCAGGACGCC 340
      |||||||
DB 73 CTGACGACACAAAGATCCCAAGCTCTGCGCGGGGACACCGGCTTCCAGGACGCC 132
      |||||||

QY 341 GGGCCACCATGGC 352
      |||||||
DB 133 GGGCCACCATGGC 144
      |||||||

RESULT 15
ARI38214 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 31 from patent US 6197930.
DEFINITION ARI38214
ACCESSION ARI38214
VERSION ARI38214.1 GI:14479723
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 31 06-MAR-2001;
FEATURES
source location/Qualifiers
1. 144
/organism="unknown"

BASE COUNT      32 a      32 c      37 g      43 t
ORIGIN

Query Match
Best Local Similarity 5.2%; Score 72; DB 6; Length 144;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 884 AGCATCAAGACAGACACCTTCTCGGATTTCTGTGTAATCGACTGGACAGCTCC 943
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DB 1 AGCATCAAGACAGACACCTTCTCGGATTTCTGTGTAATCGACTGGACAGCTCC 60
      |||||||

QY 944 CCAGTCTTGCT 955
      |||||||
DB 61 CCAGTCTTGCT 72
      |||||||
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Search completed: June 21, 2003, 13:55:52
Job time : 3723 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: June 13, 2003, 15:49:51 ; Search time 72 Seconds
(without alignments).
449.721 Million cell updates/sec

Title:	US-09-944-944-42
Perfect score:	1325
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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6: /SIDS2/gcgdata/genseq/genseqp_emb1/AA1985.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	100.0	243	20	AAV06481	Human tumour-asso
2	1325	100.0	243	20	AAV17827	Human PRO344 prote
3	1325	100.0	243	20	AAW97984	Human adipocyte-s
4	1325	100.0	243	21	AAV33461	Human adipocyte-s
5	1325	100.0	243	21	AAV71468	Human PRO344 prote
6	1325	100.0	243	21	AAV93688	Human PRO344 prote
7	1325	100.0	243	21	AAAB0318	Amino acid sequenc
8	1325	100.0	243	22	AAU12352	Human PRO344 poly
9	1325	100.0	243	22	AAAB6815	Human PRO344 poly
10	1325	100.0	243	22	AAAB4593	Human TANGO 253 SE
						Human adipocyte co

11	1325	100.0	243	22	AAB49599	Human adipocyte c
12	1323	99.8	243	22	AAB65891	Human secreted pr
13	1321	99.7	243	22	AAB65888	Human secreted pr
14	1321	99.7	243	22	AAB65889	Human secreted pr
15	1321	99.7	243	22	AAB65890	Human secreted pr
16	1271	95.9	243	21	AAV76040	Rat skin cell prot
17	1271	95.9	243	21	AAV55979	Skin cell protein,
18	1271	95.9	243	23	ABW72179	Rat protein isolat
19	1258	94.9	243	22	AAB65870	Murine TANGO 253
20	1256	94.8	228	22	AAB65816	Human mature TANG
21	1256	94.8	243	22	AAB65839	Human mature TANG
22	1254	94.6	243	22	AAB65897	Murine secreted pr
23	1254	94.6	243	22	AAB65898	Murine secreted pr
24	1243.5	93.8	242	22	AAB65896	Murine secreted pr
25	1200	90.6	228	22	AAB65821	Murine mature TANG
26	1183	89.3	220	22	ABG15744	Novel human diapo
27	1048	79.1	201	23	AAO21653	Human secreted pr
28	675	50.9	128	22	AAB65819	Human TANGO 253
29	650	49.1	128	22	AAB65824	Murine TANGO 253
30	478	36.1	151	22	ABG12753	Novel human diapo
31	449.5	33.9	225	23	ABBB0583	Human sbg103026C1
32	442.5	33.4	333	23	ABBB0582	Human sbg103026C1
33	443.5	32.7	247	18	AAW09107	Murine adipocyte c
34	433.5	32.7	247	22	AAE05528	Mouse OBG3 protein
35	433.5	32.7	247	23	ABBO8252	Mouse acrp30 prote
36	425	32.1	244	18	AAW09108	Human adipocyte co
37	424.5	32.0	247	22	AAE05527	Mouse OBG3 protein
38	424.5	32.0	247	23	ABBO8221	Mouse adipoQ protea
39	424	32.0	244	20	AAV11807	Adipose most abund
40	424	32.0	244	21	AAAB3023	Human adipocyte co
41	424	32.0	244	21	AAV71035	Human APM1 (Adipos
42	424	32.0	244	22	AAE05529	Human OBG3 protein
43	424	32.0	244	22	ABE05828	Human adipocyte co
44	424	32.0	244	22	AAB49592	Human ACRP30 prote
45	424	32.0	244	22	AAB49598	Human ACRP30 prote

ALIGNMENTS

RESULT 1	AAV06481	AAV06481 standard; Protein: 243 AA.
XX	ID	AAV06481 standard; Protein: 243 AA.
XX	AC	AAV06481;
XX	DT	27-SEP-1999 (first entry)
XX	DE	Human tumour-associated protein PRO344.
XX	KM	PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human
XX	XX	
OS		Homo sapiens.
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..15
FT	Protein	/note= "signal peptide"
FT		16..243
FT		/note= "mature protein"
FT	Modified-site	68..215
FT		/note= "N-myristoylated"
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FT		/note= "N-myristoylated"
XX		
PN	W09935170-A2.	
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PD	15-JUL-1999.	
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PE	05-JAN-1999;	99MO-US00106.
XX		
PR	20-NOV-1998;	98US-0109304.
PR	05-JAN-1998;	98US-0070440.
PR	29-APR-1998;	98US-0083500.

PR 22-MAY-1998; 98US-0086414.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WI;
 XX
 DR WPI: 1999-430385/36.
 DR N-PSDB: AAX87258.
 XX
 PT Antibody against proteins expressed in neoplastic cells, useful for
 PT tumor diagnosis and treatment
 XX
 PS Example 1; Fig 10; 162pp; English.
 XX
 CC This sequence represents human PRO344 (UN0303), a protein encoded
 CC by the novel cDNA clone DNA40592 (see AAX87258). Amplification of
 CC DNA40592 was observed in primary lung tumours and in primary colon
 CC tumours, suggesting a significant role in tumour formation and
 CC growth. Antagonists (e.g. antibodies) directed to PRO344 may have
 CC use in cancer therapy. The invention identifies 14 genes (see
 CC AAX87254-67) that are amplified in the genome of tumour cells. Such
 CC amplification is expected to be associated with overexpression of
 CC the gene product and to contribute to tumorigenesis. The encoded
 CC proteins (see AAY06477-90) may be useful targets for the diagnosis
 CC and/or treatment (including prevention) of certain cancers, and may
 CC act as predictors of the prognosis of tumour treatment. Antibodies
 CC that bind the proteins are claimed and used in claimed cancer
 CC diagnostic kits.
 CC
 XX
 SQ Sequence 243 AA;
 Query Match 100.0%; Score 1325; DB 20; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGAAG 60
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGAAG 60
 QY 61 APGKGGGRRGRLPGPRGDPGPRGAGPAGPTGAGGCSVPRAFAKRSERVPPSD 120
 DB 61 APGKGGGRRGRLPGPRGDPGPRGAGPAGPTGAGGCSVPRAFAKRSERVPPSD 120
 QY 121 APLEFDRLVNEQGHYDAVTKFTQYPGYVYFAVNAHYRASLOFDLVNKGESIASFFQ 180
 DB 121 APLEFDRLVNEQGHYDAVTKFTQYPGYVYFAVNAHYRASLOFDLVNKGESIASFFQ 180
 QY 181 FFGGMPKPAASLSGAMVRLPEDEQVWVQVGVGYIGIYASIKTDSFGFLVYSDWHSSP 240
 DB 181 FFGGMPKPAASLSGAMVRLPEDEQVWVQVGVGYIGIYASIKTDSFGFLVYSDWHSSP 240
 QY 241 VFA 243
 DB 241 VFA 243
 XX
 DE Human PRO344 protein sequence.
 XX
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 XX secreted protein; transmembrane protein; inflammation disorder.
 OS Homo sapiens.

XX
 PN WO928462-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US25108.
 XX
 PR 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069696.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 PI Yuan J;
 XX
 DR WPI: 1999-371118/31.
 DR N-PSDB: AAX80052.
 XX
 PT Nucleic acids encoding PRO secreted and transmembrane proteins
 PS
 PS
 XX
 CC Claim 12; Fig 21; 123pp; English.
 CC
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytosstatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 CC
 XX
 SQ Sequence 243 AA;
 Query Match 100.0%; Score 1325; DB 20; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGAAG 60
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGAAG 60
 QY 61 APGKGGGRRGRLPGPRGDPGPRGAGPAGPTGAGGCSVPRAFAKRSERVPPSD 120
 DB 61 APGKGGGRRGRLPGPRGDPGPRGAGPAGPTGAGGCSVPRAFAKRSERVPPSD 120
 QY 121 APLEFDRLVNEQGHYDAVTKFTQYPGYVYFAVNAHYRASLOFDLVNKGESIASFFQ 180
 DB 121 APLEFDRLVNEQGHYDAVTKFTQYPGYVYFAVNAHYRASLOFDLVNKGESIASFFQ 180
 QY 181 FFGGMPKPAASLSGAMVRLPEDEQVWVQVGVGYIGIYASIKTDSFGFLVYSDWHSSP 240
 DB 181 FFGGMPKPAASLSGAMVRLPEDEQVWVQVGVGYIGIYASIKTDSFGFLVYSDWHSSP 240
 QY 241 VFA 243
 DB 241 VFA 243
 XX
 DE Human PRO344 protein sequence.
 XX
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 XX secreted protein; transmembrane protein; inflammation disorder.
 OS Homo sapiens.

ID	AAW97984 standard; Protein; 243 AA.
XX	
AC	AAW97984;
XX	
DT	21-JUN-1999 (first entry)
XX	
DE	Human adipocyte-specific protein zslg39.
XX	
KW	Adipocyte-specific protein; zslg39; human; fatty acid metabolism;
KM	energy balance; nutrition; antimicrobial.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..15
FT	/note= "signal peptide, alternatively the signal
FT	peptide comprises residues 1..18"
FT	16..243
FT	/note= "mature protein, alternatively the mature
FT	protein comprises residues 19..243
FT	(specifically claimed in Claim 4)"
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FT	30..96
FT	/note= "collagen-like domain"
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FT	/note= "beta strand"
FT	164..171
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FT	/note= "receptor binding domain"
FT	170..174
FT	/note= "receptor binding domain"
Domain	
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PN	WO9910492-A1.
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PD	04-MAR-1999.
XX	
PF	26-AUG-1998; 98WO-US17724.
XX	
PR	26-AUG-1997; 97US-0056983.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Humes JM, Sheppard PO;
DR	WPI, 1999-204665/17.
DR	N-PSDB; AAX24684.
XX	
PT	zslg39 protein - used to modulate fatty acid metabolism
XX	
PS	Claim 1; 111-112; 132pp; English.
XX	
CC	This polypeptide comprises human adipocyte-specific protein zslg39,
CC	a protein that modulates free fatty acid metabolism. zslg39 is a
CC	member of a family of proteins having a globular domain and a
CC	collagen-like domain capable of dimerisation or oligomerisation.
CC	zslg39 polypeptides were initially identified by querying an EST
CC	database for secretory signal sequences characterised by an upstream

CC	methionine start site, a hydrophobic region of approximately 13
CC	amino acids and a cleavage site. A single EST sequence was
CC	discovered, and the novel polypeptide encoded by the full-length
CC	cDNA allowed the identification of a homologue relationship with
CC	adipocyte complement related protein Acyr30 and adipocyte secreted
CC	protein apM1. A full-length clone (see AAX24684) was obtained from a
CC	lung tissue library. Expression vectors, cultured cells and a
CC	method of producing zslg39 polypeptide are claimed, as well as
CC	zslg39 polypeptides having N- or C-terminal affinity tags, toxins,
CC	radionuclides, enzymes or fluorophores, fusion proteins
CC	including zslg39 polypeptides, an antibody that specifically
CC	binds to an epitope of zslg39, and a method for modulating free
CC	fatty acid metabolism by administering a zslg39 polypeptide. The
CC	zslg39 polypeptide may also be used in organ preservation, for
CC	cryopreservation, for surgical pretreatment to prevent injury due
CC	to ischaemia and/or inflammation, and as an antimicrobial agent,
CC	promoting lysis or phagocytosis of infectious agents.
XX	
XX	Sequence 243 AA:
SO	
XX	Query Match 100.0%; Score 1325; DB 20; Length 243;
XX	Best Local Similarity 100.0%; Pred. No. 5.3e-103;
XX	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MRPLLVLILLGLAAGSPPLDNDKITSICPHGHGLPRTGCHHSOGILPGDGRGRGATG 60
DB	1 MRPLLVLILLGLAAGSPPLDNDKITSICPHGHGLPRTGCHHSOGILPGDGRGRGATG 60
OY	61 APGEKGEGRGELPPRDPDGRGAGAPRGPGEGCVPPRSASFSAKRSRVPSPD 120
DB	61 APGEKGEGRGELPPRDPDGRGAGAPRGPGEGCVPPRSASFSAKRSRVPSPD 120
OY	121 APLPEDRVLVDEQGHYDAVTGKFTGQVPEVYFAVAHYRYSALDFLYKNESIASFQ 180
DB	121 APLPEDRVLVDEQGHYDAVTGKFTGQVPEVYFAVAHYRYSALDFLYKNESIASFQ 180
OY	181 FFGGMPKPAASISGAMVRLPEPDQVWVGVDYIGITVYSITDTSFSGFLYSDWHSSP 240
DB	181 FFGGMPKPAASISGAMVRLPEPDQVWVGVDYIGITVYSITDTSFSGFLYSDWHSSP 240
OY	241 VFA 243
DB	241 VFA 243
XX	
XX	RESULT 4
ID	AAB33461
ID	AAB33461 standard; Protein; 243 AA.
XX	AAB33461;
XX	
DT	29-JAN-2001 (first entry)
XX	
DE	Human PRO344 protein UNQ303 SEQ ID NO:241.
XX	
XX	Human; immune related disease; diagnosis; antiinflammatory; cardiac;
XX	dermatologic; antithyroid; antidiabetic; nonotropic; neuroprotective;
XX	haemostatic; antihypertensive; antidiabetic; nonotropic; neuroprotective;
XX	antianemic; hepatotropic; vitruce; antipsoriatic; antiallergic;
XX	antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
XX	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
XX	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX	systemic vasculitis; autoimmune hemolytic anemia; diabetes mellitus;
XX	autoimmune thrombocytopenia; immune-mediated renal disease;
XX	demyelinating disease; hepatobiliary disease; Whipple's disease;
XX	inflammatory bowel disease; gluten-sensitive enteropathy;
XX	autoimmune disease; immune-mediated skin disease; allergic disease;
XX	immunological disease; transplantation associated disease;
XX	graft rejection; graft-versus-host-disease.
XX	
XX	Homo sapiens.
XX	
XX	WO200053758-A2.

XX 14-SEP-2000. 2000WO-US05841.
 XX 02-MAR-2000; 2000WO-US05841.
 XX 08-MAR-1999; 99WO-US05028.
 XX 10-MAR-1999; 99US-0123618.
 XX 12-MAR-1999; 99US-0123957.
 XX 23-MAR-1999; 99US-0125775.
 XX 12-APR-1999; 99US-0128849.
 XX 20-APR-1999; 99WO-US08615.
 XX 28-APR-1999; 99US-0131445.
 XX 04-MAY-1999; 99US-0132377.
 XX 14-MAY-1999; 99US-0134287.
 XX 02-JUN-1999; 99WO-US12252.
 XX 23-JUN-1999; 99US-0141037.
 XX 20-JUL-1999; 99US-0144758.
 XX 26-JUL-1999; 99US-0145698.
 XX 28-JUL-1999; 99US-0146222.
 XX 01-SEP-1999; 99WO-US20111.
 XX 08-SEP-1999; 99WO-US20594.
 XX 13-SEP-1999; 99WO-US20944.
 XX 15-SEP-1999; 99WO-US21090.
 XX 05-OCT-1999; 99WO-US23089.
 XX 29-OCT-1999; 99US-0162506.
 XX 29-NOV-1999; 99WO-US28214.
 XX 30-NOV-1999; 99WO-US28313.
 XX 30-NOV-1999; 99WO-US28409.
 XX 01-DEC-1999; 99WO-US28301.
 XX 01-DEC-1999; 99WO-US28634.
 XX 02-DEC-1999; 99WO-US28551.
 XX 02-DEC-1999; 99WO-US28564.
 XX 02-DEC-1999; 99WO-US28565.
 XX 16-DEC-1999; 99WO-US30095.
 XX 20-DEC-1999; 99WO-US30099.
 XX 30-DEC-1999; 99WO-US31274.
 XX 05-JAN-2000; 2000WO-US00219.
 XX 06-JAN-2000; 2000WO-US00277.
 XX 06-JAN-2000; 2000WO-US00376.
 XX 11-FEB-2000; 2000WO-US03565.
 XX 18-FEB-2000; 2000WO-US04341.
 XX 18-FEB-2000; 2000WO-US04342.
 XX 22-FEB-2000; 2000WO-US04414.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 XX Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;
 XX WPI: 2000-572271/53.
 XX N-PSDB; AAC58626.
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX Claim 33; Fig 96; 309pp; English.
 XX The present invention describes sixty four human PRO proteins which can
 XX be used in the treatment of immune related diseases. The human PRO
 XX proteins, anti-PRO antibodies, agonists and antagonists are useful for
 XX treating and diagnosing immune related disorders. The disorders are
 XX selected from systemic lupus erythematosus, rheumatoid arthritis,
 XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 XX syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
 XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 XX immune-mediated renal disease, demyelinating diseases of the central
 XX and peripheral nervous system, hepatobiliary diseases, inflammatory
 XX bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 XX autoimmune or immune-mediated skin diseases, allergic diseases,

CC Immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX SQ Sequence 243 AA;
 XX Query Match 100.0%; Score 1325; DB 21; Length 243;
 XX Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRPLVLLILGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHGSGQLPGRDGRDGAAG 60
 OY 1 MRPLVLLILGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHGSGQLPGRDGRDGAAG 60
 DB 1 MRPLVLLILGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHGSGQLPGRDGRDGAAG 60
 OY 61 APGKGGGCGRLGCPRRDPPGPRGAGAGTGPAGGECVPPRASFASKRSESRVPPSD 120
 OY 61 APGKGGGCGRLGCPRRDPPGPRGAGAGTGPAGGECVPPRASFASKRSESRVPPSD 120
 DB 61 APGKGGGCGRLGCPRRDPPGPRGAGAGTGPAGGECVPPRASFASKRSESRVPPSD 120
 OY 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180
 DB 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180
 OY 181 FFGGMPKPRASLSGGAMVRLPEDDOVWVGVGYIGIYASIKTSTESGFLVYDWHSSP 240
 DB 181 FFGGMPKPRASLSGGAMVRLPEDDOVWVGVGYIGIYASIKTSTESGFLVYDWHSSP 240
 OY 241 VFA 243
 DB 241 VFA 243
 DB 241 VFA 243
 RESULT 5
 AAY71468
 ID AAY71468 standard; Protein: 243 AA.
 AC AAY71468;
 XX 08-NOV-2000 (first entry)
 DE Human PRO344 protein.
 XX PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative;
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;
 KW extracellular domain; ECD.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 XX Peptide 1..15
 FT /label- Signal_peptide
 FT Modified-site 11..17
 FT /note- "N-myristoylation site"
 FT Protein 16..243
 FT /label- Mature_PRO344_protein
 FT Modified-site 68..74
 FT /note- "N-myristoylation site"
 FT Binding-site 77..80
 FT /note- "Cell attachment sequence"
 FT Modified-site 216..222
 FT /note- "N-myristoylation site"
 XX WO200032778-A2.
 XX 08-JUN-2000.
 XX 30-NOV-1999; 99WO-US28409.
 XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 XX
 PA (GETH) GENENTECH INC.
 PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
 XX WPI: 2000-412325/35.
 DR N-PSDB; AAD01241.
 XX
 PT New composition useful for inhibiting neoplastic cell growth and for
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
 PT their antagonists -
 XX
 PS Claim 31; Fig 6; 108pp; English.
 XX
 CC The present sequence is the human PRO344 protein, encoded by the cDNA
 CC clone, designated as DNA40592-1242. It is isolated from human foetal
 CC lung tissue, cDNA library, identified using probes based on a consensus
 CC sequence DNA34396, derived from secreted protein extracellular domain
 CC (ECD) expressed sequence tag (EST). This clone is assigned ATCC deposit
 CC No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and
 CC is used for treating tumours, using an effective amount of PRO655, PRO364
 CC and PRO344. This composition is especially useful for treatment of human
 CC cancers such as breast, prostate, colon, lung, renal, ovarian and CNS,
 CC leukemia and melanoma.
 CC
 XX
 SQ Sequence 243 AA:
 Query Match 100.0%; Score 1325; DB 21; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLGTPGHHGSGQLPGRDGRDGDAG 60
 DB 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLGTPGHHGSGQLPGRDGRDGDAG 60
 QY 61 APGEKGEGRGRLPGPRDPCPRGAGPAGPTGAGGECVPPRASFSAKRSESRVPPSD 120
 DB 61 APGEKGEGRGRLPGPRDPCPRGAGPAGPTGAGGECVPPRASFSAKRSESRVPPSD 120
 QY 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESIASPFQ 180
 DB 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESIASPFQ 180
 QY 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240
 DB 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240
 QY 241 VFA 243
 DB 241 VFA 243
 RESULT 6
 ID AAY93688 standard; Protein: 243 AA.
 AC AAY93688;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of novel polypeptide PRO344.
 XX
 KM PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
 KM PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 KM tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..15
 FT /note= "signal peptide"
 FT Modified-site 11..17
 FT /note= "N-myristoylation site"
 FT Modified-site 68..74
 FT /note= "N-myristoylation site"
 FT Region 77..80
 FT /note= "cell attachment sequence"
 FT Modified-site 216..222
 FT /note= "N-myristoylation site"
 XX
 PN WO200037640-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 16-DEC-1999; 99WO-US30095.
 XX
 PR 22-DEC-1998; 98US-0113296.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WI;
 DR WPI: 2000-452188/39.
 DR N-PSDB; AAA46907.
 XX
 PT New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -
 XX
 PS Claim 61; Fig 10; 220pp; English.
 XX
 CC The present sequence represents a novel human polypeptide. The
 CC specification describes novel polypeptides designated PRO201, PRO292,
 CC PRO327, PRO1265, PRO343, PRO347, PRO357, PRO715, PRO1017,
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
 CC the genome of tumour cells. The polypeptides are believed to contribute
 CC to tumorigenesis. The polypeptides are useful target for the
 CC identification of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies against these polypeptides
 CC are useful in the treatment and diagnosis of neoplastic cell growth
 CC and proliferation in mammals.
 CC
 XX
 SQ Sequence 243 AA:
 Query Match 100.0%; Score 1325; DB 21; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLGTPGHHGSGQLPGRDGRDGDAG 60
 DB 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLGTPGHHGSGQLPGRDGRDGDAG 60
 QY 61 APGEKGEGRGRLPGPRDPCPRGAGPAGPTGAGGECVPPRASFSAKRSESRVPPSD 120
 DB 61 APGEKGEGRGRLPGPRDPCPRGAGPAGPTGAGGECVPPRASFSAKRSESRVPPSD 120
 QY 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESIASPFQ 180
 DB 121 APLEPDRVLVNEQGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESIASPFQ 180
 QY 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240
 DB 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240

QY 241 VFA 243
DB 241 VFA 243

RESULT 7
AAB01318
ID AAB01318 standard; Protein: 243 AA.
XX
AC AAB01318;
DT 25-SEP-2000 (first entry)
XX
DE Human PRO344 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO244; PRO241; PRO233; PRO299; PRO344; PRO347;
KW PRO355; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..15 Location/Qualifiers
FT Modified-site 11..17 /label= Signal peptide
FT Modified-site 68..74 /note= "N-myristoylation site"
FT /note= "N-myristoylation site"
FT Region 77..80
FT Modified-site 216..222 /label= Cell attachment sequence
FT /note= "N-myristoylation site"
XX
PN W0200032776-A2.
XX
PD 08-JUN-2000.
XX
PE 01-DEC-1999; 99WO-US28301.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 22-DEC-1998; 98US-0113296.
XX
PA (GETH) GENENTECH INC.
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerlitsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kijavlin IJ, Napier MA, Roy MA, Tumas D, Wood WT;
XX
DR WPI; 2000-412324/35.
DR N-PSDB; AAA49560.
XX
PT New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
PS Claim 12; Fig 18; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1325; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 5, 3e-103;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPTPGHNGSGGLPGRDGRDGAAG 60
DB 1 MRPLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPTPGHNGSGGLPGRDGRDGAAG 60
QY 61 APGEKGGGRGRLGPPRGDGPREGAPAGPTGAGGCSVPPRAFAFAKSESVPSPSD 120
DB 61 APGEKGGGRGRLGPPRGDGPREGAPAGPTGAGGCSVPPRAFAFAKSESVPSPSD 120
QY 121 APLEPDRVLYNEQGHYAVTGKFTQYGVYFFAVHATVYRASLQFDLVNKGESIASFFQ 180
DB 121 APLEPDRVLYNEQGHYAVTGKFTQYGVYFFAVHATVYRASLQFDLVNKGESIASFFQ 180
QY 181 FFGGMPKRPASISGGAMVRLPEPDQVWVQVGVDTIGIYASIKDSTSGFLVYSDMSSP 240
DB 181 FFGGMPKRPASISGGAMVRLPEPDQVWVQVGVDTIGIYASIKDSTSGFLVYSDMSSP 240
QY 241 VFA 243
DB 241 VFA 243

RESULT 8
AAU12352
ID AAU12352 standard; Protein: 243 AA.
XX
AC AAU12352;
DT 24-OCT-2001 (first entry)
XX
DE Human PRO344 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIa; gene therapy.
XX
OS Homo sapiens.
XX
PN W020014046-A2.
XX
PD 07-JUN-2001.
XX
PE 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX

PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2001-408281/43.
 DR N-PSDB: AAS21424.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX Claim 12; Fig 362; 813pp: English.
 PS
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes; the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 CC
 SQ Sequence 243 AA:

Query Match 100.0%; Score 1325; DB 22; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLILGLAASPLDDNKIPSLCPGHPGLPOTPGHSGSLPGRDGRDGRGAG 60
 DB 1 MRPLVLLILGLAASPLDDNKIPSLCPGHPGLPOTPGHSGSLPGRDGRDGRGAG 60
 QY 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
 DB 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
 QY 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180
 DB 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180
 QY 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIYASITDSTFSGLVYSDWHSSP 240
 DB 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIYASITDSTFSGLVYSDWHSSP 240
 QY 241 VFA 243
 DB 241 VFA 243

RESULT 9
 AAB65815
 ID AAB65815 standard; Protein; 243 AA.
 XX
 AC AAB65815;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Human TANGO 253 SEQ ID NO: 3.

XX Human: mouse; secreted protein; TANGO253; TANGO 257; TANGO 261;
 KW INTERCEPT 258; coronary disorder; olfactory disorder;
 KW neurological disorder; pulmonary disorder; immunological disorder;
 KW developmental disorder; kidney disorder.
 XX Homo sapiens.
 PN WO200078808-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 19-JUN-2000; 2000WO-US16883.
 XX
 PR 18-JUN-1999; 99US-0336536.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Leiby KR, McKay C, Bossone S;
 XX WPI: 2001-050109/06.
 DR
 XX New nucleic acids for treating diseases and disorders, e.g.
 PT atherosclerosis, infection, autoimmune diseases, obesity, ear
 PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
 PT sclerosis and asthma -
 XX
 PS Claim 9; Page 211-212; 332pp: English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
 CC TANGO 261 and INTERCEPT 258. These are useful in the treatment of
 CC coronary, pulmonary, olfactory, immunological, neurological,
 CC developmental and kidney disorders.
 CC
 SQ Sequence 243 AA:

Query Match 100.0%; Score 1325; DB 22; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPLVLLILGLAASPLDDNKIPSLCPGHPGLPOTPGHSGSLPGRDGRDGRGAG 60
 DB 1 MRPLVLLILGLAASPLDDNKIPSLCPGHPGLPOTPGHSGSLPGRDGRDGRGAG 60
 QY 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
 DB 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
 QY 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180
 DB 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180
 QY 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIYASITDSTFSGLVYSDWHSSP 240
 DB 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIYASITDSTFSGLVYSDWHSSP 240
 QY 241 VFA 243
 DB 241 VFA 243

RESULT 10
 AAB49593
 ID AAB49593 standard; Protein; 243 AA.
 XX
 AC AAB49593;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human adipocyte complement related protein homolog zs1939.
 XX
 DE Human; zacrps; gene therapy; complement inhibition; C1q domain;

KW adipocyte complement related protein homolog;
KW inflammation; hormone secretion; inositol phosphate; arachidonate;
KW phospholipase C activation; gastric emptying; neutrophil activation;
KW superoxide anion production; antimicrobial; acute vascular injury;
KW wound healing; zsig39.
XX
OS Homo sapiens.
XX
PN WO200073444-A1.
XX
PD 07-DEC-2000.
XX
PE 18-MAY-2000; 2000WO-US13608.
XX
PR 27-MAY-1999; 99US-0321372.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Pliddington CS, Sheppard FO;
XX
DR WPI: 2001-061531/07.
XX
PT Novel adipocyte complement related protein homolog, ZACRP5, useful for
PT diagnosing and treating inflammation, vascular injury microbial
PT infections, and in wound healing
XX
PS Disclosure; Fig 1; 121pp; English.
XX
XX The present invention relates to human adipocyte complement related
XX protein homolog, zacrps protein and coding sequence (see ABA49590 and
XX AAC90045). ZACRP5 has a carboxyl-terminal C1q domain. The zacrps gene is
XX located on human chromosome 16. zacrps gene and protein are useful for
XX diagnosing and treating inflammations, for determining arterial
XX remodeling, for modulating calcium ion concentration, hormone
XX secretion, DNA synthesis or cell growth, inositol phosphate turnover,
XX arachidonate release, phospholipase C activation, gastric emptying, human
XX neutrophil activation or ADCC capability and superoxide anion production.
XX zacrps gene and protein are also useful as antimicrobial applications,
XX preferably against bacteria and virus, for complement inhibition, for
XX treating acute vascular injury, and for wound healing. The present
XX sequence is human adipocyte complement related protein homolog, zsig39
XX protein. This protein was used in a sequence homology alignment with
XX zacrps protein.
XX
SQ Sequence 243 AA:
Query Match 100.0%; Score 1325; DB 22; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.3e-103;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPLVLLLLGLAAGSPPLDDNKTPLSCPGHPLGTPRGHHSGLRGDRGDRGAPG 60
Db 1 MRPLVLLLLGLAAGSPPLDDNKTPLSCPGHPLGTPRGHHSGLRGDRGDRGAPG 60
QY 61 APGEKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120
Db 61 APGEKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120
QY 121 APLEFDRVLVNEGSHYDAVTGKFTQVPYGYFFAVHATYVRASLQFDLVNKGESIASFFQ 180
Db 121 APLEFDRVLVNEGSHYDAVTGKFTQVPYGYFFAVHATYVRASLQFDLVNKGESIASFFQ 180
QY 181 PFGGWPKPASLSGAMVRLPEDDQVWQVGVGYDIGIYASIKTDTSTSGFLVYSDMHSSP 240
Db 181 PFGGWPKPASLSGAMVRLPEDDQVWQVGVGYDIGIYASIKTDTSTSGFLVYSDMHSSP 240
QY 241 VFA 243
Db 241 VFA 243

ID ABA49599 standard; Protein: 243 AA.
XX
XX ABA49599;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human adipocyte complement related protein homolog zsig39.
XX
XX Human; zacrps6; gene therapy; complement inhibition; C1q domain;
KW adipocyte complement related protein homolog;
KW inflammation; hormone secretion; inositol phosphate; arachidonate;
KW phospholipase C activation; gastric emptying; neutrophil activation;
KW superoxide anion production; antimicrobial; acute vascular injury;
KW wound healing; zsig39.
XX
OS Homo sapiens.
XX
PN WO200073446-A2.
XX
PD 07-DEC-2000.
XX
PE 22-MAY-2000; 2000WO-US14024.
XX
PR 27-MAY-1999; 99US-0321262.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Pliddington CS, Sheppard FO;
XX
DR WPI: 2001-061532/07.
XX
PT Novel adipocyte complement related protein homolog, ZACRP6, useful as
PT modulators of neurotransmission and for treating disseminated
PT intravascular coagulation, arteriosclerosis and acute vascular injury
XX
PS Disclosure; Fig 1; 119pp; English.
XX
XX The present invention relates to human adipocyte complement related
XX protein homolog, ZACRP6 protein and coding sequence (see ABA49596 and
XX AAC90051). ZACRP6 has a carboxyl-terminal C1q domain. The zacrps6 gene is
XX located on human chromosome 21q. zacrps6 gene and protein are useful for
XX diagnosing and treating inflammations, for determining arterial
XX remodeling, for modulating calcium ion concentration, hormone
XX secretion, DNA synthesis or cell growth, inositol phosphate turnover,
XX arachidonate release, phospholipase C activation, gastric emptying, human
XX neutrophil activation or ADCC capability and superoxide anion production.
XX zacrps6 gene and protein are also useful as antimicrobial applications,
XX preferably against bacteria and virus, for complement inhibition, for
XX treating acute vascular injury, disseminated intravascular coagulation,
XX arteriosclerosis and for wound healing. The present sequence is human
XX adipocyte complement related protein homolog zsig39. This protein was
XX used in a sequence homology comparison with ZACRP6 protein.
XX
SQ Sequence 243 AA:
Query Match 100.0%; Score 1325; DB 22; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.3e-103;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPLVLLLLGLAAGSPPLDDNKTPLSCPGHPLGTPRGHHSGLRGDRGDRGAPG 60
Db 1 MRPLVLLLLGLAAGSPPLDDNKTPLSCPGHPLGTPRGHHSGLRGDRGDRGAPG 60
QY 61 APGEKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120
Db 61 APGEKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120
QY 121 APLEFDRVLVNEGSHYDAVTGKFTQVPYGYFFAVHATYVRASLQFDLVNKGESIASFFQ 180
Db 121 APLEFDRVLVNEGSHYDAVTGKFTQVPYGYFFAVHATYVRASLQFDLVNKGESIASFFQ 180
QY 181 PFGGWPKPASLSGAMVRLPEDDQVWQVGVGYDIGIYASIKTDTSTSGFLVYSDMHSSP 240
Db 181 PFGGWPKPASLSGAMVRLPEDDQVWQVGVGYDIGIYASIKTDTSTSGFLVYSDMHSSP 240

DB 181 FFGGMPKPKPASISGGAMVRLPEPDQWVGVGDYIGIYASIKTDSITFSGLVYSDWHSSP 240
QY 241 VFA 243
DB 241 VFA 243

RESULT 12

AAB65891
ID AAB65891 standard; Protein: 243 AA.

XX AAB65891;

DT 28-MAR-2001 (first entry)

DE Human secreted protein related protein SEQ ID NO: 108.

XX Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

KW INTERCEPT 258; coronary disorder; olfactory disorder;

KW neurological disorder; pulmonary disorder; immunological disorder;

KW developmental disorder; kidney disorder.

XX Homo sapiens.

OS WO200078808-A1.

PN 28-DEC-2000.

PD 19-JUN-2000; 2000WO-US16883.

PF 18-JUN-1999; 99US-0336536.

PR (MILL-) MILLENNIUM PHARM INC.

PA Leiby KR, McKay C, Bossone S;

PI WPI; 2001-050109/06.

DR New nucleic acids for treating diseases and disorders, e.g.

PT atherosclerosis, infection, autoimmune diseases, obesity, ear

PT disorders, brain disorders, tumors, diabetes, arthritis, multiple

PT sclerosis and asthma -

XX Disclosure; Page 274; 332pp; English.

XX The present invention provides the protein and coding sequences of the

CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,

CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of

CC coronary, pulmonary, olfactory, immunological, neurological,

CC developmental and kidney disorders.

XX Sequence 243 AA:

Query Match 99.8%; Score 1323; DB 22; Length 243;

Best Local Similarity 99.6%; Pred. No. 7.8e-103;

Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPPILDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGDRDAGG 60
DB 1 MRPLVLLLLGLAASPPILDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGDRDAGG 60
QY 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
DB 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
QY 121 APLPDRVLVNBQGHYDAVTGKFTQCPGVYFAVAHATYRASLQFDLVKNESIASFQ 180
DB 121 APLPDRVLVNBQGHYDAVTGKFTQCPGVYFAVAHATYRASLQFDLVKNESIASFQ 180
QY 181 FFGGMPKPKPASISGGAMVRLPEPDQWVGVGDYIGIYASIKTDSITFSGLVYSDWHSSP 240
DB 181 FFGGMPKPKPASISGGAMVRLPEPDQWVGVGDYIGIYASIKTDSITFSGLVYSDWHSSP 240

QY 241 VFA 243
DB 241 VFA 243

RESULT 13

AAB65888
ID AAB65888 standard; Protein: 243 AA.

XX AAB65888;

DT 28-MAR-2001 (first entry)

DE Human secreted protein related protein SEQ ID NO: 102.

XX Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

KW INTERCEPT 258; coronary disorder; olfactory disorder;

KW neurological disorder; pulmonary disorder; immunological disorder;

KW developmental disorder; kidney disorder.

XX Homo sapiens.

OS WO200078808-A1.

PN 28-DEC-2000.

PD 19-JUN-2000; 2000WO-US16883.

PF 18-JUN-1999; 99US-0336536.

PR (MILL-) MILLENNIUM PHARM INC.

PA Leiby KR, McKay C, Bossone S;

PI WPI; 2001-050109/06.

DR New nucleic acids for treating diseases and disorders, e.g.

PT atherosclerosis, infection, autoimmune diseases, obesity, ear

PT disorders, brain disorders, tumors, diabetes, arthritis, multiple

PT sclerosis and asthma -

XX Disclosure; Page 270-271; 332pp; English.

XX The present invention provides the protein and coding sequences of the

CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,

CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of

CC coronary, pulmonary, olfactory, immunological, neurological,

CC developmental and kidney disorders.

XX Sequence 243 AA:

Query Match 99.7%; Score 1321; DB 22; Length 243;

Best Local Similarity 99.6%; Pred. No. 1.1e-102;

Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPPILDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGDRDAGG 60
DB 1 MRPLVLLLLGLAASPPILDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGDRDAGG 60
QY 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
DB 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCSVPPRSASFSAKRSRVPSPD 120
QY 121 APLPDRVLVNBQGHYDAVTGKFTQCPGVYFAVAHATYRASLQFDLVKNESIASFQ 180
DB 121 APLPDRVLVNBQGHYDAVTGKFTQCPGVYFAVAHATYRASLQFDLVKNESIASFQ 180
QY 181 FFGGMPKPKPASISGGAMVRLPEPDQWVGVGDYIGIYASIKTDSITFSGLVYSDWHSSP 240
DB 181 FFGGMPKPKPASISGGAMVRLPEPDQWVGVGDYIGIYASIKTDSITFSGLVYSDWHSSP 240
QY 241 VFA 243

Db 241 VFA 243

RESULT 14
AAB65889
ID AAB65889 standard; Protein: 243 AA.
XX
AC AAB65889;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human secreted protein related protein SEQ ID NO: 104.
XX
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW INTERCEPT 258; coronary disorder; olfactory disorder;
KW neurological disorder; pulmonary disorder; immunological disorder;
KW developmental disorder; kidney disorder.
XX
OS Homo sapiens.
XX
PN WO200078808-A1.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16883.
XX
PR 18-JUN-1999; 99US-0336536.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Leiby KR, McKay C, Bossone S;
XX
DR WPI: 2001-050109/06.
XX
PT New nucleic acids for treating diseases and disorders, e.g.
PT atherosclerosis, infection, autoimmune diseases, obesity, ear
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT sclerosis and asthma
XX
PS Disclosure; Page 271-272; 332pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC coronary, pulmonary, olfactory, immunological, neurological,
CC developmental and kidney disorders.
XX
SQ Sequence 243 AA;

Query Match 99.7%; Score 1321; DB 22; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.le-102;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPTGPHHGSQGLRGDRGDRDAPG 60
DB 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPTGPHHGSQGLRGDRGDRDAPG 60
QY 61 APGEKGGRRPGLPGPRGDPGRGEGAPAGPTGAGGCSVPPRSASFSAKSESSESVPPSPD 120
DB 61 APGEKGGRRPGLPGPRGDPGRGEGAPAGPTGAGGCSVPPRSASFSAKSESSESVPPSPD 120
QY 121 APLEPDRVLYNEGCHYAVTGKFTCOVPGYVYFAVNAVTVYRASLQDFLVNNGESIASFFQ 180
DB 121 APLEPDRVLYNEGCHYAVTGKFTCOVPGYVYFAVNAVTVYRASLQDFLVNNGESIASFFQ 180
QY 181 FFGGWPAPASLSGAMVRLPEPDQVWVQVGVGDIYASIKTIDSTSGFLVYSMDHSSP 240
DB 181 FFGGWPAPASLSGAMVRLPEPDQVWVQVGVGDIYASIKTIDSTSGFLVYSMDHSSP 240
QY 241 VFA 243
DB 241 VFA 243

Db 241 VFA 243

RESULT 15
AAB65890
ID AAB65890 standard; Protein: 243 AA.
XX
AC AAB65890;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human secreted protein related protein SEQ ID NO: 106.
XX
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW INTERCEPT 258; coronary disorder; olfactory disorder;
KW neurological disorder; pulmonary disorder; immunological disorder;
KW developmental disorder; kidney disorder.
XX
OS Homo sapiens.
XX
PN WO200078808-A1.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16883.
XX
PR 18-JUN-1999; 99US-0336536.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Leiby KR, McKay C, Bossone S;
XX
DR WPI: 2001-050109/06.
XX
PT New nucleic acids for treating diseases and disorders, e.g.
PT atherosclerosis, infection, autoimmune diseases, obesity, ear
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT sclerosis and asthma
XX
PS Disclosure; Page 272-273; 332pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC coronary, pulmonary, olfactory, immunological, neurological,
CC developmental and kidney disorders.
XX
SQ Sequence 243 AA;

Query Match 99.7%; Score 1321; DB 22; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.le-102;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPTGPHHGSQGLRGDRGDRDAPG 60
DB 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPTGPHHGSQGLRGDRGDRDAPG 60
QY 61 APGEKGGRRPGLPGPRGDPGRGEGAPAGPTGAGGCSVPPRSASFSAKSESSESVPPSPD 120
DB 61 APGEKGGRRPGLPGPRGDPGRGEGAPAGPTGAGGCSVPPRSASFSAKSESSESVPPSPD 120
QY 121 APLEPDRVLYNEGCHYAVTGKFTCOVPGYVYFAVNAVTVYRASLQDFLVNNGESIASFFQ 180
DB 121 APLEPDRVLYNEGCHYAVTGKFTCOVPGYVYFAVNAVTVYRASLQDFLVNNGESIASFFQ 180
QY 181 FFGGWPAPASLSGAMVRLPEPDQVWVQVGVGDIYASIKTIDSTSGFLVYSMDHSSP 240
DB 181 FFGGWPAPASLSGAMVRLPEPDQVWVQVGVGDIYASIKTIDSTSGFLVYSMDHSSP 240
QY 241 VFA 243
DB 241 VFA 243

Mon Jun 23 10:16:11 2003

Search completed: June 13, 2003, 16:00:38
Job time : 73 secs

us-09-944-944-42.rag

Page 11

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 21, 2003, 14:32:46 ; Search time 202 Seconds

(without alignments)
1816.694 Million cell updates/sec

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Perfect score: 2540
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	52.2	243	20	AAV06481	Human tumour-assoc
2	1325	52.2	243	20	AAV17827	Human PRO344 prote
3	1325	52.2	243	20	AAW97984	Human adipocyte-sp
4	1325	52.2	243	21	AAW33461	Human PRO344 prote
5	1325	52.2	243	21	AAV71468	Human PRO344 prote
6	1325	52.2	243	21	AAV93688	Amino acid sequenc
7	1325	52.2	243	21	AAAB0318	Human PRO344 polyp
8	1325	52.2	243	22	AAU12352	Human PRO344 polyp
9	1325	52.2	243	22	AAAB65815	Human TANGO 253 SE
10	1325	52.2	243	22	AAAB49593	Human adipocyte co
11	1325	52.2	243	22	AAAB49599	Human adipocyte co
12	1323	52.1	243	22	AAAB65891	Human secreted pro
13	1321	52.0	243	22	AAAB65888	Human secreted pro
14	1321	52.0	243	22	AAAB65889	Human secreted pro
15	1321	52.0	243	22	AAAB65890	Human secreted pro
16	1271	50.0	243	21	AAV76040	Rat skin cell prot
17	1271	50.0	243	22	AAAB55979	Skin cell protein,
18	1271	50.0	243	23	AAV72179	Rat protein isolat
19	1258	49.5	243	22	AAAB65820	Human mature TANGO
20	1256	49.4	228	22	AAAB65816	Human mature TANGO
21	1256	49.4	243	22	AAAB65899	Murine secreted pr
22	1254	49.4	243	22	AAAB65897	Murine secreted pr
23	1254	49.4	243	22	AAAB65898	Murine secreted pr
24	1243.5	49.0	242	22	AAAB65896	Murine mature TANG
25	1200	47.2	228	22	AAAB65821	Novel human diagno
26	1183	46.6	220	22	ABG12724	Human secreted pro
27	1048	41.3	201	23	AAO21663	Human TANGO 253 C1
28	675	26.6	128	22	AAAB65819	Murine TANGO 253 C
29	650	25.6	128	22	AAAB65824	Human colon cancer
30	518	20.4	95	22	AAAG74016	Human colon cancer
31	480.5	18.9	151	22	ABG12723	Novel human diagno
32	449.5	17.7	225	23	AAAB80583	Human sbp1033026C1
33	446	17.6	333	23	ABBB80588	Human sbp1033026C1
34	433.5	17.1	247	18	AAW09107	Murine adipocyte c
35	433.5	17.1	247	22	AAE05528	Mouse OB33 protein
36	433.5	17.1	247	23	ABB08222	Mouse OB33 protein
37	427	16.8	289	23	ABW72306	Rat protein isolat
38	425	16.7	244	18	AAW09108	Mouse adipocyte co
39	424.5	16.7	247	22	AAE05527	Mouse OB33 protein
40	424.5	16.7	247	23	ABB08221	Mouse adipocyte co
41	424	16.7	244	20	AAAB21807	Adipose most abund
42	424	16.7	244	21	AAAB30233	Human adipocyte co
43	424	16.7	244	21	AAV71035	Human APW1 (Adipos
44	424	16.7	244	22	AAE05529	Human OB33 protein
45	424	16.7	244	22	AAAB65828	Human adipocyte co

ALIGNMENTS

RESULT 1
AAV06481 standard; Protein: 243 AA.

AAV06481:

27-SEP-1999 (first entry)

Human tumour-associated protein PRO344.

PRO344: UNQ303; cancer; tumour; diagnosis; therapy; human.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..15

Protein /note= "signal peptide" 16..243
/note= "mature protein"

FT		Modified-site	/note="N-myristoylated"	68..215
FT		Modified-site	216..243	
ET		/note="N-myristoylated"		
XX	PV	MW9935170-A2.		
XX	PD	15-JUL-1999.		
XX	PF	05-JAN-1999;	99WO-US00106.	
XX	PR	20-NOV-1998;	98US-0109304.	
XX	PR	05-JAN-1998;	98US-0070440.	
XX	PR	29-APR-1998;	98US-0083500.	
XX	PR	22-MAY-1998;	98US-0086414.	
XX	PR	10-JUN-1998;	98US-0088742.	
XX	PA	10-NOV-1998;	98US-0107783.	
XX	(GETH) GENENTECH INC.			
XX	Botstein D., Goddard A,	Gurney AL,	Hillan KJ,	Lawrence DA:
PI	Roy MA,	Wood WJ;		
DR	N-PSDB; AA#67256.			
XX	WP1: 1999-430385/36.			
XX				
PT	Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment			
XX	Example 1; Fig 10; 16zpp; English.			
CC	<p>This sequence represents human PR0344 (UHQ303), a protein encoded by the novel cDNA clone DNA40592 (see AAX87258). Amplification of DNA40592 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PR0344 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnostic kits.</p>			
XX	Sequence	243 AA;		
XX	-50			
	Alignment Scores:			
	Pred. NO.:	5.37e-86	Length: 243	
	Score:	1325.00	Matches: 243	
	Percent Similarity:	100.00%	Conservative: 0	
	Best Local Similarity:	100.00%	Mismatches: 0	
	Query Match:	52.17%	Indels: 0	
		20	Gaps: 0	
US-09-944-944-41 (1-1377)	x	AAY06481 (1-243)		
OY	227	ATGAGCGCACTCCTGCCTGGTGTTCCTGACGCCGTGCGCGGCTGCCCCACTGGAC	286	
Dd	1	MetArgProIeuLeuValIeuLeuLeuLeuLgLYleAlalAagLYSerProIleuAsp	20	
OY	287	GACAAGAATCCCACGACTTGCCCGGGGACCACCCGGGCTTCAGAGCACCGGGCAC	348	
Dd	21	ASPasnlySllePrOserlenucySProglYhtSPROglyLeuPROglYTThrPROghis	40	
OY	347	CATGGACGCCAGGCGTTGCCGGGGCCGATGAGCCCGACAGCCCGGACGGCGCCGGG	406	
Dd	41	HtsGLySercLnclnLYleuProlYArGaSpGlYAraGaSpGlYAraGaSpGlYAlarPGLy	60	
OY -	407	GCATCCGGAGAAAGAACGAGGCGGAGGCGGGAAGCCCGGAGTCCCGGAGCCTCGAGGGGACCC	466	
	61	AlarPGLyGIlnLYseLYslnLYslnLYslnLYArGPProglYleuPROAtggLYaspTo	80	

QY	467	GGCGCGGAGAGAAAGCGGGGACCCGGGGGGCCACGGGGGCGTGGCGGGAGATGCTGCTG	526
Db	81	GLYPRALRGELYGELNALGLPRDLAAGLYPRDLHGLYPRDLAAGLYGLUCYSSEVAL	1000
QY	527	CCACCGGAGATCCGCTTTCAGCGCCCAAGCGCTCCAGAGCCGGGATGCCCGCGCTTGAC	586
Db	101	PROPRALRGSERIALAHESERIALALYSALYSERGISUSERALGYVALPROPROPISERASP	1200
QY	587	GCAACCTTGCCCTTTCAGCCGCGCTGCTGTGAACGAGAGGACATTAAGACCCGCTCAC	646
Db	121	ALAPROLEUPROPHESAPRGVALLEUVALASNGIUNGINGLIHISTYDASPAALAVALTHT	140
QY	647	GGCAAGTTTACACTCCGACAGGTGGCTGGGTCTACTCTCGCCGCTGCATGCCACCGTCTAC	706
Db	141	GLYLSHETHRHYSGLSINALPRGGLYVALTYTYTPHEALAVAIHISALATHIVALTYT	1600
QY	707	CGGGACGACGCTTGATGATGTTGATGCGAAGATGCGAATGCATTCGCTCTTTCACG	766
Db	161	ARGALASERLEUCLINPHEASPRLEUVALYLSAANGLYGUSERLLEALASERPHENEGIN	1800
QY	767	TTTTTGGGGGGGTGGCCCAAGCCAGCCTGCTCTCGGGGGGGCCATGCTGAGGCTGAG	826
Db	181	PHAPHEGLYGLYTPRPROLYSPROALASERLEUSERGLYGLYALMETVALATGLAUGLN	2000
QY	827	CCGAGAGACCAAGTGTGGGTGAGGTGGGTGGGTGACTCATTTGGCATCTATGCCAC	886
Db	201	PROGLINSPGLINVALITTPALGINVALGLYVALGLYASPTYTLIEGLYLTETRYALASER	2200
QY	887	ATCCAGACAGACAGACACTTCTCCGATTTCTGTGTACTGCTACGCTGCAGTGCAGCTCCCA	946
Db	221	ILELTYTHASPERTHRPHESERGLYRHEUVALTYRSEARPTPHISSESRERO	2400
QY	947	GTCCTTGCT 955	
Db	241	VALPHEALA 243	
RESULT 2			
ID	AAI17827	standard; protein; 243 AA.	
XX	AAI17827:		
AC	12-AUG-1999	(first entry)	
XX			
DE	Human PRO344 protein sequence.		
XX			
KW	Human; PRO protein; tumour necrosis factor family; TNF; cytokine;		
XX	secreted protein; transmembrane protein; inflammation disorder.		
OS	Homo sapiens.		
XX			
EN	W09928462-A2.		
XX			
DD	10-JUN-1999.		
XX			
PF	01-DEC-1998;	98WC-US25108.	
XX			
PR	25-FEB-1998;	98US-0075945.	
PR	03-DEC-1997;	97US-0067411.	
PR	11-DEC-1997;	97US-0069278.	
PR	11-DEC-1997;	97US-0069334.	
PR	11-DEC-1997;	97US-0069335.	
PR	12-DEC-1997;	97US-0069425.	
PR	16-DEC-1997;	97US-0069694.	
PR	16-DEC-1997;	97US-0069696.	
PR	16-DEC-1997;	97US-0069702.	
PR	17-DEC-1997;	97US-0069870.	
PR	17-DEC-1997;	97US-0069873.	
PR	18-DEC-1997;	97US-0068017.	
PR	05-JAN-1998;	98US-0070440.	
PR	09-FEB-1998;	98US-0074086.	
PR	09-FEB-1998;	98US-0074092.	

QY	347	CATGGCAGCAGGAGGCTTGGCCGGGGCCGCAATGGCCGGCAGAGCCGCGCAGACGGCCGGCCGGG	406
Db	41		60
QY	407	GCTCCGGGAGAAAGGCGAGGGCCGGGAGCCGGGACTCCGGGACTCGAGGAGGAGCC	466
Db	61		80
QY	467	GGGCGCGCAGAGAGAGGGGAGCCCGGGGGCCACCGGGGCTCGCGGGAGTCTGGTG	526
Db	81		100
QY	527	CCTCCGCGATCCCGCTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTGGCTCCGCGCTGAC	586
Db	101		120
QY	587	GCACCTTGCCCTTGACCGCGCTGCTGGTGAACAGCAGAGGACATTACAGCCGCTACC	646
Db	121		140
QY	647	GGCAGATTACCTGGCGAGGTGCTGGGGGCTCTACTTGCCGCTCATGCGACGCTTC	706
Db	141		160
QY	707	CGGGCGACCTGCACTTTGATCTTGGTGAAGATGGCGAATGCCATTCCTCTTCCAG	766
Db	161		180
QY	767	TTTTTCGGGGGGTGGCCCAAGCCAGCTGCTCTCGGGGGGGCCATGGTAGGCTGGAG	-826
Db	181		200
QY	827	CCTGAGGACCAAGTGTGGGTGACAGGCGGTGTGGGTGAGTCAATTGGCATTCATGGCAGC	886
Db	201		220
QY	887	ATCAAGACAGACAGCAGCACTTCTCCGATTCTGTGTACTCCGACTGGCAGACGCTCCCA	946
Db	221		240
QY	947	GTCCTTGCT 955	
Db	241	ValpheA 243	
RESULT 10			
AAB49593			
ID	AAB49593 standard; Protein; 243 AA.		
AC	AAB49593;		
XX			
DT	13-MAR-2001 (first entry)		
XX			
DE	Human adipocyte complement related protein homolog zsig39.		
XX			
KW	Human; zacrpf; gene therapy; complement inhibition; C1q domain;		
KW	adipocyte complement related protein homolog;		
KW	inflammation; hormone secretion; inositol phosphate; arachidonate;		
KW	phospholipase C activation; gastric emptying; neutrophil activation;		
KW	superoxide anion production; antimicrobial; acute vascular injury;		
XX	wound healing; zsig39.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200073444-A1.		
XX			
PD	07-DEC-2000.		
XX			
PF	18-MAY-2000; 2000WO-US13608.		
XX			
PR	27-MAY-1999; 99US-0321372.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		

PI	Piddington CS, Sheppard PO;
XX	
XX	WPI; 2001-061531/07.
XX	
PT	Novel adipocyte complement related protein homolog, zACRP5, useful for
PT	diagnosing and treating inflammation, vascular injury microbial
PT	infections, and in wound healing -
XX	
PS	Disclosure; Fig 1; 121pp; English.
XX	
CC	The present invention relates to human adipocyte complement related
CC	protein homolog, zacrps protein and coding sequence (see AAB49590 and
CC	AAC90045). ZACRP5 has a carboxyl-terminal Ctg domain. The zacrps gene is
CC	located on human chromosome 16. zacrps gene and protein are useful for
CC	diagnosing and treating inflammations, for determining arterial
CC	remodelling, for modulating calcium ion concentration, hormone
CC	secretion, DNA synthesis or cell growth, inositol phosphate turnover,
CC	arachidonate release, phospholipase C activation, gastric emptying, human
CC	neutrophil activation or ADPC capability and superoxide anion production.
CC	zacrps gene and protein are also useful as antimicrobial applications,
CC	preferably against bacteria and virus, for complement inhibition, for
CC	treating acute vascular injury, and for wound healing. The present
CC	sequence is human adipocyte complement related protein homolog, zs1g39
CC	protein. This protein was used in a sequence homology alignment with
XX	
SQ	Sequence 243 AA;
Alignment Scores:	
Pred. No.:	5,37e-86 Length: 243
Score:	1325.00 Matches: 243
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	52.17% Indels: 0
DB:	Gaps: 0
US-09-944-944-41 (1-1377) x AAB49593 (1-243)	
OY	227 ATGAGGCCACTCCTCGTCTGTCTGTCCTGGGCGTGCGGCAGCCGCCCCCATGTGAC 286
Db	1 MetirgrProleuLeuValLeuLeuLeuLeuLeuLgLyLeuAlaLaIlgSerProProLeuAsp 20
OY	287 GACAACAAGATCCCAGCCCTCTGCCCCGGGGGCAACCCCGGCTTCCAGGACCGCGGGCCAC 346
Db	21 AspAsnlySlleProSerLeucySProGlylnSProGlyLeuProGlylThrProGlyHis 40
OY	347 CATGGCAGCAGCGGCTTGCCCGGGCCCGATGGACCAGCGAGCGCGGCGCGCGG 408
Db	41 HislgyserclndlyLeuProGlylAraSpRglYlAraSpRglYlAraSpRglYlAraProGly 60
OY	407 GCTCCGGGAGAAGAGCGAGGCGGAGCGGAGCCGGGAATTGCGGAACTCGAAGGGACCCC 466
Db	61 AlAProGlYgluISgLygluISglYlAraGrProGlyLeuProGlyProArglYAspPro 80
OY	467 GGCGCCGGAGAAAGCGCGGACCCGGGGGCCACCGGGCTCCCGGGGAATGCTGGTG 528
Db	81 GlYProArGlYgluAlaIgLPProAlaIgLProlInGlyProAlaIgLYluCySseVal 1000
OY	527 CTCGCCGGAATCGCCTTCAGCGCGCAAGCGCTCGAGAGCGGGGTGCTCCGCGCTGAC 586
Db	101 ProPolarGerlAlaPheSerAlaLysAlaySerglUSeRAlYvalProProPoleSerAsp 1200
OY	587 GCACCCCTTGCCCTTCAGCCGCGTGGCGTGAACAGACAGAGACATTACAGACCGCTCAC 646
Db	121 AlaProleuProrheAsprArYalLeuValaAnsglInglnISlYlAraAlaValThr 1400
OY	647 GGCAGATTCACTGTCCAGGTGCTGGGGCTTAATACTTGGCGCTGCATGCCACCGTTAC 706
Db	141 GlYlYSerPherhICySglnglnAlProGlylValYtTYlPhAlaValAlnISlaIThrValTyx 1600
OY	707 CGGGCCAGCCTGAGATTGATCTGGTGAAGAATGGCGAATGCATTTGCTCTTCCAG 766
Db	161 AtYAlaSerleuNdlnPheAspLeuValLYlSaSnGlylUSeRIleAlaSerPhePheGln 1800

Oy		767	TTTTTGGGGGGGTGCCCCAAGCCACCTCGTCCTGGGGGGGGGCCATGCTGAGCGTGAG	826
Dd		181	PhePheGlyGlyTrpProIysProAlaSerLeuSeGlyAlaMetValArgLeuGln	200
Oy		827	CCTGAGCACCAGTTGGTGCAGCTGGGTGGGTGCATCAATTGGCATCTATGCGCAC	886
Dd		201	ProGluAspGlnValTrpValcInlValGlyValGlyAspTyrlleGlylleTryAlaSer	220
Oy		887	ATCAAGACAGACAGCACCCTTCGCGGATTTCTGTGTGTACTCCGACTGGACAGACCTCCCA	946
Dd		221	IleIysThrAspSerThrPheSerGlyPheLeuValTySeraSprHisSerSerPro	240
Oy		947	GTCCTTGCT	955
Dd		241	VAlPheAla	243
RESULT 11				
ID	AAB49599			
XX	AAB49599 standard; Protein; 243 AA.			
AC	AAB49599;			
DT	13-MAR-2001 (first entry)			
XX				
DE	Human adipocyte complement related protein homolog zsig39.			
XX				
KM	Human; zacrpf gene therapy; complement inhibition; C1q domain;			
KW	adipocyte complement related protein homolog;			
KV	inflammation; hormone secretion; inositol phosphate; arachidonate;			
KW	phospholipase C activation; gastric emptying; neutrophil activation;			
KM	superoxide anion production; antimicrobial; acute vascular injury;			
KX	wound healing; zsig39.			
OS	Homo sapiens.			
XX				
PN	WO200073446-A2.			
PD	07-DEC-2000.			
XX				
PF	22-MAY-2000; 2000MO-US14024.			
PR	27-MAY-1999; 99US-0321262.			
XX				
PA	(ZYMO) ZYMOGENETICS INC.			
PI	Piddington CS, Sheppard PO;			
DR	WP1; 2001-061532/07.			
PT	Novel adipocyte complement related protein homolog, ZACRP6, useful as			
PT	modulators of neurotransmission and for treating disseminated			
PT	intravascular coagulation, arteriosclerosis and acute vascular injury			
XX				
PS	Disclosure: Fig 1; 119pp; English.			
XX				
CC	The present invention relates to human adipocyte complement related			
CC	protein homology, ZACRP6 protein and coding sequence (see AAB49596 and			
CC	AAC30051). ZACRP6 has a carboxyl-terminal C1q domain. The zacrp6 gene is			
CC	located on human chromosome 21q. zacrp6 gene and protein are useful for			
CC	diagnosing and treating inflammations, for determining arterial			
CC	remodelling, for modulating calcium ion concentration, hormone			
CC	secretion, DNA synthesis or cell growth, inositol phosphate turnover,			
CC	arachidonate release, phospholipase C activation, gastric emptying, human			
CC	neutrophil activation, or ABC capability and superoxide anion production.			
CC	zacrp6 gene and protein are also useful as antimicrobial applications,			
CC	preferably against bacteria and virus, for complement inhibition, for			
CC	treating acute vascular injury, disseminated intravascular coagulation,			
CC	arteriosclerosis and for wound healing. The present sequence is human			
CC	adipocyte complement related protein homolog zsig39. This protein was			
XX	used in a sequence homology comparison with ZACRP6 protein.			

[illegible]

Pred. No.: 1.03e-85 Length: 243
Score: 1321.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 52.01% Indels: 0
DB: 22 Gaps: 0

US-09-944-944-41 (1-1377) x AAB65888 (1-243)

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OY 227 ATGAGGCGACATCGTCCTGCTCTGCTGCGGCGCTGGGCGGCGGCTGCCCCCACTGGAC 286
    |||||||
DB 1 MetArgProLeuLeuValLeuLeuLeuValLeuAlaAlaGlySerProProLeuasp 20
OY 287 GACAACAAGATCCCGAGCCTCTGCCGGGCGACCCCGGCTTCCAGGACGCGGGCCAC 346
    |||||||
DB 21 AspAsnLysIleProSerLeuCySerProGlyHisProGlyLeuProGlyThrProGlyHis 40
OY 347 CATGGCAGCAGGCTTCCCGGCGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGG 406
    |||||||
DB 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyValProGly 60
OY 407 GCTCCGGGAGAAAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
    |||||||
DB 61 AlaProGlyGluLysGlyGlyGlyGlyArgProGlyLeuProGlyProArgGlyAspPro 80
OY 467 GGGCGCGAGAGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526
    |||||||
DB 81 GlyProArgGlyGlyAlaGlyProAlaGlyProThrGlyProAlaGlyGlyGlyGlySerVal 100
OY 527 CCTCCGCGATCCGCTTACGCGCAAGCGCTCCGAGACCGGCGGCTCCGCGCTGTAC 586
    |||||||
DB 101 ProProArgSerAlaPheSerAlaLysArgSerGlnSerArgValProProProSerasp 120
OY 587 GCACCTTGCCCTCGACGCGCTGCTGTGTGAACGAGCGGACGATATAGACCGCTCAC 646
    |||||||
DB 121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140
OY 647 GCGAGTTCACCTGCGCAGGTGCTGCGGCTCTACTACTGCGGCTCCATGCCACGCTTAC 706
    |||||||
DB 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
OY 707 CGGGCGACGCTGAGTTGATCTGTGTGAAGATGGCGAATCCATTCCTCTTCTTCAG 766
    |||||||
DB 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlnSerIleAlaSerPheGln 180
OY 767 TTTTTCGGGGGGGCGCAAGCGCCTGCTGCTGGGGGGGCGCATGCTAGCGTGGAG 826
    |||||||
DB 181 PhePheGlyLysTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
OY 827 CCTGAGCAGCAAGTGTGGGTGCGAGTGGGTGCTGCTACTGATGATGCGATGATGCCAC 886
    |||||||
DB 201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220
OY 887 ATCAAGACAGACAGCCTTCTCGGATTTCTGTGTACTCGACTGGCAGACTGCCCA 946
    |||||||
DB 221 IleLysIleThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheSerPro 240
OY 947 GTCCTTGGCT 955
    |||||||
DB 241 ValPheAla 243
```

RESULT 14

AAB65889 standard; Protein: 243 AA.

AC AAB65889;

XX 28-MAR-2001 (first entry)

DE Human secreted protein related protein SEQ ID NO: 104.

XX Human; mouse; secreted protein: TANCO253; TANCO 257; TANCO 281;
KW INTERCEPT 258; coronary disorder; olfactory disorder;

KW neurological disorder; pulmonary disorder; immunological disorder;
KW developmental disorder; kidney disorder.

OS Homo sapiens.

PN WO200078808-A1.

PD 28-DEC-2000.

PF 19-JUN-2000; 2000WO-US16883.

FR 18-JUN-1999; 99US-0336536.

PA (MILL-) MILLENNIUM PHARM INC.

PI leiby KR, McKay C, Bossone S;

DR WPI; 2001-050109/06.

PT New nucleic acids for treating diseases and disorders, e.g.
PT atherosclerosis, infection, autoimmune diseases, obesity, ear
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT sclerosis and asthma -

PS Disclosure: Page 271-272; 332pp; English.

The present invention provides the protein and coding sequences of the
human and murine secreted or transmembrane proteins TANCO 253, TANCO 257,
TANCO 281 and INTERCEPT 258. These are useful in the treatment of
coronary, pulmonary, olfactory, immunological, neurological,
developmental and kidney disorders.

Sequence 243 AA:

Alignment Scores:

Pred. No.: 1.03e-85 Length: 243
Score: 1321.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 52.01% Indels: 0
DB: 22 Gaps: 0

US-09-944-944-41 (1-1377) x AAB65889 (1-243)

```
OY 227 ATGAGGCGACATCGTCCTGCTCTGCTGCGGCGCTGGGCGGCGGCTGCCCCCACTGGAC 286
    |||||||
DB 1 MetArgProLeuLeuValLeuLeuLeuValLeuAlaAlaGlySerProProLeuasp 20
OY 287 GACAACAAGATCCCGAGCCTCTGCCGGGCGACCCCGGCTTCCAGGACGCGGGCCAC 346
    |||||||
DB 21 AspAsnLysIleProSerLeuCySerProGlyHisProGlyLeuProGlyThrProGlyHis 40
OY 347 CATGGCAGCAGGCTTCCCGGCGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 406
    |||||||
DB 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyValProGly 60
OY 407 GCTCCGGGAGAAAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
    |||||||
DB 61 AlaProGlyGluLysGlyGlyGlyGlyArgProGlyLeuProGlyProArgGlyAspPro 80
OY 467 GGGCGCGAGAGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526
    |||||||
DB 81 GlyProArgGlyGlyAlaGlyProAlaGlyProThrGlyProAlaGlyGlyGlyGlySerVal 100
OY 527 CCTCCGCGATCCGCTTACGCGCAAGCGCTTCCGAGACCGGCGGCTTCCGCGCTGTAC 586
    |||||||
DB 101 ProProArgSerAlaPheSerAlaLysArgSerGlnSerArgValProProProSerasp 120
OY 587 GCACCTTGCCCTGACGCGCTGCTGTGTGAACGAGCGGACGATATAGACGCGGCTCAC 646
    |||||||
DB 121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140
OY 647 GCGAGTTCACCTGCGCAGGTGCTGCGGCTCTACTACTGCGGCTCCATGCCACGCTTAC 706
```


Db	21	AspaanlytIleProserIeucysProglIyHisProglIyLeuProglIyThrProglIyHis	40
QY	347	CATGGCAGCCAGGCGCTTGGCCGGGCGCGGATGGCCGGAGCGGCCGACGGCGGCCGGG	406
Db	41	HisglYserGlnGlyLeuProglIyAgsaPglYarAspElYaragsPglYalAProglY	60
QY	407	GCTCCGGGAGAGAAAGCGGAGGGCGGAGGCCGGAGCTGGCGGGAGCCTCGAGGGACCCC	466
Db	61	AlaProglIyGlnLysLyluGlylueGlylYalYgProglIyLeuProglIyProAlnglYAsPro	80
QY	467	GGCGCGCAGAGAGAGCGGGAGCCCGCGGGGCCACCAGCGGGCTCGGGGAGTCTCGGTG	536
Db	81	GlyProAlnglYgluAluAglYProAlnglYProThGlyProAlnglYlucYsserVal	100
QY	527	CCTCCGGCGATTCGGCCTTCAGCGGCAAGCGCTCCAGAGCGGGAGCGGGTGGCTCCGGCTCGAC	586
Db	101	ProProAlnglYserAlaPheSerAlaYsaYserGluSerArYalProProPserAsp	120
QY	587	GCACCCCTTGCCTTCGACCGCGGCTGTGTGAACGACAGGAGGACATTACAGCGCGTCACC	646
Db	121	AlaProLeuProPheAspArYalLeuValAsnGluGlnGlyIstYrAspaAlaValThr	140
QY	647	GGCAGATTACCTTCGCGAGGTGGCTGCTACTACTTGGCCGTCCATGGCACCGCTTAC	706
Db	141	GlyLysPheThrCysGlnValProglYalTYrTYrPheAlaAlaHisAlaThrValTYr	160
QY	707	CGGCGCAGCGCTCAGATTGTATGTGTGAAGAATGGCGAATTCATTCCTCTTCTTCAG	766
Db	161	ArgAlaSerLeuGlnPheAspLeuValYlsasnGlyGluSerIleAlaSerPhePheGln	180
QY	767	TTTTTCGGGGGGTGGCCCAAGCCAGCCTGTCTCGGGGGGGGCCATGTGAGGCTGGAG	826
Db	181	PhePheGlyGlyTYrProLysProAlaSerLeuSerGlyYalAlaMetValArgLeuGlu	200
QY	827	CCTGAGGACCAAGTGGGGGTGCGAGGTTGGTGGTGAGGATCTTGGATCTATGGCAGC	886
Db	201	ProGluAspGlnValTYrValGlnValGlyValGlyAspTYrIleGlyIleTYrAlaSer	220
QY	.887	ATCAAGACAGACAGCACCTTCTCCGGATTTCTGTGTACTCCGACGTGGCACAGCTCCCA	946
Db	221	IleLysThrAspSerThrPheSerGlyPheLeuValTYrSerAspTrpHisSerPro	240
QY	947	GNCTTGGT 955	
Db	241	ValPheAla 243	
RESULT 2			
US-09-336-536-3			
Sequence 3, Application US/09336536			
Patent No. 6406884			
GENERAL INFORMATION:			
APPLICANT: Leiby, K.			
APPLICANT: McKay, C.			
APPLICANT: Bossone, S.			
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF			
FILE REFERENCE: 7853-144			
CURRENT APPLICATION NUMBER: US/09/336,536			
CURRENT FILING DATE: 1999-06-18			
NUMBER OF SEQ ID NOS: 75			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 3			
LENGTH: 243			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-336-536-3			
Alignment Scores:			
Pred. No.: 3,55e-88			
Score: 1325.00			
Percent Similarity: 100.00%			
Percent Local Similarity: 100.00%			
Query Match: 52.17%			
Length: 243			
Matches: 243			
Conservative: 0			
Mismatches: 0			
Indels: 0			

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DB:      4          Gaps:      0
US-09-944-944-41 (1-1377) x US-09-336-356-3 (1-243)
OY       227 ATGAGGCCATCTCGTCTCCTGTGCTCTCTGGGGCTGGCCGCAGCTCGCCCCACTGGAC 286
         |||||||
Db        1 MetArgProLeuLeuValLeuLeuLeuLeuGlyLeuAlaIalaglySerProProLeuAsp 20
OY       287 GACCAACAAGATCCCACAGCTTGCCCGGGGGGACACCCCGGCTTCAGAGCACGGCGGGCAC 346
         |||||||
Db        21 AspaInLysIlePheSerLeuLysProGlyHisProGlyLeuProGlyThrProGlyHis 40
OY       347 CATGCGAGCCAGCGGCTTCCCGGGCCCGCATGGCCCGAGCGGGCCGCGACGGCGGCCCGGG 406
         |||||||
Db        41 HisGlySerGlnGlyLeuProGlyArgAspArgGlyArgAspArgGlyArgAlaProGly 60
OY       407 GCTCCGGGAGAAAGAGCGGAGGGCGGAGCGGGAGCTCCGGGACCCTGAGGGGAGACCC 466
         |||||||
Db        61 AlaProGlyGluLysLeuGlyGlnGlyGlyAsnProGlyLeuProGlyProAlaGlyAspPro 80
OY       467 GGGCGCGGAGAGAGCGGGAGCCCGCGGGGCCACCGGGGCTCCGCGGAGTGTCTGGTG 526
         |||||||
Db        81 GlyProAlaGlyGlyAlaGlyProAlaGlyProAlaGlyProAlaGlyGlyGlySerVal 100
OY       527 CCTCCGCGATCCGCTTCAGCGCCAAGCGCTCCGAGAGCCGGGCTGCTCGCCGCTTGAC 586
         |||||||
Db        101 ProProAlaGlySerAlaPheSerAlaLysArgSerGlySerArgValProProPheSerAsp 120
OY       587 GCACCTTGCCCTTGACCGCGGTGCTGTAACAGACAGGAGACATTACGACCGCGGTAC 646
         |||||||
Db        121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140
OY       647 GGCAAGTTCACTGCGCAGGTGCGCTTGAGGCTCTACTACTTCGCGCTCATGCGCCAGTCTAC 706
         |||||||
Db        141 GlyLysPheThrhcryGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
OY       707 CGGGCCAGCTTCGATTTGATCTGTGGAGAATGGGAATCCATTCGCTCTTCTCCAG 766
         |||||||
Db        161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyLysSerIleAlaSerPhePheGln 180
OY       767 TTTTTGGGGGGGTGGCCCAAGCGCTTCGCTTCGGGGGGGCGCATGGTGAGGCTGGAG 826
         |||||||
Db        181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
OY       827 CCGTAGGACCAAGTGGTGGTCAGTGGGTGTGGTACTACATTGGCATCTATGGCAGC 886
         |||||||
Db        201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220
OY       887 ATCAAGACAGACAGCAGCTTCCTCCGATTCTGGTGTACTCGAGTGGAGCAGCAGCTCCCA 946
         |||||||
Db        221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspIrrPhisSerPro 240
OY       947 GTCTTGGCT 955
         |||||||
Db        241 ValPheAla 243

RESULT 3
US-09-188-930-295
; Sequence 295, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Iorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188, 930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
```


QY 947 GTCTTGGCT 955
Db 241 ValPheala 243

RESULT 5

US-09-336-536-4
; Sequence 4, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-4

Alignment Scores:

Pred. No.:	3,336-83	Length:	228
Score:	1256.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	49.45%	Indels:	0
DB:	4	Gaps:	0

US-09-944-944-41 (1-1377) x US-09-336-536-4 (1-228)

QY 272 TCGCCCCCAGTGGACGACACAAAGATCCAGCCTCGCCGGGGACACCCGGCCTTCCA 331
Db 1 SerProProleuaspaspasnlylIleProSerleuCySProclglnhSpProglYleuPro 20
QY 332 GGCACGCGGGGCGGCACCATGGACGCGGCTTCCGGGCGCGCATGGCGCGACGCGCGC 391
Db 21 G1YThrProclglnhShSlgYserGlnGlyLeuProclYArGaspGlyArG 40
QY 392 GAGCGCGCGCGCGCGGCTCCGGGAGAGAAAGCGGAGCGCGGCGGACCTGCGCGGA 451
Db 41 AspGlyAlaProclYAlaProglYglnYglnYglnYglnYArGProglYleuProglY 60
QY 452 CPTCGAGGGAGACCCCGGCGCGAGAGAGCGGAGACCCGCGGCGCCACCGGGCCTGCC 511
Db 61 ProArGlyAspProclYProArGlyGlnAlaGlyProAlaGlyProThrGlyProAla 80
QY 512 GGGAGTGTCTGGTGCCTCCGCGATCCGCTTACGCGCCAAAGCGCTCCGAGAGCGGCTG 571
Db 81 G1YglnCySerValProProArGSerAlaPheSerAlaYsArGSerGlnSerArGVal 100
QY 572 CPTCCGCGCGTACGACGACCTTGCCTTGCAGCGCGCTGCTGTGAACGACGAGGACAT 631
Db 101 ProProProSerAspAlaProleuProPheAspArgValIleuValnsnGlnGlnYHis 120
QY 632 TACGAGCGCGTACCGGCAAGTTCACCTGCAGGTGCTGGGTCTACTACTTCCGCGTC 691
Db 121 TyrAspAlaValAlhThrGlyYsPheThrCySglnValAlProclYAlYrYrPheAlaVal 140
QY 692 CATGCCACGCTACCGGGCGACCTGCATTTGATCTGGTGAAGATGGCAATCCATT 751
Db 141 HisAlaThrValYrArgAlaSerLeuGlnPheAspLeuValYlsasnGlnYglnSerIle 160
QY 752 GCCTCTTCTTCCAGTTTTCGGGGGTGGCCCAAGCCCTGCTCTGGGGGGGCC 811
Db 161 AlaSerPhehGlnPhePheGlnYglnYrProlySProAlaSerleuSerGlnYglnAla 180
QY 812 ATGGTAGGCTGAGGCTGAGACCAAGTGTGGTGCAGGTGGGTGGTGGTGGTGGTGGTGGT 871
Db 181 MetValAlaArgLeuGlnProGlnuAspGlnValITrPValGlnValGlnYAlGlnAspTrYIle 200

QY 872 GGCATCTATGCCAGCATCAAGACAGACGACCTTTCGGAATTTGTGTACTCCGAC 931
Db 201 GlyIleYrAlaSerIleYsThrAspSerThrPheSerGlyPheLeuValYrSerAsp 220
QY 932 TGGCAGAGCTCCCGACGCTTTGCT 955
Db 221 TrpHisSerSerProValPheala 228

RESULT 6

US-09-336-536-11
; Sequence 11, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-11

Alignment Scores:

Pred. No.:	3,646-79	Length:	228
Score:	1200.00 <td>Matches:</td> <td>216</td>	Matches:	216
Percent Similarity:	96.93% <td>Conservative:</td> <td>5</td>	Conservative:	5
Best Local Similarity:	94.74% <td>Mismatches:</td> <td>7</td>	Mismatches:	7
Query Match:	47.24%	Indels:	0
DB:	4	Gaps:	0

US-09-944-944-41 (1-1377) x US-09-336-536-11 (1-228)

QY 272 TCGCCCCCAGTGGACGACACAAAGATCCAGCCTTCCGGGCGGCACCCGGCCTTCCA 331
Db 1 SerProProleuaspaspasnlylIleProSerleuCySProclglnhSpProglYleuPro 20
QY 332 GGCACGCGGGGCGGCACCATGGACGCGGCTTCCGGGCGCGCATGGCGCGACGCGCGC 391
Db 21 G1YThrProclglnhShSlgYserGlnGlyLeuProclYArGaspGlyArG 40
QY 392 GAGCGCGCGCGCGGCTCCGGGAGAGAAAGCGGAGCGCGGCGGACCTGCGCGGA 451
Db 41 AspGlyAlaProclYAlaProglYglnYglnYglnYglnYArGProglYleuProglY 60
QY 452 CPTCGAGGGAGACCCCGGCGCGAGAGAGCGGAGACCCGCGGCGCCACCGGGCCTGCC 511
Db 61 ProArGlyAspProclYProArGlyGlnAlaGlyProAlaGlyProThrGlyProAla 80
QY 512 GGGAGTGTCTGGTGCCTCCGCGATCCGCTTACGCGCCAAAGCGCTCCGAGAGCGGCTG 571
Db 81 G1YglnCySerValProProArGSerAlaPheSerAlaYsArGSerGlnSerArGVal 100
QY 572 CPTCCGCGCGTACGACGACCTTGCCTTGCAGCGCGCTGCTGTGAACGACGAGGACAT 631
Db 101 ProProProAlaSpThrProleuProPheAspArgValIleuValnsnGlnGlnYHis 120
QY 632 TACGAGCGCGTACCGGCAAGTTCACCTGCAGGTGCTGGGTCTACTACTTCCGCGTC 691
Db 121 TyrAspProThrThrGlyYsPheThrCySglnValAlProclYAlYrYrPheAlaVal 140
QY 692 CATGCCACGCTACCGGGCGACCTGCATTTGATCTGGTGAAGATGGCAATCCATT 751
Db 141 HisAlaThrValYrArgAlaSerLeuGlnPheAspLeuValYlsasnGlnYglnSerIle 160
QY 752 GCCTCTTCTTCCAGTTTTCGGGGGTGGCCCAAGCCCTGCTCTGGGGGGGCC 811

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Db      161 AlaSerPhepneIntyRPhneGlyGlyTrpProLysProAlaSerLeuSerGlyGlyAla 180
Oy      812 ATGTGAGCGCGAGCGCGAGAGCGAGCGCGGTGCGAGCGCGGTGCGACTACTT 871
Db      181 MetValArgLeuGluProGluAspGlnValTrpAlaGlyValGlyAspTrpLe 200
Oy      872 GGCATCTATGCGCAGCATCAAGACAGACAGACACTTCTCCGATTTCGGTACTGCGAC 931
Db      201 GlyLeuTrpAlaSerLeuIleLysThrAspSerThrPheSerGlyPheLeuValTrpSer 220
Oy      932 TGGCAGAGCTCCCGAGCTTGTGCT 955
Db      221 TrpHisSerSerProValPheAla 228

RESULT 7
US-09-336-536-7
; Sequence 7, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leidy, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-7

Alignment Scores:
Pred. No.:      2,42e-41      Length:      128
Score:          675.00        Matches:      128
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    26.57%        Indels:      0
DB:             4            Gaps:        0

US-09-944-41 (1-1377) x US-09-336-536-7 (1-128)
Oy      539 GCCTTCAGCGCCAGCGCGCTCGAGAGCGCGGTGCGCTCGCGTCAAGCAGCCCTTGCC 598
Db      1 AlaPheSerAlaLysArgSerGluSerArgValProProPheSerAspAlaProLeuPro 20
Oy      599 TTCGACCGCGTGTGTGAACAGACAGAGGACATTACGAGCGCGTCAAGCGGCAAGTTCACC 658
Db      21 PheAspArgValLeuValAsnGluGlnGlyHisTrpAspAlaValThrGlyLysPheThr 40
Oy      659 TGGCAGGCGCTGGGGGTCTACTACTTGGCGCTCATGCGCAGCGCTCTACCGGCGCAGCCTG 718
Db      41 CysGlnValProGlyValTyrTrpPheAlaValHisAlaThrValTyrArgAlaSerLeu 60
Oy      719 CAGTTGATCTGTGTGAAGATGCGGAATCCATTGCCCTCTCTCCAGTTTTCGGGGGG 778
Db      61 GlnPheAspLeuValLysAsnGlyGluSerIleAlaSerPhePheGlnPheGlyGly 80
Oy      779 TGGCCCAAGCCAGCGCTGCTCTCGGGGGGCGCATGTGTGAGCGCTGAGAGCCCTGAGACCAA 838
Db      81 TrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGln 100
Oy      839 GTGTGGGTGAGGTGGGTGGGTGACTACTTGGCATCTATGCGCATCAAGCATCAAGACAGAC 898
Db      101 ValTrpValGlnValGlyValGlyAspTrpIleGlyIleTrpAlaSerIleLysThrAsp 120
Oy      899 AGCAGCTTCTCCGAGATTCTGTGCTG 922
Db      121 SerThrPheSerGlyPheLeuVal 128

RESULT 8
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US-09-336-536-14
; Sequence 14, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leidy, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-14

Alignment Scores:
Pred. No.:      1,54e-39      Length:      128
Score:          650.00        Matches:      121
Percent Similarity: 97.66%    Conservative: 4
Best Local Similarity: 94.53% Mismatches: 3
Query Match:    25.59%        Indels:      0
DB:             4            Gaps:        0

US-09-944-944-41 (1-1377) x US-09-336-536-14 (1-128)
Oy      539 GCCTTCAGCGCCAGCGCGCTCGAGAGCGCGGTGCGCTCGCGTCAAGCAGCCCTTGCC 598
Db      1 AlaPheSerAlaLysArgSerGluSerArgValProProPheSerAspAlaProLeuPro 20
Oy      599 TTCGACCGCGTGTGTGAACAGACAGAGGACATTACGAGCGCGTCAAGCGGCAAGTTCACC 658
Db      21 PheAspArgValLeuValAsnGluGlnGlyHisTrpAspProThrThrGlyLysPheThr 40
Oy      659 TGGCAGGCGCTGGGGGTCTACTACTTGGCGCTCATGCGCAGCGCTCTACCGGCGCAGCCTG 718
Db      41 CysGlnValProGlyValTyrTrpPheAlaValHisAlaThrValTyrArgAlaSerLeu 60
Oy      719 CAGTTGATCTGTGTGAAGATGCGGAATCCATTGCCCTCTCTCCAGTTTTCGGGGGG 778
Db      61 GlnPheAspLeuValLysAsnGlyGluSerIleAlaSerPhePheGlnPheGlyGly 80
Oy      779 TGGCCCAAGCCAGCGCTGCTCTCGGGGGGCGCATGTGTGAGCGCTGAGAGCCCTGAGACCAA 838
Db      81 TrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGln 100
Oy      839 GTGTGGGTGAGGTGGGTGGGTGACTACTTGGCATCTATGCGCATCAAGCATCAAGACAGAC 898
Db      101 ValTrpValGlnValGlyValGlyAspTrpIleGlyIleTrpAlaSerIleLysThrAsp 120
Oy      899 AGCAGCTTCTCCGAGATTCTGTGCTG 922
Db      121 SerThrPheSerGlyPheLeuVal 128

RESULT 9
US-08-463-911-2
; Sequence 2, Application US/08463911
; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp E.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
```



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Db      44 AlaGlyIleProGlyIleProGlyIleAsnGlyIleThrProGlyIleArgAspSer--- 62
OY      369 CGGAGCGGCGCCCGGGGCGCTCCGGAGAGAAAGCGAGGCGGAGCGGAGCGGAGCTGCGG 448
Db      63 -----GlyIleProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleLeu 77
OY      449 GGACCTCGAGGGAGCGCCCGCGCGCGAGAGAGAGCGGAGCGGAGCGGCGGCGGCGGCGG 499
Db      78 GlyProIleGlyIleGlyIleThrGlyIleAspValGlyMetIleGlyAlaGlyIleProAlaGlyIlePhe 97
OY      500 -----ACCGGCGCTCGCGGGGAGTGCCTCGGTGCTCCCGGATCGCGC 541
Db      98 ProGlnIleIleProGlyIleArgIleGlyIleGlyIleGlyIleAlaIleGlyIleMetIleGlyIleArgSerIleAla 117
OY      542 TTCACGCGGCAAGCGCTCCGAGAGCGGCGGTGCTCCGCGCTGACGACCGACCTTGCGCTTC 601
Db      118 PheSerIleVal---GlyLeuGlnIleIleArgValIleIleValPro---AsnValProIleAlaGlyPhe 135
OY      602 GACGCGGTGCTGCTGTAACAGAGAGCGGAGCATTAACGAGCGGCGCTGACCGGCAAGTTCACCTGC 661
Db      136 ThrIleIlePheIleTyrAsnGlnGlnAsnIleTyrAspGlySerIleThrGlyIlePheIleTyrGly 155
OY      662 CAGGCGCTCGGGGTCTACTACTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
Db      156 AsnIleProGlyIleIleTyrIleTyrPheSerIleTyrIleIleIleIleIleIleIleIleIleIle 175
OY      722 TTGTGATCTGCTGTAACAAATGAGCGCAATTCATGCTCTCTTCTCCAGCTGTTTTCGGGGGGGTGG 781
Db      176 ValSerIlePheIleTyrIleAspIleValIleValIleValIlePheIleThrIleTyrAspIleIleGlnIle 194
OY      782 CCGAAGCCAGCGCTCGCTCGGGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841
Db      195 LysAsnValIleAspGlnIleAspIleSerIleGlySerValIleLeuIleIleIleGlnIleValIleAspGlnIleVal 214
OY      842 TGGGCGGACGATG---GCTGCGGCGTACTACTATGTCGATGTCATGCGCATGCAAGACAGAG 898
Db      215 TrpLeuGlnValTyrGlyIleAspIleAspIleAsnIleGlyIleIleTyrIleAlaIleAspIleValIleAsp 234
OY      899 AGCACCTTCTCGGATTTCTGCTGCTACTCCGAC 931
Db      235 SerIlePheIleIleGlyIlePheIleLeuIleIleTyrIleAsp 245

RESULT 13
US-08-463-911-7
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05

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1 TELECOMMUNICATION INFORMATION
2 TELEPHONE: (617) 861-6240
3
4 TELEFAX: (617) 861-9540
5
6 INFORMATION FOR SEQ ID NO: 7:
7
8 SEQUENCE CHARACTERISTICS:
9
10 LENGTH: 244 amino acids
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12 TYPE: amino acid
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14 TOPOLOGY: linear
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16 MOLECULE TYPE: protein
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Alignment Scores:

Pred. No.:	3,49e-23	Length:	24
Score:	424.00	Matches:	10
Percent Similarity:	50.38%	Conservative:	26
Best Local Similarity:	40.46%	Mismatches:	72
Query Match:	16.69%	Indels:	58
DB:	2	Gaps:	10

US-09-944-944-41 (1-1377) x US-08-463-911-7 (1-244),

242 GTCCCTGCTCCTGGGCGCTGGCGCGGCTGCCCCCACTGGACGACAACAAGATCCCC 301

Db	7 ValLeuLeuLeuAlaLeu-----	13
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302 AGCCTCTGCGCGGCAC-----CCGCGC-----323

14 -----PrognosisrglglulmrlnglglrPrognValleuLeurto 30

[illegible]

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110

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db
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85 ValProGlyValGlyProArgLysPheProGlyIleGlyNGlyArgLysGlyValPro 104

512 GGGGAGTGCCTCGGTGCCCTCCGGATCCGCCCTCAGCGGCCAAGCCCTCCGAGAGCCGGTG 571

Db 105 GLYGLUGLYALATyrValTyrArgSerAlapheserVal---GLYLEUGLuthrTyrVal 123

572 CCTCCGCGTCTGACGCACCTTGCCCTTCGACCGCGTGTGTGAACGAGCAGGACAT 631

Db 124 ThrIlePro--AsnMetProIleArgPheThrLysIlePheTyrAsnGlnGlnAsnHis 142

632 TAGGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCCTGGGCTACTACTTCGCCGTC 691

Db 143 TyrAspGlySerThrGlyLysPheHisCysAsnIleProGlyLeuTyrTyrPheAlaTyr 162

692 CATGCCACCGTCTACCGGGCCAGCCTGCAGTTGATCTGGTGAAGATGGCGATCC--- 748

Db 163 HisIleThrValTyrMetLysAspValLysValSerLeuphellysAspLysAlaMet 1822

749 ATGCGCTCTTCTTCAGTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGG 808

Db 183 LeuphethrTyraspGlnTyrGlnIuAsnAsnValaspGlnAla-----SerGlySer 200

809 GCCATGGTGAAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAAGTGC--GGTGTGGGTGAC 865

201 VALLLEUENHISLEUGLUVALGLYASPRINVALITRPREUGINVALITYRGLYGLUGLUGLU 220

866 TACATGGCACTTATGCCAGCACTCAAGACAGACAGACACCCTTCTCCGGATTCTGGGTAC 925

221 **ALY** **AS** **UN** **LY** **LE** **U** **Y** **LA** **AS** **PR** **AS** **IN** **SP** **SE** **I** **N** **RI** **EN** **GL** **Y** **FI** **EB** **EA** **LE** **U** **Y** 240


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Db      105 G|YGLUG|L|A|T|Y|T|A|T|Y|T|A|T|S|E|T|A|P|H|E|S|E|T|A|V|A|---G|L|Y|L|E|U|G|L|U|T|H|T|Y|T|A|T|
QY      572 CCTCCGCCGCTGTGACGACCCCTTCCCTGACCCGCTGCTGTGTAACGACGACGACAT 631
Db      124 Thr|Leu|Pro|---Asn|Met|Pro|Leu|Arg|Phe|Thr|Leu|Tyr|Ser|Leu|Gln|Asn|His 142
QY      632 TACGACGCCGCTACCCGCAAGTTACCTGACGAGTGGCTGGGCTACTACTTCCGCGTC 691
Db      143 Tyr|Asp|G|L|Y|S|E|T|H|G|L|Y|S|P|H|E|N|I|C|Y|A|S|N|I|L|E|P|O|G|L|Y|L|E|U|T|Y|T|Y|P|H|E|A|L|A|T|Y|T|
QY      692 CATGCCACGCTGTACCGGCGACGCTGACGTTGATCTGTGTAAGATGGGAATCC--- 748
Db      163 His|Leu|Thr|Val|I|Y|Met|L|Y|S|P|Val|S|er|Leu|Phe|L|Y|S|Asp|L|Y|S|Ala|Met 182
QY      749 ATTGCCCTCTTCTTCACGTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCGGGGGG 808
Db      183 Leu|Phe|Thr|Tyr|Asp|G|L|N|T|Y|G|L|G|L|U|A|S|N|A|S|N|V|A|L|Asp|G|L|N|A|I|A|-----Ser|G|L|Y|Ser 200
QY      809 GCCATGGGTGAGGCTGAGACCTGAGACCAAGTGTGGTGCAAGTG---GGTGTGGGTGAC 865
Db      201 Val|Leu|Leu|His|Leu|G|L|U|Val|G|L|Y|Asp|G|L|N|Val|T|P|Leu|G|L|N|Val|T|Y|G|L|Y|G|L|U|G|L|Y|G|L|U 220
QY      866 TACATGGCATCTATGGCAGCATCAAGACAGACGACACTTCGCCGATTTCTGTGTAC 925
Db      221 Arg|Asn|G|L|Y|Leu|Tyr|Ala|Asp|Asn|Asp|Asn|Asp|Ser|Thr|Phe|Thr|G|L|Y|Phe|Leu|Leu|Tyr 240
QY      926 TCCGAC 931
Db      241 His|Asp 242

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Search completed: June 21, 2003, 16:09:18
 Job time : 55.5 secs

1	PRIOR APPLICATION NUMBER: 60/067,411
2	PRIOR FILING DATE: December 3, 1997
3	PRIOR APPLICATION NUMBER: 60/069,334
4	PRIOR FILING DATE: December 11, 1997
5	PRIOR APPLICATION NUMBER: 60/069335
6	PRIOR FILING DATE: December 11, 1997
7	PRIOR APPLICATION NUMBER: 60/069,278
8	PRIOR FILING DATE: December 11, 1997
9	PRIOR APPLICATION NUMBER: 60/069,425
10	PRIOR FILING DATE: December 12, 1997
11	PRIOR APPLICATION NUMBER: 60/069,696
12	PRIOR FILING DATE: December 16, 1997
13	PRIOR APPLICATION NUMBER: 60/069,694
14	PRIOR FILING DATE: December 16, 1997
15	PRIOR APPLICATION NUMBER: 60/069,702
16	PRIOR FILING DATE: December 16, 1997
17	PRIOR APPLICATION NUMBER: 60/069,870
18	PRIOR FILING DATE: December 17, 1997
19	PRIOR APPLICATION NUMBER: 60/069,873
20	PRIOR FILING DATE: December 17, 1997
21	PRIOR APPLICATION NUMBER: 60/068,017
22	PRIOR FILING DATE: December 18, 1997
23	PRIOR APPLICATION NUMBER: 60/070,440
24	PRIOR FILING DATE: January 5, 1998
25	PRIOR APPLICATION NUMBER: 60/074,086
26	PRIOR FILING DATE: February 9, 1998
27	PRIOR APPLICATION NUMBER: 60/074,092
28	PRIOR FILING DATE: February 9, 1998
29	PRIOR APPLICATION NUMBER: 60/075,945
30	PRIOR FILING DATE: February 25, 1998
31	PRIOR APPLICATION NUMBER: 60/112,850
32	PRIOR FILING DATE: December 16, 1998
33	PRIOR APPLICATION NUMBER: 60/113,296
34	PRIOR FILING DATE: December 22, 1998
35	PRIOR APPLICATION NUMBER: 60/146,222
36	PRIOR FILING DATE: January 28, 1999
37	PRIOR APPLICATION NUMBER: PCT/US98/19330
38	PRIOR FILING DATE: September 16, 1998
39	PRIOR APPLICATION NUMBER: PCT/US98/25108
40	PRIOR FILING DATE: December 1, 1998
41	PRIOR APPLICATION NUMBER: 09/216,021
42	PRIOR FILING DATE: December 16, 1998
43	PRIOR APPLICATION NUMBER: 09/218,517
44	PRIOR FILING DATE: December 22, 1998
45	PRIOR APPLICATION NUMBER: 09/234,311
46	PRIOR FILING DATE: March 3, 1999
47	PRIOR APPLICATION NUMBER: PCT/US99/12252
48	PRIOR FILING DATE: June 22, 1999
49	PRIOR APPLICATION NUMBER: PCT/US99/21090
50	PRIOR FILING DATE: September 15, 1999
51	PRIOR APPLICATION NUMBER: PCT/US99/28409
52	PRIOR FILING DATE: No. US20020156004A1embder 30, 1999
53	PRIOR APPLICATION NUMBER: PCT/US99/28313
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55	PRIOR APPLICATION NUMBER: PCT/US99/28301
56	PRIOR FILING DATE: December 1, 1999
57	PRIOR APPLICATION NUMBER: PCT/US99/30095
58	PRIOR FILING DATE: December 16, 1999
59	PRIOR APPLICATION NUMBER: PCT/US00/03565
60	PRIOR FILING DATE: February 11, 2000
61	PRIOR APPLICATION NUMBER: PCT/US00/04414
62	PRIOR FILING DATE: February 22, 2000
63	PRIOR APPLICATION NUMBER: PCT/US00/05841
64	PRIOR FILING DATE: March 2, 2000
65	PRIOR APPLICATION NUMBER: PCT/US00/08439
66	PRIOR FILING DATE: March 30, 2000
67	PRIOR APPLICATION NUMBER: PCT/US00/14042
68	PRIOR FILING DATE: May 22, 2000
69	PRIOR APPLICATION NUMBER: PCT/US00/20710
70	PRIOR FILING DATE: July 28, 2000
71	PRIOR APPLICATION NUMBER: PCT/US00/32678
72	PRIOR FILING DATE: December 1, 2000
73	PRIOR APPLICATION NUMBER: PCT/US01/06520

P R I O R F I L I N G D A T E : F e b r u a r y 2 8 , 2 0 0 1			
N U M B E R O F S E Q I D N O S : 1 2 0			
S E Q I D N O : 4 2			
L E N G T H : 2 4 3			
T Y P E : P R T			
O R G A N I S M : H o m o S a p i e n			
U S - 0 9 - 9 4 4 - 4 1 3 - 4 2			
A l i g n m e n t S c o r e s :			
P r e d . N o . :	1 . 0 1 e - 5 7	L e n g t h :	2 4 3
S c o r e :	1 3 2 5 . 0 0	M a t c h e s :	2 4 3
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Q u e r y M a t c h :	5 2 . 1 7 %	I n d e l s :	0
D b :	9	G a p s :	0
U S - 0 9 - 9 4 4 - 9 4 4 - 4 1 (1 - 1 3 7 7) x U S - 0 9 - 9 4 4 - 4 1 3 - 4 2 (1 - 2 4 3)			
Q Y	2 2 7	A T G A G G C C A C T C C T C G C T G C T G C T C C T G G G C C T T G G C G C C G C C C C C A C T G G A C	2 8 6
D b	1	M e t a r p r o b l e u n V a l l e u n l e u l e u l e u l e u l a l a l a g l y s e r p r o b l e u n a s p	2 0
Q Y	2 8 7	G A C A A C A A G A T C C C C A C C C T C G C C C G G G G A C C C C G C C T T G C A G G A C C G C G G C C A C	3 4 6
D b	2 1	A s p a n m y s t l l e p r o s e r l e u c y s p r o g l y n h s p r o g l y l e n p r o g l y t h n p r o g l y n h s	4 0
Q Y	3 4 7	C A T G C A C C A G G G C T T G C C G G G C C G C G A T G G C C G C G A C G C C G C G A C G G C C G C C G G G	4 0 6
D b	4 1	H i s t l y e r t n g l y l e u n p r o g l y a n g a s p g l y a n g a s p g l y a n g a s p g l y a l a p r o g l y	6 0
Q Y	4 0 7	G C T C C G G A G A A A G G C G A G G C G G G A G C C G G G A C T G C C G G A C T C G A G G G A C C C	4 6 6
D b	6 1	A l a p r o g l y l u n s g l y n g l y n g l y a r g p r o g l y l e n p r o g l y p r o a r g l y a s p r o	8 0
Q Y	4 6 7	G G G C G G G A G A G A G G G G G A C C C G G G G G C C A C C G G G C T G C C G G G A G T G C T G G T G	5 2 6
D b	8 1	G l y p r o a r g e l y l u n a l a g l y p r o a l a g l y p r o t h n g l y p r o a l a g l y l u c y s s e r a l	1 0 0
Q Y	5 2 7	C C T C C G G A T C C G C C T T C A C G C C A A C G C C T C C G A G A C C G G G T C C T C C G C C T T G A C	5 8 6
D b	1 0 1	P r o p r o a r g e r a l a p h e s e r a l a l a y s a r g s e r g l u s e r a r g v a l p r o p r o s e r a s p	1 2 0
Q Y	5 8 7	G C A C C T T G C C T T C G A C G C G T G C T G G T G A A C G A C A G C A C A T T A C A G C C G T C A C	6 4 6
D b	1 2 1	A l a p r o l e u p r o p h e a s p a r y a l l e u n l a a n g l u n g l n g l y n h s t y r a s p a l a v a l t h r	1 4 0
Q Y	6 4 7	G G C A A G T T C A C T G C C A G G G C C T G G G T C T A C T T C G C C G T C A C C A C C G C T C A C	7 0 6
D b	1 4 1	G l y l y s p h e r t h r y s g l n a l p r o g l y a l t y r t y r p h e a l a v a l n h s l a l t h v a l t y r	1 6 0
Q Y	7 0 7	C G G G C C A C C T T G C A G T T T G A T C T G T G A A A T G C G A T C C A T T G C T C T T T C T C A G	7 6 6
D b	1 6 1	A r g a l a s e r l e u g l n p h e a s p l e u n l y s a a n g l y l u s e r l l e a l a s e r P h e p h e g l n	1 8 0
Q Y	7 6 7	T T T T T C G G G G G T G C C C A A C C A G C C T G C T C T G G G G G G G C C A T G T G A G C T G A G	8 2 6
D b	1 8 1	P h e p h e g l y g l y r p r o l y s p r o a l a s e r l e u s e r g l y g l a l a m e l v a l a r g l e u g l n	2 0 0
Q Y	8 2 7	C C G A G A C C A A T G T G G T G C A G G G G T G G T G A C T A C A T T G C A T C A T T G C A T T A G C A G C	8 8 6
D b	2 0 1	P r o g l i a s p l n a l t r p a l a l n a l g l y a l g l y a s p t y r l l e g l y l t e t y r a l a s e r	2 2 0
Q Y	8 8 7	A T C A A G A C A G A C A C T T T C C G A A T T T G T G T A C T C C G A C T G G A C A G C T C C C A	9 4 6
D b	2 2 1	I l e l y s t h r a s p s e r t h r p h e s e r e l y p h e u n e u a l t y r s e r a s p t r p h i s e r s e r p r o	2 4 0
Q Y	9 4 7	G T C T T T G C T 9 5 5	
D b	2 4 1	V a l p h e a l a 2 4 3	
R E S U L T 2			
U S - 0 9 - 9 4 4 - 4 0 3 - 4 2			
: S e q u e n c e 4 2 , A p p l i c a t i o n U S / 0 9 9 4 4 4 0 3			

```

Patent No:US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999

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	PRIOR APPLICATION NUMBER:	PCT/US99/21090	
	PRIOR FILING DATE:	September 15, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28409	
	PRIOR FILING DATE:	No. US20020165143A1ember 30, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28313	
	PRIOR FILING DATE:	No. US20020165143A1ember 30, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28301	
	PRIOR FILING DATE:	December 1, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/30095	
	PRIOR FILING DATE:	December 16, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US00/03565	
	PRIOR FILING DATE:	February 11, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/04414	
	PRIOR FILING DATE:	February 22, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/05841	
	PRIOR FILING DATE:	March 2, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/08439	
	PRIOR FILING DATE:	March 30, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/14042	
	PRIOR FILING DATE:	May 22, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/20710	
	PRIOR FILING DATE:	July 28, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/32678	
	PRIOR FILING DATE:	December 1, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US01/06520	
	PRIOR FILING DATE:	February 28, 2001	
	NUMBER OF SEQ ID NOS:	120	
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	LENGTH:	243	
	TYPE:	PRT	
	ORGANISM:	Homo Sapien	
	US-09-944-403-42		
	Alignment Scores:		
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	Percent Similarity:	100.00%	Conservative: 0
	Best Local Similarity:	100.00%	Mismatches: 0
	Query Match:	52.17%	Indels: 0
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Dy	227 ATGAGGCCACATCCTCGTCCGTCTGTCCTGGAGCCGTGGAGCCGCCTGCCCCCATGGAC	286	
Dd	1 MetaAgProleuleuValLeuLeuLeuLeuLgLYLeuAlAlAdlySerProProleuAsp	20	
Dy	287 GACACACAGATCCCAAGCCTCTGCCCCGGGGCACCCCGGCTTCCAGGCACCGGGGCAC	346	
Dd	21 AspaNlySlIerProSerIeuCySProglYnASPrOglYLemProdlYThrProglYhtS	40	
Dy	347 CATGCGAGCCAGGGCTGCGCGGGCCGCGCATGGCCCGCGAGGGCCGCGAGCGGGCCGGG	406	
Dd	41 HIsGlYSegInGLylneuProdlYArGaSPglYArGaSPglYArGaSPglYAlaProglY	60	
Dy	407 GCTCCGGGAGAGAAGGCGAGGGCGGAGCGCGGGAAGTCCCGGACCTCGAGGGGACCCC	466	
Dd	61 AlaProglYglulYsglYslubLYelYArGrProglYleuProglYProArgrglYaspro	80	
Dy	467 GGGCCGCGAGAGAGCGGGGACC CGCGGGGCCACCGGGCTTCGCGGGAGTGCTGGTG	526	
Dd	81 GlYProlArGlgLYlualadlyProAlaclyProThnglyProAlaglyluCYsserval	100	
Dy	527 CTTCCGGCATCCGCTTCAGCGCCCAAGCCCTCCGAGAGCCGGGTGCTCCCGCGGTGAC	586	
Dd	101 ProProArGserAlaPheserialalysaTssegluSerArYalVAlProProProserASP	120	
Dy	587 GCACCTTGCCCTTGACCGCGCTGCTGCTGAACGAGACGAGGACATTACGACGCGCTCAC	646	
Dd	121 AlaProleuProPheaspArgvalLeuValaSnGLuInGLYhtISyrAspaAlaValThr	140	
Dy	647 GGCAAGTTCACCTGCGAGGTGCTGGGGGTCTACTACTTTCGCGGTTCATCGACACCGTTCAC	706	

OY		347	CATGGCAGCCAGGCGTTCCGGGCCGCATGGCCCAAGCGCGGACGCGCGCCGGG	406
Dd		41	HtselSertgInglYleuProGlYlArgSprglYlAdSRglYlArgSPrlYalArProGlY	60
OY		407	GCTCCGGGAGAAAGGCGAGGCGCGAGGCCGGACTCCCGGAACSTTCGAGGGACCCC	466
Dd		61	AlArProGlYglYlUGlYglUGlYlYrLmGrProGlYleuProGlYProArMgLYlsArPro	80
OY		467	GGGCGCGGAGAGAGGCGGGACCCCGGGGGCCCCACCGGGCTCCGGGGAGTGTGGTG	526
Dd		81	GLYrPrArMgLYglYglYlAglYrPrOlaGlYrPrOrHnGlYrPrOlaGlYlUcYSerSerVal	100
OY		527	CCCTCCGGCATCCCGCTTCAGCGGCCCAAGGGCTCCGAGCGCGGGGTGGCTCCGGCGATTGAC	586
Dd		101	ProFroArMgSerAlArPheSerAlAlaYSarTSerGIuSerAlYlValProFroProSerAsp	120
OY		587	GCACCCTTGGCCTTCGACCGCGGTGGTGGTGAACAAGCAGAGGACATTAACGCGCCGTACCC	646
Dd		121	AlArProIeuProPhArSPrgValLeuValAsnglUGlnGlYhIStYrAlsrAlaValAlThr	140
OY		647	GGCAAGTTACCTGCGCAAGGTGCTGGGTCTACTCTTCGGCCGTGCATGCSACCGCTTAC	706
Dd		141	GLYrsPrrThrCYSGlnValArProGlYAlTYrTYrPhrAlaValAlHisAlaThrValAlTYr	160
OY		707	CGGGCCAGCCCGCATGTTGATCTGGTGAAGAATGGCGMATCGATTGCCCTTTCTTCGAC	766
Dd		161	ArgAlaslerLeuglnPhArSPleuValLYlsasnGlYglUserTlleAlaserPhePheGln	180
OY		767	TTTTTCGGGGGTGGCCCAAGCCACGACTCGCTCTCGGGGGGGGCCATGGTGAAGCTTGAG	826
Dd		181	PhePheGlyglYTrProLYrProLYrProAlaserLeuSerGlYglYAlAmetValArgLeuGln	200
OY		827	CCTAGAGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATATTGGCATCTATGCCACG	886
Dd		201	ProGlnASprGlnValAlTYrPrValGlnValAlGlyAsPTyrTlleGlYlleLYrAlaser	220
OY		887	ATCAAGACAGACAGACGACCTTCGCCGATTTCGTGTACTCCGACATGGACAGAGCTCCCA	946
Dd		221	TlleYrThrArSPrrThrPheSerGlyPheLeuValTYrSerAspTrHisSerPro	240
OY		947	GTCCTTTGCT	955
Dd		241	ValPheAla	243
 RESULT 4 US-09-944-944-42 Sequence 42, Application US/09944944 Patent NO. US20020173463A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin APPLICANT: Botstein, David APPLICANT: Baton, Dan APPLICANT: Ferrara, Napoleone APPLICANT: Filvaroff, Ellen APPLICANT: Gerritsen, Mary APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul APPLICANT: Grimaldi, Christopher APPLICANT: Gurney, Austin APPLICANT: Hillan, Kenneth APPLICANT: Kijavlin, Iyar APPLICANT: Napier, Mary APPLICANT: Roy, Margaret APPLICANT: Tumas, Daniel APPLICANT: Wood, William TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/944, 944 PRIOR FILING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: 09/866, 028 PRIOR FILING DATE: 2001-05-25				

PRIOR FILING DATE:	December 3, 1997
PRIOR APPLICATION NUMBER:	60/069,334
PRIOR FILING DATE:	December 11, 1997
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PRIOR APPLICATION NUMBER:	60/069,278
PRIOR FILING DATE:	December 11, 1997
PRIOR APPLICATION NUMBER:	60/069,425
PRIOR FILING DATE:	December 12, 1997
PRIOR APPLICATION NUMBER:	60/069,696
PRIOR FILING DATE:	December 16, 1997
PRIOR APPLICATION NUMBER:	60/069,694
PRIOR FILING DATE:	December 16, 1997
PRIOR APPLICATION NUMBER:	60/069,702
PRIOR FILING DATE:	December 16, 1997
PRIOR APPLICATION NUMBER:	60/069,870
PRIOR FILING DATE:	December 17, 1997
PRIOR APPLICATION NUMBER:	60/069,873
PRIOR FILING DATE:	December 17, 1997
PRIOR APPLICATION NUMBER:	60/068,017
PRIOR FILING DATE:	December 18, 1997
PRIOR APPLICATION NUMBER:	60/070,440
PRIOR FILING DATE:	January 5, 1998
PRIOR APPLICATION NUMBER:	60/074,086
PRIOR FILING DATE:	February 9, 1998
PRIOR APPLICATION NUMBER:	60/074,092
PRIOR FILING DATE:	February 9, 1998
PRIOR APPLICATION NUMBER:	60/075,945
PRIOR FILING DATE:	February 25, 1998
PRIOR APPLICATION NUMBER:	60/112,850
PRIOR FILING DATE:	December 16, 1998
PRIOR APPLICATION NUMBER:	60/113,296
PRIOR FILING DATE:	December 22, 1998
PRIOR APPLICATION NUMBER:	60/146,222
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PRIOR FILING DATE:	September 16, 1998
PRIOR APPLICATION NUMBER:	PCr/US98/25108
PRIOR FILING DATE:	December 1, 1998
PRIOR APPLICATION NUMBER:	09/216,021
PRIOR FILING DATE:	December 16, 1998
PRIOR APPLICATION NUMBER:	09/218,517
PRIOR FILING DATE:	December 22, 1998
PRIOR APPLICATION NUMBER:	09/254,311
PRIOR FILING DATE:	March 3, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/12252
PRIOR FILING DATE:	June 22, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/21090
PRIOR FILING DATE:	September 15, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/28409
PRIOR FILING DATE:	No. US20020117346A1amber 30, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/28313
PRIOR FILING DATE:	No. US20020117346A1amber 30, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/28301
PRIOR FILING DATE:	December 1, 1999
PRIOR APPLICATION NUMBER:	PCr/US99/30095
PRIOR FILING DATE:	December 16, 1999
PRIOR APPLICATION NUMBER:	PCr/US00/03565
PRIOR FILING DATE:	February 11, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/04414
PRIOR FILING DATE:	February 22, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/05841
PRIOR FILING DATE:	March 2, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/08439
PRIOR FILING DATE:	March 30, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/14042
PRIOR FILING DATE:	May 22, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/20710
PRIOR FILING DATE:	July 28, 2000
PRIOR APPLICATION NUMBER:	PCr/US00/32678
PRIOR FILING DATE:	December 1, 2000
PRIOR APPLICATION NUMBER:	PCr/US01/06520

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OY 707 CGGCCAGCCTGACATTTGATCTGGTGAAGAATGGCGAATCCATTCCTTTCTTCAG 766
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OY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTCTCTCGGGGGGGGCCCATGGTGAAGCTGGAG 826
181 PhepegIylGlyTyrProIylsProIylaserIleuSerIylGlyAlMetValArgIeuGln 200
OY 827 CCTGAGGACCAAGTGTGGGTGAGGTGGGTGGGTGACATTCATTCGATTCGAC 886
DB 201 ProGluaspGlnValTyrValGlnValIylGlyaspTyrIleGlyIleTyrAlaser 220
OY 887 ATCAAGACAGACAGACCTTCCTCGGATTTCTGTGTACTCCAGCTGGACAGCTCCCA 946
DB 221 IleIylsIlnaspSerIlnPheSerIylPheLeuValTyrSeraspIlnPheSerPro 240
OY 947 GTCTTTGCT 955
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DB 241 ValPheAla 243

RESULT 6

US-09-944-929-42
; Sequence 42, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT FILING DATE: 2001-08-31
; CURRENT APPLICATION NUMBER: US/09/944,929
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/866,028
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 42
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-929-42

Alignment Scores:

Pred. No.: 1,01e-57 Length: 243
Score: 1325.00 Matches: 243
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 52.17% Indels: 0
DB: 9 Gaps: 0

US-09-944-944-41 (1-1377) x US-09-944-929-42 (1-243)

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OY 287 GACAACAAGATCCCAAGCTCTGCGCGGGGACCCCGGGCTTCACAGGACGCGGGGAC 346
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DB 21 AspaenIylsIleProSerIeuGlyProGlyHisProGlyLeuProGlyThrProGlyHis 40

OY 347 CATGGCAGCCAGGCGCTTGCCGGGCGCGATGGCCGGACGCGGACGCGGCGCGCCGGG 406
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DB 41 HisGlySerGlnGlyLeuProIylAspGlnValArgaspGlyArgaspIylAlaProGly 60
OY 407 GCTCCGGGAGAAAGGCGAGGCGGAGCGGAGCCGCGGACTCCCGGACCTTCAGAGGAGACCC 466
DB 61 AlaProGlyGlyIyluGlyIyluGlyIyluGlyIyluGlyIyluGlyIyluGlyIyluGly 80
OY 467 GGGCGCGAGAGAGAGGCGGAGCCCGGGGCGCCACCGGGCTCCCGGGGAGTCTCGGTG 526
DB 81 GlyProArgGlyIyluAlaIyluAlaIyluAlaIyluAlaIyluAlaIyluAlaIyluAla 100
OY 527 CCTCGGCAATCCGCTTCACAGCCCAAGGCTCCGAGAGCGGGGTGCTCCGCGCTCGAC 586
DB 101 ProProArgSerAlaPheSerAlaIyluArgSerGlyIyluArgValProProSerasp 120
OY 587 GCACCTTGCCCTTCGACCGCGCTGCTGTGAAGACAGACATTACAGCCCGCTCAC 646
DB 121 AlaProLeuProPheaspArgValIeuValAsngIuGlnGlyHisTyrAspAlaValThr 140
OY 647 GGCAGGTACCTGCCAGGTGCTGGGTCTACTTGGCGGTCCATCCACCGCTCAC 706
DB 141 GlyIylsPheThrCysGlnValIylProGlyValIylTyrPheAlaValHisAlaThrValTyr 160
OY 707 CGGGCAGCCTGACATTTGATCTGGTGAAGAATGGGANTCCATTCCTTTCTTCAG 766
DB 161 ArgAlaserLeuGlnPheaspLeuValIylsasngIyluSerIleAlaserPhepegln 180
OY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTCTCTCGGGGGGGGCCCATGGTGAAGCTGGAG 826
DB 181 PhepegIylGlyTyrProIylsProIylaserIleuSerIylGlyAlMetValArgIeuGln 200
OY 827 CCTGAGGACCAAGTGTGGGTGAGGTGGGTGGGTGACATTCATTCGATTCGAC 886
DB 201 ProGluaspGlnValTyrValGlnValIylGlyaspTyrIleGlyIleTyrAlaser 220
OY 887 ATCAAGACAGACAGACCTTCCTCGGATTTCTGTGTACTCCAGCTGGACAGCTCCCA 946
DB 221 IleIylsIlnaspSerIlnPheSerIylPheLeuValTyrSeraspIlnPheSerPro 240
OY 947 GTCTTTGCT 955
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DB 241 ValPheAla 243

RESULT 7

US-10-028-072-362
; Sequence 362, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18

1	PRIOR APPLICATION NUMBER: 60/056597
2	PRIOR FILING DATE: 1997-08-26
3	PRIOR APPLICATION NUMBER: 60/059113
4	PRIOR FILING DATE: 1997-09-17
5	PRIOR APPLICATION NUMBER: 60/059115
6	PRIOR FILING DATE: 1997-09-17
7	PRIOR APPLICATION NUMBER: 60/059111
8	PRIOR FILING DATE: 1997-09-11
9	PRIOR APPLICATION NUMBER: 60/059122
10	PRIOR FILING DATE: 1997-09-17
11	PRIOR APPLICATION NUMBER: 60/051818
12	PRIOR FILING DATE: 1997-09-11
13	PRIOR APPLICATION NUMBER: 60/059265
14	PRIOR FILING DATE: 1997-09-18
15	PRIOR APPLICATION NUMBER: 60/059352
16	PRIOR FILING DATE: 1997-09-19
17	PRIOR APPLICATION NUMBER: 60/059588
18	PRIOR FILING DATE: 1997-09-19
19	PRIOR APPLICATION NUMBER: 60/059836
20	PRIOR FILING DATE: 1997-09-24
21	PRIOR APPLICATION NUMBER: 60/062255
22	PRIOR FILING DATE: 1997-10-17
23	PRIOR APPLICATION NUMBER: 60/062288
24	PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-03-12	PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081222
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PRIOR FILING DATE: 1998-04-24	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084622
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PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22	PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22	PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088741

[illegible]

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Db          241 ValphaAa 243

RESULT 12
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; Sequence 362, Application US/10175746
; Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Guiney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Saplen
US-10-175-746-362

Alignment Scores:
Pred. No.:      1,01e-57      Length:      243
Score:          1325.00      Matches:     243
Percent Similarity: 100.00%   Conservative: 0
Best local Similarity: 100.00% Mismatches:    0
Query Match:      52.17%      Indels:      0
Db:               9          Gaps:           0

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QY 287 GACACACAGATCCCCAGCCTCTGCCCCGGGGCACCCCAGGCGCTTCACAGGACGGCGGCAC 346
Dd 21 AspAsnIlysIleProSerLeuLysProGlyHisProGlyLeuProGlyThrProGlyHis 40
QY 347 CARGGAGGCGAGGGGCTGCCGGGGCGCGATGGCGCGACGGCGCGACGGCGGCGCCGGG 406
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QY 407 GCTCCGGGAGAGAAAGCGAGGCGGAGGCGGGAAGCGGCACTGCCGGGACCTCGAGGGAGACCC 466
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QY 527 CCACCGGAGATCGGCTTCAGGCCCAAGGCGTCGAGAGACGGGGGCGCTCCGCGCTGAC 586
Dd 101 ProProlArgSerAlaPheSerAlaLysTrpSerGlnSerIleValPropioProSerAsp 120
QY 587 GCACCTTTGCCCTTGACCGCGTGTGCTGACGACGACGAGGACATTACGACGCGCTCAC 646

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Db	181	PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu	200
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Db	201	ProGlnAspGlnValTyrValGlnValGlyAspTyrIleGlyIleTyrAlaSer	220
OY	887	ATCAAGACAGACACACCTTCTCCGATTCTGGTGTACTCGACTGGCAGAGTCCCA	946
Db	221	IleLysThrAspSerThrPheSerClyPheLeuValTyrSerAspTyrPheSerPro	240
OY	947	GTCCTTGCT	955
Db	241	ValPheAla	243

Search completed: June 21, 2003, 16:41:47
 Job time : 166 secs

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ALIGNMENTS

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RESULT 1
US-09-140-804-1
Sequence 1, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97/49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1347
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (198)...(926)
US-09-140-804-1

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Query Match	94.8%	Score 1305;	DB 4;	Length 13477
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Matches 1305; Conservative				

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QY	524	GTGGCTCCGGATCCGGCTTACGCGCCAAAGCGCTCCGAGAGCGGGGTGGCTCCGCGCTCT	583
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QY	644	ACGGGCAAGTTCACCTTCGACAGGTGCTGGGGTCTACTACTTCGCGCTCCATGCAACGTC	703
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QY	704	TACCGGGGACACGCTGCAAGTTGATTCGTCGTAAGAAATGGGGAATCCATTGCTTTCTTC	763
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QY	764	CAGTTTTCGGGGGGGTGGCCCAAGCCAGCGCTGCTTCGGGGGGGGGSCATGGTGAAGCTC	823
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RESULT 1
US-09-140-804-2
; Sequence 2, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-2

Query Match 100.0%; Score 1325; DB 4; Length 243;
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Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	241	VFA	243

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